

```
Seq. No.
                  164009
Seq. ID
                  LIB3177-070-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  328
E value
                  4.0e-47
Match length
                  106
% identity
                  91
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
Seq. No.
                  164010
Seq. ID
                  LIB3177-070-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q4678385
BLAST score
                  162
E value
                  4.0e-11
Match length
                  62
                  55
% identity
NCBI Description (AL049656) putative protein [Arabidopsis thaliana]
                  164011
Seq. No.
                  LIB3177-070-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g585536
NCBI GI
BLAST score
                  724
E value
                  6.0e-77
Match length
                  135
% identity
                  99
NCBI Description
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                  >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)
                  thioglucosidase [Arabidopsis thaliana]
Seq. No.
                  164012
Seq. ID
                  LIB3177-070-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  q3659491
BLAST score
                  404
E value
                  0.0e + 00
Match length
                  462
% identity
                  100
NCBI Description
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164013
Seq. ID
                  LIB3177-071-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g4510376
BLAST score
                  210
E value
                  1.0e-16
Match length
                  106
```

Seq. No. 164014

46

% identity

NCBI Description

(AC007017) unknown protein [Arabidopsis thaliana]



Seq. ID LIB3177-071-P1-K1-A11 Method BLASTX NCBI GI g2129639 BLAST score 549 E value 1.0e-56 Match length 108 % identity 99 NCBI Description luminal binding protein (BiP) - Arabidopsis thaliana >gi 1303695 dbj BAA12348 (D84414) luminal binding protein (BiP) [Arabidopsis thaliana] Seq. No. 164015 Seq. ID LIB3177-071-P1-K1-A12 Method BLASTX NCBI GI q3717948 BLAST score 446 E value 2.0e-44 Match length 106 % identity 89 NCBI Description (AJ005902) vaq2 [Arabidopsis thaliana] Seq. No. 164016 Seq. ID LIB3177-071-P1-K1-A2 Method BLASTX NCBI GI g1922944 BLAST score 351 E value 2.0e-33 Match length 73 % identity 97 NCBI Description (AC000106) Strong similarity to Picea histone H2A (gb_X67819). ESTs gb ATTS3874,gb_T46627,gb_T14194 come from this gene. [Arabidopsis thaliana] Seq. No. 164017 Seq. ID LIB3177-071-P1-K1-A3 Method BLASTX NCBI GI q2398679 BLAST score 407 E value 9.0e-40 Match length 84 % identity 90 NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia] 164018 Seq. No. Seq. ID LIB3177-071-P1-K1-A4 Method BLASTX NCBI GI q3395441 BLAST score 513 E value 3.0e-52 Match length 98 100 % identity NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 164019

Seq. ID LIB3177-071-P1-K1-A5

Method BLASTX



```
NCBI GI
                   q2499973
BLAST score
                   228
E value
                   1.0e-18
Match length
                   105
% identity
                   52
NCBI Description
                   PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                   >gi_1465366 emb CAA66701 (X98078) photosystem II
                   [Arabidopsis thaliana]
Seq. No.
                   164020
Seq. ID
                  LIB3177-071-P1-K1-A6
Method
                  BLASTN
NCBI GI
                   q2160155
BLAST score
                   59
E value
                   1.0e-24
Match length
                  161
% identity
                   92
NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164021
Seq. ID
                  LIB3177-071-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2088654
BLAST score
                  111
E value
                   6.0e-18
Match length
                  58
% identity
                  91
                  (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  164022
Seq. ID
                  LIB3177-071-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  572
E value
                  3.0e-59
Match length
                  112
% identity
                  99
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                  164023
Seq. ID
                  LIB3177-071-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  600
E value
                  2.0e-62
Match length
                  116
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
```

% identity

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 164024

Seq. ID LIB3177-071-P1-K1-B1



Method BLASTN
NCBI GI g4757411
BLAST score 53
E value 6.0e-22
Match length 53
% identity 62

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXC7, complete sequence

Seq. No. 164025

Seq. ID LIB3177-071-P1-K1-B10

Method BLASTX
NCBI GI g115783
BLAST score 601
E value 1.0e-62
Match length 113
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 164026

Seq. ID LIB3177-071-P1-K1-B11

Method BLASTX
NCBI GI g135860
BLAST score 576
E value 1.0e-59
Match length 116
% identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic

protein gamma - Arabidopsis thaliana

>gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic

protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma

[Arabidopsis thaliana]

Seq. No. 164027

Seq. ID LIB3177-071-P1-K1-B12

Method BLASTX
NCBI GI g2494299
BLAST score 167
E value 1.0e-11
Match length 97
% identity 40

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT

(EIF-2-BETA) >gi_1732361 (U80269) translation initiation

factor 2 beta [Malus domestica]

Seq. No. 164028

Seq. ID LIB3177-071-P1-K1-B2

Method BLASTX NCBI GI g417073 BLAST score 510 E value 5.0e-52



```
Match length
                   116
% identity
                   84
NCBI Description
                  GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
                   >gi_484529 pir JQ1977 glutamate synthase (NADH) (EC
                   1.4.1.14) - alfalfa >gi 166412 (L01660) NADH-glutamate
                   synthase [Medicago sativa]
                   164029
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q131360
BLAST score
                   241
                   3.0e-20
E value
Match length
                   61
                   80
% identity
NCBI Description
                  PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                   >gi_81727_pir__S02115 photosystem II protein psbK precursor
                   - white mustard chloroplast >gi 12209 emb CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.
                  164030
Seq. ID
                  LIB3177-071-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g114591
BLAST score
                  393
E value
                  2.0e-38
Match length
                  80
% identity
                  100
NCBI Description ATP SYNTHASE EPSILON CHAIN >gi_81663_pir__S01903
                  H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain -
                  Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_
                   (X12889) Cf1 ATPase epsilon subunit (AA 1 - 13\overline{2})
                   [Arabidopsis thaliana]
Seq. No.
                  164031
Seq. ID
                  LIB3177-071-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q2341034
BLAST score
                  424
E value
                  6.0e-42
Match length
                  87
% identity
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  164032
Seq. ID
                  LIB3177-071-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3869062
BLAST score
                  141
E value
                  2.0e-73
Match length
                  393
                  98
% identity
```

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K11II, complete sequence [Arabidopsis thaliana]

Seq. No. 164033

Seq. ID LIB3177-071-P1-K1-B7



```
Method
                   BLASTX
                   g3182922
NCBI GI
BLAST score
                   233
E value
                   2.0e-19
Match length
                   51
% identity
                   94
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 1654142 (U38470) small
                   GTP-binding protein ARF [Brassica rapa]
Seq. No.
                   164034
                  LIB3177-071-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3763930
BLAST score
                   415
E value
                   9.0e-41
Match length
                  137
% identity
                   66
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164035
Seq. ID
                  LIB3177-071-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                   60
                  5.0e-32
E value
                  107
Match length
% identity
                  76
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  164036
Seq. ID
                  LIB3177-071-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1170170
BLAST score
                  349
                  5.0e-33
E value
Match length
                  91
                  76
% identity
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT3 (HD-ZIP PROTEIN 3)
NCBI Description
                  >gi_549889 (U09338) homeobox protein [Arabidopsis thaliana]
                  >gi_549890 (U09339) homeobox protein [Arabidopsis thaliana]
Seq. No.
                  164037
Seq. ID
                  LIB3177-071-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  623
```

E value 4.0e-65 Match length 115 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (\overline{EC} 4. $\overline{1.1.39}$) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Method

BLASTX



```
Seq. No.
                   164038
Seq. ID
                   LIB3177-071-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   110
                   2.0e-55
E value
Match length
                   150
% identity
                   94
NCBI Description Arabidopsis thaliana chromosome I BAC F13011 genomic
                   sequence, complete sequence
Seq. No.
                   164039
Seq. ID
                   LIB3177-071-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2335094
BLAST score
                   101
E value
                   2.0e-57
Match length
                   118
% identity
                   87
NCBI Description
                  (AC002339) putative polygalacturonase [Arabidopsis
                   thaliana]
                   164040
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   g4469023
BLAST score
                   259
E value
                   8.0e-23
Match length
                  70
% identity
                   70
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  164041
Seq. ID
                  LIB3177-071-P1-K1-C5
Method
                  BLASTX
                  q3885343
NCBI GI
BLAST score
                  185
E value
                   7.0e-14
Match length
                  99
% identity
                  33
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164042
Seq. ID
                  LIB3177-071-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2062164
BLAST score
                  156
E value
                  1.0e-58
Match length
                  116
                  97
% identity
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  164043
Seq. ID
                  LIB3177-071-P1-K1-C9
```

BLAST score

Match length

E value

825

157

9.0e-89



```
g2398679
NCBI GI
BLAST score
                  239
E value
                  2.0e-20
Match length
                  59
% identity
                  81
NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                  synthase [Morinda citrifolia]
                  164044
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-D1
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  119
E value
                  7.0e-65
Match length
                  132
% identity
                  91
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                  164045
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g517330
BLAST score
                  440
E valué
                  0.0e + 00
                  448
Match length
% identity
                  100
NCBI Description A.thaliana mRNA for ribosomal protein S10
Seq. No.
                  164046
                  LIB3177-071-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494174
BLAST score
                  615
E value
                  3.0e-64
Match length
                  126
% identity
                  97
NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
                  glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.
                  164047
Seq. ID
                  LIB3177-071-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  593
E value
                  1.0e-61
Match length
                  131
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  164048
Seq. ID
                  LIB3177-071-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1363489
```



```
% identity
                   99
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164049
Seq. ID
                  LIB3177-071-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g2760167
BLAST score
                  83
E value
                  7.0e-39
Match length
                  99
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164050
Seq. ID
                  LIB3177-071-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q4757394
BLAST score
                  19
E value
                  2.0e-01
Match length
                  74
                  88
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1904, complete sequence
                  164051
Seq. No.
                  LIB3177-071-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710114
BLAST score
                  245
E value
                  4.0e-21
Match length
                  74
% identity
                  74
NCBI Description (U53865) PRH26 [Arabidopsis thaliana]
Seq. No.
                  164052
Seq. ID
                  LIB3177-071-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  51
E value
                  1.0e-64
Match length
                  121
% identity
                  99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  164053
Seq. ID
                  LIB3177-071-P1-K1-D9
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1871199
BLAST score 240
E value 3.0e-20
Match length 127



```
% identity
NCBI Description (U91318) pM5 (3' partial) [Homo sapiens]
Seq. No.
                   164054
Seq. ID
                   LIB3177-071-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2924792
BLAST score
                   502
E value
                   7.0e-51
Match length
                   120
% identity
                   82
NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
Seq. No.
                   164055
Seq. ID
                   LIB3177-071-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   589
E value
                   4.0e-61
Match length
                   114
% identity
                   97
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   164056
Seq. ID
                   LIB3177-071-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   q4220636
BLAST score
                   235
E value
                   1.0e-129
Match length
                   474
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164057
Seq. ID
                  LIB3177-071-P1-K1-E12
Method
                  BLASTX
NCBI GI
                   g3914740
BLAST score
                   443
E value
                   3.0e-44
Match length
                  95
% identity
                  92
NCBI Description
                  60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_
                   (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  164058
Seq. ID
                  LIB3177-071-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  58
E value
                  2.0e-70
Match length
                  136
% identity
                  96
```

21933

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

BLAST score

E value

54 7.0e-25



(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No. 164059 Seq. ID LIB3177-071-P1-K1-E3 Method BLASTN NCBI GI g3169169 BLAST score 103 E value 1.0e-50 Match length 473 % identity 97 NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 164060 Seq. ID LIB3177-071-P1-K1-E5 Method BLASTX NCBI GI g1709825 BLAST score 719 E value 2.0e-76 Match length 151 % identity 96 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana] Seq. No. 164061 Seq. ID LIB3177-071-P1-K1-E6 Method BLASTX NCBI GI g1345681 BLAST score 96 E value 8.0e-40 Match length 106 % identity 72 NCBI Description CATALASE ISOZYME 3 >gi 862456 dbj BAA09508 (D55647) catalase [Cucurbita pepo] Seq. No. 164062 Seq. ID LIB3177-071-P1-K1-E7 Method BLASTX NCBI GI g548355 BLAST score 418 E value 4.0e-48 Match length 139 % identity 73 NCBI Description NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase
[Arabidopsis thaliana] >gi_448286_prf_ 1916406A nitrate reductase [Arabidopsis thaliana] Seq. No. 164063 Seq. ID LIB3177-071-P1-K1-E8 Method BLASTX NCBI GI g462174



Match length 95 % identity 69

NCBI Description GERANYLGERANYL PYROPHOSPHATE SYNTHETASE PRECURSOR (GGPP

SYNTHETASE) (DIMETHYLALLYLTRANSFERASE /

GERANYLTRANSTRANSFERASE / FARNESYLTRANSTRANSFERASE

>gi_413730 (L25813) geranylgeranyl pyrophosphate synthase

[Arabidopsis thaliana]

Seq. No. 164064

Seq. ID LIB3177-071-P1-K1-E9

Method BLASTX
NCBI GI g4680212
BLAST score 165
E value 2.0e-11
Match length 106
% identity 41

NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]

Seq. No. 164065

Seq. ID LIB3177-071-P1-K1-F1

Method BLASTN
NCBI GI g2618602
BLAST score 260
E value 1.0e-144

Match length 450 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 164066

Seq. ID LIB3177-071-P1-K1-F10

Method BLASTX
NCBI GI g2529674
BLAST score 190
E value 3.0e-14
Match length 69
% identity 57

NCBI Description (AC002535) hypothetical protein [Arabidopsis thaliana]

Seq. No. 164067

Seq. ID LIB3177-071-P1-K1-F12

Method BLASTN
NCBI GI g217842
BLAST score 33
E value 7.0e-09
Match length 61
% identity 89

NCBI Description A.thaliana mRNA for protein kinase

Seq. No. 164068

Seq. ID LIB3177-071-P1-K1-F3

Method BLASTX
NCBI GI g4587525
BLAST score 347
E value 1.0e-32
Match length 145
% identity 48



NCBI Description (AC007060) Contains the PF 00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb Z25700 come from this gene.

[Arabidopsis thaliana]

164069 Seq. No.

LIB3177-071-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI g3273743 BLAST score 616 E value 3.0e-64 Match length 118 % identity 99

NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis

thaliana] >gi 3786019 (AC005499) unknown protein

[Arabidopsis thaliana]

164070 Seq. No.

LIB3177-071-P1-K1-F5 Seq. ID

Method BLASTX NCBI GI g4455183 BLAST score 116 E value 9.0e-31Match length 123 % identity 60

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 164071

Seq. ID LIB3177-071-P1-K1-F6

Method BLASTN NCBI GI g4337026 BLAST score 73 E value 6.0e-33 Match length 161

% identity 88

NCBI Description Arabidopsis thaliana MFP2 mRNA, complete cds

Seq. No. 164072

Seq. ID LIB3177-071-P1-K1-F7

Method BLASTX NCBI GI q2618723 BLAST score 294 E value 1.0e-26 Match length 69 % identity 86

NCBI Description (U49073) IAA17 [Arabidopsis thaliana] >gi_2921756

(AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]

>gi_4389514_gb_AAB70451_ (AC000104) Identical to
Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis

thaliana]

Seq. No. 164073

Seq. ID LIB3177-071-P1-K1-F8

Method BLASTX NCBI GI g3688799 BLAST score 225



E value 5.0e-19
Match length 60
% identity 80

NCBI Description (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis

thaliana]

Seq. No. 164074

Seq. ID LIB3177-071-P1-K1-F9

Method BLASTN
NCBI GI g1279568
BLAST score 41
E value 1.0e-13
Match length 72
% identity 96

NCBI Description Nicotiana acuminata chloroplast JLB region, 1-250bp

Seq. No. 164075

Seq. ID LIB3177-071-P1-K1-G1

Method BLASTX
NCBI GI g4454036
BLAST score 796
E value 2.0e-85
Match length 147
% identity 99

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 164076

Seq. ID LIB3177-071-P1-K1-G10

Method BLASTX
NCBI GI g464707
BLAST score 556
E value 3.0e-57
Match length 110
% identity 99

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273 (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 164077

Seq. ID LIB3177-071-P1-K1-G11

Method BLASTX
NCBI GI g3885511
BLAST score 396
E value 1.0e-38



```
Match length
                   105
% identity
                   78
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  164078
                  LIB3177-071-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4490331
BLAST score
                   417
E value
                   6.0e-41
Match length
                  97
                  84
% identity
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164079
                  LIB3177-071-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3510254
BLAST score
                  352
                  3.0e-33
E value
Match length
                  154
% identity
                  58
NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  164080
Seq. ID
                  LIB3177-071-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1749676
BLAST score
                  222
E value
                  4.0e-18
Match length
                  121
% identity
                  40
NCBI Description
                  (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
                  EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                  164081
Seq. ID
                  LIB3177-071-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q3914442
BLAST score
                  403
E value
                  2.0e-39
Match length
                  105
% identity
                  78
                 PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  164082
Seq. ID
                  LIB3177-071-P1-K1-G7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3914940
BLAST score 125
E value 4.0e-09
Match length 70
% identity 56

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR



164083

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. ID LIB3177-071-P1-K1-G8
Method BLASTN
NCBI GI g3402745
BLAST score 185
E value 1.0e-100
Match length 305
% identity 96

Seq. No.

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

(ESSAII project)

Seq. No. 164084

Seq. ID LIB3177-071-P1-K1-H1

Method BLASTX
NCBI GI g2583108
BLAST score 498
E value 2.0e-50
Match length 132
% identity 78

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 164085

Seq. ID LIB3177-071-P1-K1-H10

Method BLASTX
NCBI GI g1805652
BLAST score 717
E value 4.0e-76

E value 4.0e-76
Match length 140
% identity 100

NCBI Description (X98927) thylakoid-bound ascorbate peroxidase [Arabidopsis

thaliana]

Seq. No. 164086

Seq. ID LIB3177-071-P1-K1-H11

Method BLASTX
NCBI GI g1071913
BLAST score 353
E value 2.0e-33
Match length 134
% identity 61

NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial

- spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine

synthase [Spinacia oleracea]

Seq. No. 164087

Seq. ID LIB3177-071-P1-K1-H12

Method BLASTX
NCBI GI g421826
BLAST score 655
E value 8.0e-69
Match length 147
% identity 83

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana



>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
thaliana]

Seq. No. 164088

Seq. ID LIB3177-071-P1-K1-H2

Method BLASTN
NCBI GI g4432847
BLAST score 199
E value 1.0e-108
Match length 331
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F13B15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164089

Seq. ID LIB3177-071-P1-K1-H4

Method BLASTX
NCBI GI g2160158
BLAST score 534
E value 1.0e-54
Match length 103
% identity 99

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb_EF1G_XENLA). ESTs gb_T20564,gb T45940,gb T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 164090

Seq. ID LIB3177-071-P1-K1-H5

Method BLASTN
NCBI GI g3046847
BLAST score 152
E value 6.0e-80
Match length 160
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 164091

Seq. ID LIB3177-071-P1-K1-H6

Method BLASTX
NCBI GI g4741952
BLAST score 594
E value 9.0e-62
Match length 117
% identity 73

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 164092

Seq. ID LIB3177-071-P1-K1-H7

Method BLASTN
NCBI GI g4544435
BLAST score 139
E value 4.0e-72
Match length 436
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F14M13 genomic

sequence, complete sequence



```
Seq. No.
                   164093
Seq. ID
                  LIB3177-071-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1418990
BLAST score
                   575
E value
                   2.0e-59
Match length
                  155
% identity
                   68
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                  164094
                  LIB3177-071-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2246620
BLAST score
                  33
E value
                   3.0e-09
Match length
                  45
                  93
% identity
NCBI Description Arabidopsis thaliana salt-stress induced tonoplast
                  intrinsic protein mRNA, complete cds
Seq. No.
                  164095
Seq. ID
                  LIB3177-072-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2739371
BLAST score
                  541
E value
                  2.0e-55
Match length
                  110
% identity
                  95
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                  164096
Seq. No.
Seq. ID
                  LIB3177-072-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1703227
BLAST score
                  229
E value
                  7.0e-19
Match length
                  60
% identity
                  72
NCBI Description
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC
                  2.6.1.2) - barley >gi_46\overline{9148} emb CAA81231 (Z26322) alanine
                  aminotransferase [Hordeum vulgare]
Seq. No.
                  164097
Seq. ID
                  LIB3177-072-P1-K1-A11
Method
                  BLASTN
```

Method BLASTN
NCBI GI g3212846
BLAST score 142
E value 6.0e-74
Match length 414
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]



```
164098
Seq. No.
Seq. ID
                   LIB3177-072-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   g4455322
BLAST score
                   221
E value
                   6.0e-18
                   43
Match length
                   100
% identity
NCBI Description
                 (AL035525) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  164099
                  LIB3177-072-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3286693
BLAST score
                   703
E value
                   2.0e-74
Match length
                  139
                  100
% identity
NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  164100
Seq. ID
                  LIB3177-072-P1-K1-A4
Method
                  BLASTX
NCBI GI
                   g4467134
BLAST score
                  83
E value
                   2.0e-46
Match length
                  96
% identity
                   99
NCBI Description
                  (AL035540) protein kinase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  164101
Seq. ID
                  LIB3177-072-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  q4757409
BLAST score
                  278
E value
                  1.0e-155
Match length
                   462
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
Seq. No.
                  164102
Seq. ID
                  LIB3177-072-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4567232
BLAST score
                  342
E value
                  4.0e-32
Match length
                  72
% identity
                  96
                  (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. Seq. ID LIB3177-072-P1-K1-A7

164103

Method BLASTX



```
g4406780
NCBI GI
BLAST score
                  519
E value
                  5.0e - 53
Match length
                  111
% identity
                  84
NCBI Description
                  (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  164104
                  LIB3177-072-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  647
E value
                  6.0e-68
Match length
                  129
% identity
                  71
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164105
Seq. ID
                  LIB3177-072-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3746065
BLAST score
                  426
E value
                  4.0e-42
Match length
                  126
% identity
                  63
NCBI Description (AC005311) putative lipase [Arabidopsis thaliana]
Seq. No.
                  164106
Seq. ID
                  LIB3177-072-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3914740
BLAST score
                  418
E value
                  4.0e-41
Match length
                  109
                  77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi_2160300 dbj BAA18941
                  (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  164107
Seq. ID
                  LIB3177-072-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2062164
BLAST score
                  504
E value
                  4.0e-51
Match length
                  94
% identity
                  59
```

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 164108

Seq. ID LIB3177-072-P1-K1-B11



Method BLASTX
NCBI GI g1200205
BLAST score 461
E value 4.0e-46
Match length 98
% identity 88

NCBI Description (X95753) DAG [Antirrhinum majus]

Seq. No. 164109

Seq. ID LIB3177-072-P1-K1-B12

Method BLASTX
NCBI GI g3915023
BLAST score 513
E value 3.0e-52
Match length 134
% identity 75

NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1

(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate

synthase [Citrus unshiu]

Seq. No. 164110

Seq. ID LIB3177-072-P1-K1-B2

Method BLASTX
NCBI GI g3367536
BLAST score 412
E value 2.0e-40
Match length 100
% identity 88

NCBI Description (AC004392) Contains similarity to symbiosis-related like

protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 164111

Seq. ID LIB3177-072-P1-K1-B4

Method BLASTX
NCBI GI 94406775
BLAST score 270
E value 1.0e-23
Match length 119
% identity 42

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 164112

Seq. ID LIB3177-072-P1-K1-B5

Method BLASTX
NCBI GI g4406804
BLAST score 221
E value 5.0e-18
Match length 50
% identity 84

NCBI Description (AC006304) proline iminopeptidase [Arabidopsis thaliana]

Seq. No. 164113

Seq. ID LIB3177-072-P1-K1-B6

Method BLASTX



q166867 NCBI GI BLAST score 697 E value 9.0e-74 Match length 151 % identity 89 (J05216) ribosomal protein S11 (probable start codon at bp NCBI Description 67) [Arabidopsis thaliana] Seq. No. 164114 Seq. ID LIB3177-072-P1-K1-B7 Method BLASTX NCBI GI g2522417 BLAST score 153 E value 3.0e-10 Match length 29 % identity 100 NCBI Description (AF013984) alpha-tubulin [Cryptosporidium parvum] Seq. No. 164115 Seq. ID LIB3177-072-P1-K1-B8 Method BLASTN NCBI GI g4218109 BLAST score 166 E value 2.0e-88 Match length 220 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project) Seq. No. 164116 Seq. ID LIB3177-072-P1-K1-B9 Method BLASTX NCBI GI q3153207 BLAST score 531 E value 3.0e-54 Match length 129 % identity 82 NCBI Description (AF001949) ATHB-12 [Arabidopsis thaliana] Seq. No. 164117 Seq. ID LIB3177-072-P1-K1-C1 Method BLASTX g1419090

NCBI GI BLAST score 279 E value 9.0e-25 Match length 108 % identity 53

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 164118

Seq. ID LIB3177-072-P1-K1-C10

Method BLASTX NCBI GI g4583542 BLAST score 608 E value 3.0e-63 Match length 151

Match length

% identity

126

63



```
% identity
NCBI Description
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
                   [Arabidopsis thaliana]
Seq. No.
                   164119
Seq. ID
                   LIB3177-072-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1076289
BLAST score
                   731
E value
                   9.0e-78
Match length
                   138
                   98
% identity
NCBI Description
                   amino acid permease AAP5 - Arabidopsis thaliana
                   >gi_608673_emb_CAA54632_ (X77501) amino acid permease
                   [Arabidopsis thaliana]
Seq. No.
                   164120
                   LIB3177-072-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2983755
BLAST score
                   279
E value
                   9.0e-25
                   86
Match length
% identity
                   60
NCBI Description
                  (AE000735) ATP-dependent Clp protease proteolytic subunit
                   [Aquifex aeolicus]
Seq. No.
                   164121
Seq. ID
                   LIB3177-072-P1-K1-C3
Method
                  BLASTX
NCBI GI
                   g4754913
BLAST score
                   313
E value
                   1.0e-52
Match length
                   140
% identity
                   74
NCBI Description
                   (AF132854) carbonic anhydrase isoform 1 [Gossypium
                  hirsutum]
Seq. No.
                   164122
Seq. ID
                   LIB3177-072-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   g3286693
BLAST score
                   657
E value
                   4.0e-69
Match length
                   131
% identity
NCBI Description
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  164123
Seq. ID
                  LIB3177-072-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  552
E value
                  9.0e-57
```



NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 164124

Seq. ID LIB3177-072-P1-K1-C7

Method BLASTX
NCBI GI 94220523
BLAST score 823
E value 2.0e-88
Match length 154
% identity 99

NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No. 164125

Seq. ID LIB3177-072-P1-K1-C8

Method BLASTX
NCBI GI g166834
BLAST score 155
E value 4.0e-30
Match length 69
% identity 100

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase

activase [Arabidopsis thaliana] >gi_2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 164126

Seq. ID LIB3177-072-P1-K1-C9

Method BLASTX
NCBI GI g1351272
BLAST score 202
E value 2.0e-16
Match length 39
% identity 97

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550

(U02949) cytosolic triose phosphate isomerase [Arabidopsis

thaliana] >gi_742408_prf 2009415A triose phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 164127

Seq. ID LIB3177-072-P1-K1-D1

Method BLASTX
NCBI GI 94490725
BLAST score 787
E value 3.0e-84
Match length 150
% identity 100

NCBI Description (AL035709) endo-xyloglucan transferase-like protein

[Arabidopsis thaliana]

Seq. No. 164128

Seq. ID LIB3177-072-P1-K1-D10

Method BLASTX
NCBI GI g140285
BLAST score 207
E value 3.0e-16
Match length 42
% identity 95

NCBI Description HYPOTHETICAL 19 KD PROTEIN (ORF 168)





```
>gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana
tabacum]
```

```
Seq. No.
                    164129
  Seq. ID
                    LIB3177-072-P1-K1-D11
 Method
                    BLASTX ·
 NCBI GI
                    g2341034
 BLAST score
                    455
 E value
                    2.0e-45
 Match length
                    86
                    100
  % identity
 NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                    164130
 Seq. ID
                    LIB3177-072-P1-K1-D12
 Method
                    BLASTN
                    g3985954
 NCBI GI
 BLAST score
                    398
 E value
                    0.0e+00
 Match length
                    456
 % identity
                    98
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MRG21, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    164131
 Seq. ID
                    LIB3177-072-P1-K1-D2
 Method
                    BLASTN
 NCBI GI
                    g3510343
 BLAST score
                    443
 E value
                    0.0e + 00
 Match length
                    454
 % identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MJC20, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    164132
 Seq. ID
                    LIB3177-072-P1-K1-D3
 Method
                    BLASTX
 NCBI GI
                    g4587526
 BLAST score
                    242
 E value
                    2.0e-20
 Match length
                    130
 % identity
                    38
                    (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
 NCBI Description
                    berberine bridge enzyme from Arabidopsis thaliana BAC
                    gb_AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come
                    from this gene
```

Seq. No. 164133

Seq. ID LIB3177-072-P1-K1-D4

Method BLASTN
NCBI GI g2924505
BLAST score 142
E value 5.0e-74
Match length 240
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13



(ESSAII project)

Seq. No. 164134 Seq. ID LIB3177-072-P1-K1-D5 Method BLASTN NCBI GI g2244950 BLAST score 179 E value 5.0e-96 Match length 316 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No Seq. No. 164135 LIB3177-072-P1-K1-D6 Seq. ID Method BLASTX NCBI GI g3334144 BLAST score 336 E value 8.0e-35 Match length 114 % identity 68 NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj BAA13181 (D86925) C-type cyclin [Oryza sativa] Seq. No. 164136 Seq. ID LIB3177-072-P1-K1-D7 Method BLASTN NCBI GI g2264315 BLAST score 201 E value 1.0e-109 Match length 273 97 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana] Seq. No. 164137 Seq. ID LIB3177-072-P1-K1-D8 Method BLASTX NCBI GI q3402676 BLAST score 148 E value 2.0e-34 Match length 91 % identity 44 NCBI Description (AC004697) putative myrosinase-binding protein [Arabidopsis thaliana] Seq. No. 164138 Seq. ID LIB3177-072-P1-K1-D9 Method BLASTX NCBI GI q4741952 BLAST score 723 E value 8.0e-77 Match length 134 % identity 77 NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 164139



```
Seq. ID
                   LIB3177-072-P1-K1-E10
Method
                  BLASTX
NCBI GI
                   q461550
BLAST score
                  154
E value
                   2.0e-10
Match length
                   63
% identity
                   60
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
                   >gi_81635_pir__B39732 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma-1 chain precursor, chloroplast -
                   Arabidopsis thaliana >gi_166632 (M61741) ATP synthase
                   gamma-subunit [Arabidopsis thaliana]
Seq. No.
                   164140
Seq. ID
                  LIB3177-072-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q4006827
BLAST score
                  231
E value
                  4.0e-19
Match length
                  145
% identity
NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No. Seq. ID
                  164141
                  LIB3177-072-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q3687228
BLAST score
                  638
E value
                  8.0e-67
Match length
                  145
% identity
                  87
NCBI Description (AC005169) putative malate dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  164142
Seq. ID
                  LIB3177-072-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g4220644
BLAST score
                  154
E value
                  4.0e-81
Match length
                  415
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164143
Seq. ID
                  LIB3177-072-P1-K1-E4
                  BLASTN
Method
NCBI GI
                  g4733968
BLAST score
                  33
                  3.0e-09
E value
Match length
                  227
% identity
                  92
NCBI Description Arabidopsis thaliana chromosome II BAC F12P23 genomic
```

Seq. No. 164144

sequence, complete sequence



Seq. ID LIB3177-072-P1-K1-E5 Method BLASTX NCBI GI a2738248 BLAST score 711 E value 2.0e-75 Match length 151 % identity NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana] Seq. No. 164145 LIB3177-072-P1-K1-E6 Seq. ID Method BLASTN NCBI GI g3702724 BLAST score 42 E value 2.0e-14 Match length 128 % identity 94 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K17N15, complete sequence [Arabidopsis thaliana] 164146 Seq. No. Seq. ID LIB3177-072-P1-K1-E7 Method BLASTX g1363489 NCBI GI BLAST score 746 E value 1.0e-79 Match length 140 97 % identity NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana] Seq. No. 164147 Seq. ID LIB3177-072-P1-K1-E8 Method BLASTX NCBI GI q132792 BLAST score 506 E value 2.0e-51 Match length 130 % identity 75 NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >qi 343153 (M60953) ribosomal protein CL22 [Pelargonium hortorum] Seq. No. 164148 Seq. ID LIB3177-072-P1-K1-E9 Method BLASTX NCBI GI g4741952 BLAST score 415 E value 8.0e-41 81 Match length 95 % identity NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 164149

Seq. ID LIB3177-072-P1-K1-F1

Method BLASTN



NCBI GI q2828182 BLAST score 335 E value 0.0e + 00Match length 335 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No. 164150

LIB3177-072-P1-K1-F10 Seq. ID

Method BLASTN NCBI GI q2182286 BLAST score 401 E value 0.0e+00Match length 409 % identity 100

NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 164151

Seq. ID LIB3177-072-P1-K1-F11

Method BLASTX NCBI GI q1169867 BLAST score 162 E value 5.0e-11 Match length 123 % identity 13

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi 881422 (U27537) G beta like protein

[Dictyostelium discoideum]

Seq. No. 164152

Seq. ID LIB3177-072-P1-K1-F12

Method BLASTX NCBI GI g115767 BLAST score 732 E value 7.0e-78 Match length 139 % identity 100

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164153

Seq. ID LIB3177-072-P1-K1-F2

Method BLASTX NCBI GI g2129640 BLAST score 748 E value 1.0e-79 Match length 144 % identity 100

NCBI Description magnesium chelatase chain - Arabidopsis thaliana

>gi 1154627_emb_CAA92802_ (Z68495) magnesium chelatase

Method

BLASTX



subunit [Arabidopsis thaliana]

```
Seq. No.
                   164154
Seq. ID
                   LIB3177-072-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2880051
BLAST score
                   348
E value
                   8.0e-33
Match length
                   101
% identity
                   71
NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   164155
Seq. ID
                   LIB3177-072-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q2494275
BLAST score
                   222
E value
                   4.0e-18
Match length
                   66
% identity
                   62
NCBI Description ELONGATION FACTOR P (EF-P) >gi 1399829 (U59235) elongation
                   factor P [Synechococcus PCC7942]
Seq. No.
                   164156
Seq. ID
                  LIB3177-072-P1-K1-F5
Method
                  BLASTX
NCBI GI
                   q4689366
BLAST score
                   146
E value
                   3.0e-09
Match length
                   60
% identity
                   45
NCBI Description (AF134155) RING finger protein [Arabidopsis thaliana]
Seq. No.
                   164157
Seq. ID
                  LIB3177-072-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3269287
BLAST score
                  286
E value
                  7.0e-26
Match length
                  95
% identity
                   61
NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]
Seq. No.
                  164158
Seq. ID
                  LIB3177-072-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q2832623
BLAST score
                  640
E value
                  4.0e-67
Match length
                  125
% identity
                  98
NCBI Description
                  (AL021711) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  164159
Seq. ID
                  LIB3177-072-P1-K1-F8
```



q417103

NCBI GI

BLAST score 441 E value 5.0e-44Match length 89 % identity 99 HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone NCBI Description H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 164160

Seq. ID LIB3177-072-P1-K1-F9

Method BLASTX
NCBI GI g4581146
BLAST score 471
E value 1.0e-59
Match length 135
% identity 91

NCBI Description (AC006919) putative fructose-bisphosphate aldolase,

cytoplasmic [Arabidopsis thaliana]

Seq. No. 164161

Seq. ID LIB3177-072-P1-K1-G1

Method BLASTX
NCBI GI g2281631
BLAST score 646
E value 9.0e-68
Match length 134
% identity 91

NCBI Description (AF003096) AP2 domain containing protein RAP2.3

[Arabidopsis thaliana]

Seq. No. 164162

Seq. ID LIB3177-072-P1-K1-G10

Method BLASTX
NCBI GI g2119846
BLAST score 657
E value 3.0e-69
Match length 124

Match length 124 % identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364 emb CAA45790 (X64460)



photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164163 Seq. ID LIB3177-072-P1-K1-G11 Method BLASTX NCBI GI g1363489 BLAST score 689 E value 8.0e-73 Match length 126 % identity 100 NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana] Seq. No. 164164 Seq. ID LIB3177-072-P1-K1-G12 Method BLASTX NCBI GI g3047082 BLAST score 262

E value 6.0e-23 Match length 48 94 % identity

NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase

precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No. 164165

Seq. ID LIB3177-072-P1-K1-G2

Method BLASTX NCBI GI q480450 BLAST score 440 E value 1.0e-43 Match length 100 % identity 89

ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis NCBI Description

thaliana >gi 402552 emb_CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 164166

Seq. ID LIB3177-072-P1-K1-G3

Method BLASTX NCBI GI q4115387 BLAST score 605 E value 5.0e-63 Match length 148 % identity 82

(AC005967) putative NADP-dependent NCBI Description

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis

thaliana]

Seq. No. 164167

Seq. ID LIB3177-072-P1-K1-G4

Method BLASTX NCBI GI g1480078

Seq. ID

Method

NCBI GI

E value

BLAST score



```
BLAST score
                    631
  E value
                    5.0e-66
 Match length
                    126
  % identity
NCBI Description
                    (X99696) shaggy-like protein kinase iota [Arabidopsis
                    thaliana] >gi_2444277 gb AAB71545.1 (AF019927)
                    GSK3/shaggy-like protein kinase [Arabidopsis thaliana]
 Seq. No.
                    164168
 Seq. ID
                    LIB3177-072-P1-K1-G5
 Method
                    BLASTX
 NCBI GI
                    g2435511
 BLAST score
                    506
 E value
                    2.0e-51
 Match length
                    126
  % identity
                    82
 NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase
                    alpha subunit [Arabidopsis thaliana]
 Seq. No.
                    164169
 Seq. ID
                    LIB3177-072-P1-K1-G6
 Method
                    BLASTN
 NCBI GI
                    q4469002
 BLAST score
                    190
 E value
                    1.0e-102
 Match length
                    459
 % identity
                    100
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                    (ESSA project)
 Seq. No.
                    164170
 Seq. ID
                    LIB3177-072-P1-K1-G7
 Method
                    BLASTX
 NCBI GI
                    g3212877
 BLAST score
                    488
 E value
                    3.0e-49
 Match length
                    114
 % identity
                    86
 NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
 Seq. No.
                    164171
 Seq. ID
                    LIB3177-072-P1-K1-G8
 Method
                    BLASTX
 NCBI GI
                    g531829
 BLAST score
                    155
 E value
                    2.0e-10
 Match length
                    78
 % identity
                    47
 NCBI Description
                   (U12390) beta-galactosidase alpha peptide [cloning vector
                    pSport1]
 Seq. No.
                    164172
```

21956

LIB3177-072-P1-K1-G9

BLASTX

736

g115767

2.0e-78



Match length 140 % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164173

Seq. ID LIB3177-072-P1-K1-H1

Method BLASTX
NCBI GI g4741952
BLAST score 239
E value 9.0e-66
Match length 136
% identity 69

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 164174

Seq. ID LIB3177-072-P1-K1-H10

Method BLASTX
NCBI GI g2119846
BLAST score 739
E value 1.0e-78
Match length 141
% identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164175

Seq. ID LIB3177-072-P1-K1-H11

Method BLASTX
NCBI GI g2809255
BLAST score 759
E value 5.0e-81
Match length 133
% identity 100

NCBI Description (AC002560) F21B7.24 [Arabidopsis thaliana]

Seq. No. 164176

Seq. ID LIB3177-072-P1-K1-H12

Method BLASTX
NCBI GI g115767
BLAST score 687
E value 2.0e-72
Match length 143
% identity 96

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana



>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
protein (LHCP AB 65) [Arabidopsis thaliana]
>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

procern (there AB 100) [Ara

Seq. No. 164177

Seq. ID LIB3177-072-P1-K1-H2

Method BLASTX
NCBI GI g119350
BLAST score 237
E value 3.0e-63
Match length 133
% identity 97

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase);identical to P25696

[Arabidopsis thaliana]

Seq. No. 164178

Seq. ID LIB3177-072-P1-K1-H3

Method BLASTX
NCBI GI g515616
BLAST score 190
E value 6.0e-68
Match length 132
% identity 91

NCBI Description (X61608) LHC II Type III chlorophyll a /b binding protein

[Brassica napus]

Seq. No. 164179

Seq. ID LIB3177-072-P1-K1-H4

Method BLASTX
NCBI GI g1170939
BLAST score 596
E value 6.0e-62
Match length 139
% identity 84

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 164180

Seq. ID LIB3177-072-P1-K1-H5

Method BLASTX
NCBI GI g1755156
BLAST score 619
E value 1.0e-64
Match length 136
% identity 90

NCBI Description (U75189) germin-like protein [Arabidopsis thaliana]



>gi_1755158 (U75190) germin-like protein [Arabidopsis thaliana] >gi 1755170 (U75196) germin-like protein [Arabidopsis thaliana] >gi 1755172 (U75197) germin-like protein [Arabidopsis thaliana] >gi 1755180 (U75201) germin-like protein [Arabidopsis thaliana] >gi 1755190 (U75206) germin-like protein [Arabidopsis thaliana] >gi_1934728 (U95035) germin-like protein [Arabidopsis thaliana] >gi 4154285 (AF090733) germin-like protein 1 [Arabidopsis thaliana] >gi 4666248 dbj BAA77207.1 (D89055) germin-like protein precursor [Arabidopsis thaliana]

Seq. No. 164181 Seq. ID LIB3177-072-P1-K1-H6 Method BLASTN NCBI GI g2191157 BLAST score 272 E value 1.0e-151 Match length 442 97 % identity

NCBI Description Arabidopsis thaliana BAC IG002P16

Seq. No. 164182

LIB3177-072-P1-K1-H7 Seq. ID

Method BLASTX NCBI GI g1362078 BLAST score 455 E value 2.0e-45 Match length 113 74 % identity

NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)

- common nasturtium >gi 311835 emb CAA48324 (X68254)

cellulase [Tropaeolum majus]

Seq. No. 164183

Seq. ID LIB3177-072-P1-K1-H9

Method BLASTX NCBI GI g4741960 BLAST score 543 E value 1.0e-55 Match length 122 % identity

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 164184

Seq. ID LIB3177-073-P1-K1-A1

Method BLASTX NCBI GI q4193320 BLAST score 420 E value 3.0e-41 Match length 121 % identity

NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 164185

Seq. ID LIB3177-073-P1-K1-A11

Method BLASTX NCBI GI g4567267



BLAST score 361 E value 2.0e-34 Match length 66 % identity 100

NCBI Description (AC006841) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 164186

Seq. ID LIB3177-073-P1-K1-A12

Method BLASTX
NCBI GI g1168607
BLAST score 452
E value 5.0e-67
Match length 131
% identity 98

NCBI Description AUXIN-INDUCED PROTEIN AUX2-11 >gi_16197_emb_CAA37526

(X53435) Aux2-11 protein [Arabidopsis thaliana] >gi 454285 (L15450) auxin-responsive protein [Arabidopsis thaliana]

Seq. No. 164187

Seq. ID LIB3177-073-P1-K1-A2

Method BLASTX
NCBI GI g4585935
BLAST score 726
E value 4.0e-77
Match length 138
% identity 99

NCBI Description (AC007211) putative chlorophyll A/B binding protein

[Arabidopsis thaliana] >gi_4741946 gb AAD28770.1 AF134123 1

(AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 164188

Seq. ID LIB3177-073-P1-K1-A3

Method BLASTX
NCBI GI g4566614
BLAST score 181
E value 1.0e-13
Match length 49
% identity 71

NCBI Description (AF112887) actin depolymerizing factor [Populus alba x

Populus tremula]

Seq. No. 164189

Seq. ID LIB3177-073-P1-K1-A4

Method BLASTX
NCBI GI g2499973
BLAST score 226
E value 1.0e-18
Match length 105
% identity 52

NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)

>gi 1465366 emb CAA66701 (X98078) photosystem II

[Arabidopsis thaliana]

Seq. No. 164190

Seq. ID LIB3177-073-P1-K1-A5

Method BLASTX



NCBI GI g4376158 BLAST score 449 E value 6.0e-45 Match length 107 % identity 88

NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No. 164191

Seq. ID LIB3177-073-P1-K1-A6

Method BLASTX
NCBI GI g4127456
BLAST score 440
E value 9.0e-44
Match length 97
% identity 62

NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 164192

Seq. ID LIB3177-073-P1-K1-A7

Method BLASTX
NCBI GI g136251
BLAST score 778
E value 3.0e-83
Match length 151
% identity 99

NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR

>gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20)
beta chain - Arabidopsis thaliana >gi_166892 (M23872)
tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No. 164193

Seq. ID LIB3177-073-P1-K1-A8

Method BLASTN
NCBI GI g3985952
BLAST score 445
E value 0.0e+00
Match length 469
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 164194

Seq. ID LIB3177-073-P1-K1-B1

Method BLASTN
NCBI GI g4406776
BLAST score 351
E value 0.0e+00
Match length 462
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F14H2O genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164195

Seq. ID LIB3177-073-P1-K1-B10

Method BLASTN NCBI GI g2618605

BLAST score 36



E value 5.0e-11 Match length 119 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 164196

Seq. ID LIB3177-073-P1-K1-B11

Method BLASTX
NCBI GI g4049349
BLAST score 508
E value 1.0e-51
Match length 122
% identity 86

NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein

[Arabidopsis thaliana]

Seq. No. 164197

Seq. ID LIB3177-073-P1-K1-B12

Method BLASTX
NCBI GI g4646206
BLAST score 447
E value 3.0e-45

E value 3.0e-45 Match length 110 % identity 84

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 164198

Seq. ID LIB3177-073-P1-K1-B2

Method BLASTX
NCBI GI g132090
BLAST score 405
E value 8.0e-40
Match length 80
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR

(RUBISCO SMALL SUBUNIT 1B) >gi_68062 pir RKMUB1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi 16193 emb CAA32700 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164199

Seq. ID LIB3177-073-P1-K1-B3

Method BLASTX
NCBI GI g115783
BLAST score 566
E value 2.0e-58
Match length 109
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

NCBI Description



164200

```
Seq. No.
Seq. ID
                   LIB3177-073-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   q2182287
BLAST score
                   89
E value
                   2.0e-42
Match length
                   162
                   95
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   164201
                   LIB3177-073-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760833
BLAST score
                   340
                   2.0e-32
E value
                   80
Match length
                   86
% identity
NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164202
                   LIB3177-073-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g114330
BLAST score
                   379
E value
                   5.0e-37
Match length
                   78
                   95
% identity
NCBI Description
                   PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                   >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                   type 1, plasma membrane - Arabidopsis thaliana >gi 166746
                   (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                   thaliana]
Seq. No.
                   164203
Seq. ID
                   LIB3177-073-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q4835244
BLAST score
                   505
E value
                   3.0e-51
Match length
                   145
% identity
                   68
                  (AL049862) putative mitochondrial protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164204
Seq. ID
                  LIB3177-073-P1-K1-C2
Method
                  BLASTX
NCBI GI
                   g1208408
BLAST score
                   515
E value
                   2.0e-52
                  98
Match length
                   98
% identity
```

(D14824) nitrite reductase [Arabidopsis thaliana] >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase



[Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248) nitrate reductase [Arabidopsis thaliana]

Seq. No. 164205

Seq. ID LIB3177-073-P1-K1-C3

Method BLASTX
NCBI GI g1363489
BLAST score 281
E value 2.0e-25
Match length 57
% identity 93

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis

thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No. 164206

Seq. ID LIB3177-073-P1-K1-C4

Method BLASTX
NCBI GI 94539460
BLAST score 173
E value 2.0e-12
Match length 110
% identity 4

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 164207

Seq. ID LIB3177-073-P1-K1-C6

Method BLASTX
NCBI GI 94567269
BLAST score 128
E value 6.0e-44
Match length 100
% identity 98

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 164208

Seq. ID LIB3177-073-P1-K1-C7

Method BLASTN
NCBI GI g2109292
BLAST score 240
E value 1.0e-132
Match length 264
% identity 98

NCBI Description Arabidopsis thaliana serine/threonine protein kinase mRNA,

complete cds

Seq. No. 164209

Seq. ID LIB3177-073-P1-K1-C8

Method BLASTN
NCBI GI g1732569
BLAST score 75
E value 5.0e-34
Match length 154
% identity 87

NCBI Description Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA,

complete cds



164210

LIB3177-073-P1-K1-D1

Seq. No.

Seq. ID

```
Method
                   BLASTX
NCBI GI
                   g2306917
BLAST score
                   467
E value
                   6.0e-47
Match length
                   113
% identity
                   82
NCBI Description
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
                   thaliana]
Seq. No.
                   164211
Seq. ID
                  LIB3177-073-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3335340
BLAST score
                   385
E value
                   3.0e-37
Match length
                  76
% identity
                  84
NCBI Description
                  (AC004512) Strong similarity to xylglucan
                   endo-transglycolsylase (TCH4) gene gb U27609, first exon
                   contains strong similarity to meri 5 gene gb Z17989 from A.
                   thaliana. EST gb_N37583 comes from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                  164212
Seq. ID
                  LIB3177-073-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4757409
BLAST score
                  116
E value
                  2.0e-58
Match length
                  458
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
Seq. No.
                  164213
                  LIB3177-073-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1066163
BLAST score
                  243
E value
                  1.0e-20
Match length
                  51
% identity
                  92
NCBI Description (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica
                  napus]
Seq. No.
                  164214
Seq. ID
                  LIB3177-073-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g119194
BLAST score
                  449
E value
                  5.0e-45
Match length
                  93
% identity
                  96
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                  >gi_81607_pir__S09152 translation elongation factor Tu
```



precursor, chloroplast - Arabidopsis thaliana
>gi_22565_emb_CAA36498_ (X52256) elongation factor Tu
precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A
elongation factor Tu [Arabidopsis thaliana]

Seq. No. 164215

Seq. ID LIB3177-073-P1-K1-D4

Method BLASTX
NCBI GI g4240120
BLAST score 375
E value 2.0e-36
Match length 78
% identity 90

NCBI Description (AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No. 164216

Seq. ID LIB3177-073-P1-K1-D5

Method BLASTX
NCBI GI g1495269
BLAST score 562
E value 6.0e-58
Match length 136
% identity 80

NCBI Description (X97829) product similar to ccr protein, Citrus paradisi;

PIR: S52663 [Arabidopsis thaliana]

>gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis

thaliana]

Seq. No. 164217

Seq. ID LIB3177-073-P1-K1-D6

Method BLASTX
NCBI GI g2271465
BLAST score 141
E value 4.0e-09
Match length 57

% identity 49

NCBI Description (AF009563) 3-ketoacyl-CoA synthase [Brassica napus]

Seq. No. 164218

Seq. ID LIB3177-073-P1-K1-D7

Method BLASTN
NCBI GI g2252823
BLAST score 246
E value 1.0e-136
Match length 258
% identity 99

NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 164219

Seq. ID LIB3177-073-P1-K1-D8

Method BLASTX
NCBI GI g2827552
BLAST score 482
E value 8.0e-52
Match length 143
% identity 35

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]



```
Seq. No.
                  164220
                  LIB3177-073-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543841
BLAST score
                  241
E value
                  2.0e-20
Match length
                  69
                  76
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                  (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                  >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                  thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                  164221
Seq. ID
                  LIB3177-073-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3158376
BLAST score
                  244
E value
                  4.0e-21
Match length
                  51
% identity
                  90
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  164222
                  LIB3177-073-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q189496
BLAST score
                  564
E value
                  4.0e-58
Match length
                  151
% identity
                  68
NCBI Description
                 (M88565) p58 protein kinase [Homo sapiens]
Seq. No.
                  164223
Seq. ID
                  LIB3177-073-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g228210
BLAST score
                  449
E value
                  7.0e-45
Match length
                  109
% identity
                  78
NCBI Description granule-bound starch synthase [Solanum tuberosum]
```

Seq. No. 164224

Seq. ID LIB3177-073-P1-K1-E3

Method BLASTN NCBI GI q2618603 BLAST score 247 E value 1.0e-136 Match length 333 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSL3, complete sequence [Arabidopsis thaliana]



Seq. No. 164225

Seq. ID LIB3177-073-P1-K1-E5

Method BLASTX
NCBI GI g1172873
BLAST score 48
E value 3.0e-29
Match length 77
% identity 87

NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 164226

Seq. ID LIB3177-073-P1-K1-E6

Method BLASTX
NCBI GI g4056502
BLAST score 336
E value 1.0e-31
Match length 98
% identity 73

NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 164227

Seq. ID LIB3177-073-P1-K1-E7

Method BLASTX
NCBI GI 94586256
BLAST score 203
E value 7.0e-16
Match length 58
% identity 71

NCBI Description (AL049640) probable photosystem I chain XI precursor

[Arabidopsis thaliana]

Seq. No. 164228

Seq. ID LIB3177-073-P1-K1-E8

Method BLASTX
NCBI GI g2119848
BLAST score 772
E value 1.0e-82
Match length 151
% identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 164229

Seq. ID LIB3177-073-P1-K1-E9

Method BLASTX NCBI GI g404670 BLAST score 193 E value 6.0e-15



```
Match length
                   54
% identity
                   76
NCBI Description
                   (L21154) phytochrome A [Arabidopsis thaliana] >gi 3482934
                   (AC003970) phytochrome A [Arabidopsis thaliana]
Seq. No.
                  164230
Seq. ID
                  LIB3177-073-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  699
E value
                  5.0e-74
```

Match length 136 % identity 93 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 164231 LIB3177-073-P1-K1-F10 Seq. ID Method BLASTN NCBI GI g3763944

BLAST score 83

E value 5.0e-39 Match length 217 % identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No. 164232

Seq. ID LIB3177-073-P1-K1-F11

Method BLASTX NCBI GI g3033375 BLAST score 274 E value 3.0e-24Match length 134 % identity 39

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 164233

Seq. ID LIB3177-073-P1-K1-F12

Method BLASTX NCBI GI g3983125 BLAST score 560 E value 1.0e-57 Match length 138 % identity 80

(AF097648) phosphate/triose-phosphate translocator NCBI Description

precursor [Arabidopsis thaliana]

Seq. No. 164234

Seq. ID LIB3177-073-P1-K1-F2

Method BLASTX NCBI GI g1363489 BLAST score 708 E value 5.0e-75



Match length 130 % identity 100

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No. 164235

Seq. ID LIB3177-073-P1-K1-F5

Method BLASTN
NCBI GI g4559375
BLAST score 72
E value 2.0e-32
Match length 178
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic

sequence, complete sequence

Seq. No. 164236

Seq. ID LIB3177-073-P1-K1-F6

Method BLASTX
NCBI GI g115767
BLAST score 345
E value 8.0e-33
Match length 82
% identity 83

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164237

Seq. ID LIB3177-073-P1-K1-F8

Method BLASTN
NCBI GI g2264321
BLAST score 337
E value 0.0e+00
Match length 385
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 164238

Seq. ID LIB3177-073-P1-K1-F9

Method BLASTX
NCBI GI g2245093
BLAST score 71
E value 4.0e-15
Match length 52
% identity 87

NCBI Description (Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No. 164239

Seq. ID LIB3177-073-P1-K1-G1

Method BLASTX



NCBI GI g117238 BLAST score 447 E value 2.0e-44 Match length 117 % identity 78

NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN

CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)

>gi_81656_pir__S12785 protein ch-42 precursor, chloroplast
- Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411)
protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana]
>gi_2832653_emb_CAA16728_ (AL021710) protein ch-42

precursor, chloroplast [Arabidopsis thaliana]

>gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein
[Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene

[Euglena gracilis]

Seq. No. 164240

Seq. ID LIB3177-073-P1-K1-G10

Method BLASTX
NCBI GI g2119846
BLAST score 693
E value 2.0e-73
Match length 134

Match length 134 % identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164241

Seq. ID LIB3177-073-P1-K1-G11

Method BLASTN
NCBI GI g3080430
BLAST score 243
E value 1.0e-134
Match length 431
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19

(ESSAII project)

Seq. No. 164242

Seq. ID LIB3177-073-P1-K1-G12

Method BLASTN
NCBI GI g3033373
BLAST score 106
E value 1.0e-52
Match length 282
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164243

Seq. ID LIB3177-073-P1-K1-G2

Method BLASTX



NCBI GI q132074 BLAST score 618 E value 1.0e-64 Match length 112 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 164244

Seq. ID LIB3177-073-P1-K1-G3

Method BLASTX NCBI GI a3947448 BLAST score 215 E value 3.0e-17 Match length 141 % identity 39

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3

comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 164245

Seq. ID LIB3177-073-P1-K1-G4

Method BLASTX NCBI GI g115385 BLAST score 236 E value 6.0e-20 Match length 65 % identity 77

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164246

Seq. ID LIB3177-073-P1-K1-G5

Method BLASTX NCBI GI g115767 BLAST score 724 E value 6.0e-77 Match length 139 99 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164247

Seq. No.

Seq. ID

164252

LIB3177-073-P1-K1-H11



```
Seq. ID
                  LIB3177-073-P1-K1-G7
Method
                   BLASTN
                   g3859658
NCBI GI
BLAST score
                   459
E value
                   0.0e + 00
Match length
                   459
                   88
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                  164248
Seq. ID
                  LIB3177-073-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                   563
E value
                   5.0e - 58
Match length
                  138
% identity
                   84
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                   >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
                   164249
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g3193282
BLAST score
                  87
E value
                  3.0e-41
Match length
                  320
                   94
% identity
NCBI Description Arabidopsis thaliana BAC T14P8
                  164250
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g166867
BLAST score
                  695
E value
                  2.0e-73
Match length
                  152
% identity
                  89
NCBI Description
                  (J05216) ribosomal protein S11 (probable start codon at bp
                  67) [Arabidopsis thaliana]
                  164251
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q82512
BLAST score
                  538
                  3.0e-55
E value
Match length
                  109
% identity
                  43
NCBI Description
                  ubiquitin precursor - rice (fragment)
                  >gi_218189_dbj_BAA02241 (D12776) poly-ubiquitin [Oryza
                  sativa]
```



```
Method
                  BLASTX
NCBI GI
                  q4115387
BLAST score
                  500
E value
                  1.0e-50
Match length
                  98
                  99
% identity
NCBI Description
                  (AC005967) putative NADP-dependent
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  164253
                  LIB3177-073-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  388
E value
                  1.0e-37
Match length
                  74
% identity
                  100
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164254
Seq. ID
                  LIB3177-073-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  707
E value
                  6.0e-75
Match length
                  152
% identity
                  90
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164255
Seq. ID
                  LIB3177-073-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g417381
BLAST score
                  438
E value
                  1.0e-43
Match length
                  89
% identity
                  97
NCBI Description
                  NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) -
                  Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445)
                  nitrilase I [Arabidopsis thaliana]
Seq. No.
                  164256
Seq. ID
                  LIB3177-073-P1-K1-H4
```

Method BLASTN NCBI GI g555977 BLAST score 318 E value 1.0e-179 Match length 346



% identity 98

NCBI Description Arabidopsis thaliana metallothionein-like protein (AtMT-q)

mRNA, complete cds

Seq. No. 164257

Seq. ID LIB3177-073-P1-K1-H5

Method BLASTX
NCBI GI 94467359
BLAST score 513
E value 3.0e-52
Match length 109
% identity 89

NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis

thaliana]

Seq. No. 164258

Seq. ID LIB3177-073-P1-K1-H6

Method BLASTN
NCBI GI g4539448
BLAST score 217
E value 1.0e-118
Match length 217
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23

(ESSA project)

Seq. No. 164259

Seq. ID LIB3177-073-P1-K1-H7

Method BLASTX
NCBI GI g2119848
BLAST score 413
E value 2.0e-40
Match length 116
% identity 78

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 164260

Seq. ID LIB3177-073-P1-K1-H9

Method BLASTN
NCBI GI g4469002
BLAST score 293
E value 1.0e-164
Match length 464
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 164261

Seq. ID LIB3177-074-P1-K1-A4

Method BLASTN



NCBI GI g2245073 BLAST score 63 E value 4.0e-27 Match length 185 % identity 79

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 164262

Seq. ID LIB3177-074-P1-K1-A5

Method BLASTN
NCBI GI 94097337
BLAST score 188
E value 1.0e-101
Match length 235
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 164263

Seq. ID LIB3177-074-P1-K1-B12

Method BLASTN
NCBI GI g1020154
BLAST score 157
E value 4.0e-83
Match length 265
% identity 89

NCBI Description Arabidopsis thaliana clone myb6 DNA-binding protein mRNA,

complete cds

Seq. No. 164264

Seq. ID LIB3177-074-P1-K1-B6

Method BLASTN
NCBI GI g16375
BLAST score 41
E value 5.0e-14
Match length 163
% identity 78

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

protein

Seq. No. 164265

Seq. ID LIB3177-074-P1-K1-B7

Method BLASTX
NCBI GI g2623302
BLAST score 586
E value 9.0e-61
Match length 125
% identity 92

NCBI Description (AC002409) putative cysteine proteinase inhibitor

[Arabidopsis thaliana]

Seq. No. 164266

Seq. ID LIB3177-074-P1-K1-C11

Method BLASTN NCBI GI g710625 BLAST score 225



E value 1.0e-123 Match length 266 % identity 95

NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No. 164267

Seq. ID LIB3177-074-P1-K1-C12

Method BLASTN
NCBI GI g3426033
BLAST score 172
E value 6.0e-92
Match length 344
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F12C2O genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164268

Seq. ID LIB3177-074-P1-K1-C4

Method BLASTX
NCBI GI g2760834
BLAST score 694
E value 2.0e-73
Match length 143
% identity 95

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

Seq. No. 164269

Seq. ID LIB3177-074-P1-K1-C6

Method BLASTX
NCBI GI g3201613
BLAST score 375
E value 3.0e-36
Match length 100
% identity 77

NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 164270

Seq. ID LIB3177-074-P1-K1-C7

Method BLASTN
NCBI GI g4165340
BLAST score 184
E value 3.0e-99
Match length 241
% identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164271

Seq. ID LIB3177-074-P1-K1-D1

Method BLASTX
NCBI GI g1345595
BLAST score 668
E value 2.0e-70
Match length 150
% identity 89

NCBI Description 14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)



>gi_1084332_pir__S53727 14-3-3-like protein (ATF1) Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like
protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14
lambda [Arabidopsis thaliana]

 Seq. No.
 164272

 Seq. ID
 LIB3177-074-P1-K1-D11

 Method
 BLASTN

 NCBI GI
 g3492855

 BLAST score
 35

 E value
 1.0e-10

 Match length
 79

% identity 84
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2,

complete sequence [Arabidopsis thaliana]

Seq. No. 164273

Seq. ID LIB3177-074-P1-K1-D9

Method BLASTX
NCBI GI 94544419
BLAST score 575
E value 2.0e-59
Match length 146
% identity 81

NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 164274

Seq. ID LIB3177-074-P1-K1-E1

Method BLASTX
NCBI GI g3201613
BLAST score 562
E value 6.0e-58
Match length 108
% identity 99

NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 164275

Seq. ID LIB3177-074-P1-K1-E11

Method BLASTX
NCBI GI g2246621
BLAST score 328
E value 5.0e-31
Match length 78
% identity 83

NCBI Description (AF004393) salt-stress induced tonoplast intrinsic protein

[Arabidopsis thaliana]

Seq. No. 164276

Seq. ID LIB3177-074-P1-K1-E2

Method BLASTX
NCBI GI g1172977
BLAST score 344
E value 1.0e-32
Match length 87
% identity 82

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.

164282



```
164277
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g70753
BLAST score
                  375
                  3.0e-36
E value
                  79
Match length
                  95
% identity
NCBI Description histone H3 - garden pea >gi 82610 pir S00373 histone H3 -
                  wheat
                  164278
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-F11
                  BLASTX
Method
NCBI GI
                  g3212869
BLAST score
                  266
                  1.0e-23
E value
Match length
                  65
% identity
                  74
                 (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164279
Seq. ID
                  LIB3177-074-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  286
                  7.0e-26
E value
Match length
                  80
% identity
                  64
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  164280
Seq. ID
                  LIB3177-074-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g585536
BLAST score
                  425
E value
                  5.0e-42
                  92
Match length
% identity
                  86
NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                  >gi_1362006_pir_ S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi 304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)
                  thioglucosidase [Arabidopsis thaliana]
                  164281
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g512400
BLAST score
                  205
E value
                  2.0e-38
Match length
                  130
% identity
                  66
NCBI Description (X74947) annexin [Medicago sativa]
```

Seq. No.

Seq. ID

164287

LIB3177-074-P1-K1-G12



```
LIB3177-074-P1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  368
                  0.0e+00
E value
                  432
Match length
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164283
                  LIB3177-074-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4559372
BLAST score
                  652
                  2.0e-68
E value
Match length
                  140
                  87
% identity
NCBI Description
                  (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
                  >gi 4646235 gb AAD26898.1 AC007266 6 (AC007266) putative
                  CONSTANS protein [Arabidopsis thaliana]
                  164284
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  q4454004
BLAST score
                  40
                  2.0e-13
E value
Match length
                  155
                  77
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                  (ESSAII project)
Seq. No.
                  164285
Seq. ID
                  LIB3177-074-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2446981
BLAST score
                  558
E value
                  1.0e-57
Match length
                  108
% identity
                  99
NCBI Description
                  (AB005560) AtGDI2 [Arabidopsis thaliana]
                  >gi_2569936_emb CAA04727 (AJ001397) GDI2 [Arabidopsis
                  thaliana]
Seq. No.
                  164286
Seq. ID
                  LIB3177-074-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g1465365
BLAST score
                  45
E value
                  2.0e-16
Match length
                  104
                  85
% identity
NCBI Description A.thaliana mRNA for subunit T of photosystem II
```



Method BLASTX
NCBI GI g120675
BLAST score 387
E value 1.0e-37
Match length 97
% identity 78

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66011 pir DEIS3C glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis

alba]

Seq. No. 164288

Seq. ID LIB3177-074-P1-K1-G4

Method BLASTX
NCBI GI 94263525
BLAST score 600
E value 2.0e-62
Match length 139
% identity 85

NCBI Description (AC004044) putative photosystem I reaction center subunit

II precursor [Arabidopsis thaliana]

Seq. No. 164289

Seq. ID LIB3177-074-P1-K1-G8

Method BLASTN
NCBI GI g3461810
BLAST score 54
E value 8.0e-22
Match length 160
% identity 79

NCBI Description Arabidopsis thaliana chromosome II BAC T17M13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164290

Seq. ID LIB3177-074-P1-K1-H10

Method BLASTN
NCBI GI g3492855
BLAST score 52
E value 2.0e-20
Match length 193
% identity 81

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2,

complete sequence [Arabidopsis thaliana]

Seq. No. 164291

Seq. ID LIB3177-074-P1-K1-H11

Method BLASTN
NCBI GI g2739359
BLAST score 128
E value 1.0e-65
Match length 413
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T9J22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164292



Seq. ID LIB3177-074-P1-K1-H3 Method BLASTN NCBI GI g972916 BLAST score 45 3.0e-16 -E value Match length 254 76 % identity NCBI Description Arabidopsis thaliana IAA7 (IAA7) gene, complete cds 164293 Seq. No. LIB3177-074-P1-K1-H4 Seq. ID Method BLASTN NCBI GI g4455321 BLAST score 200 E value 1.0e-108 Match length 361 96 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project) 164294 Seq. No. LIB3177-074-P1-K1-H5 Seq. ID Method BLASTX NCBI GI g3688799 BLAST score 380 E value 1.0e-36 Match length 112 % identity 71 (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis NCBI Description thaliana] Seq. No. 164295 LIB3177-074-P1-K1-H6 Seq. ID Method BLASTX NCBI GI q416681 BLAST score 202 E value 9.0e-16 Match length 96 % identity 39 NCBI Description ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum] Seq. No. 164296 Seq. ID LIB3177-074-P1-K1-H7 Method BLASTX

NCBI GI g3075395 BLAST score 301 E value 2.0e-27 73 Match length % identity

NCBI Description (AC004484) nodulin-35 homologue [Arabidopsis thaliana]

Seq. No. 164297

Seq. ID LIB3177-074-P1-K1-H8



Method BLASTX
NCBI GI g4490732
BLAST score 366
E value 4.0e-35
Match length 78
% identity 91
NCBI Description (AL03570

NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like

protein [Arabidopsis thaliana]

Seq. No. 164298

Seq. ID LIB3177-074-P1-K1-H9

Method BLASTX
NCBI GI g132110
BLAST score 413
E value 1.0e-40
Match length 85
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164299

Seq. ID LIB3177-075-P1-K1-A10

Method BLASTX
NCBI GI g1076393
BLAST score 536
E value 6.0e-55
Match length 110
% identity 99

NCBI Description RCI14A protein - Arabidopsis thaliana

>gi 540559 emb CAA52237 (X74140) RCI14A [Arabidopsis

thaliana]

Seq. No. 164300

Seq. ID LIB3177-075-P1-K1-A11

Method BLASTX
NCBI GI g115783
BLAST score 607
E value 4.0e-63
Match length 126
% identity 96

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 164301

Seq. ID LIB3177-075-P1-K1-A12

Method BLASTX
NCBI GI g1669387
BLAST score 382
E value 6.0e-37
Match length 74
% identity 99



```
(U41998) actin 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164302
                  LIB3177-075-P1-K1-A2
Seq. ID
                  BLASTN
Method
                  q442528
NCBI GI
BLAST score
                  62
                  2.0e-26
E value
                  66
Match length
                  98
% identity
                  HY4=flavin-type blue-light photoreceptor [Arabidopsis
NCBI Description
                  thaliana, ecotype Columbia, Genomic/mRNA, 2458 nt]
                  164303
Seq. No.
                  LIB3177-075-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213632
                  158
BLAST score
                  1.0e-10
E value
                  98
Match length
                  43
% identity
NCBI Description
                  (AC000103) F21J9.24 [Arabidopsis thaliana]
                  164304
Seq. No.
                  LIB3177-075-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  q1769905
NCBI GI
BLAST score
                  60
                  1.0e-48
E value
Match length
                  114
                  88
% identity
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
                  164305
Seq. No.
                  LIB3177-075-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2947063
                  194
BLAST score
                  8.0e-15
E value
                  92
Match length
% identity
                   47
                  (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164306
Seq. ID
                  LIB3177-075-P1-K1-A6
Method
                  BLASTN
NCBI GI
                   q4589440
BLAST score
                   362
E value
                   0.0e + 00
Match length
                   408
% identity
                   96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

Seq. No. 164307

MSD21, complete sequence



Seq. ID LIB3177-075-P1-K1-A7 ${\tt BLASTX}$ Method g1041702 NCBI GI 729 BLAST score 2.0e-77 E value Match length -146 90 % identity (U30476) expansin At-EXP1 [Arabidopsis thaliana] NCBI Description 164308 Seq. No. LIB3177-075-P1-K1-A8 Seq. ID Method BLASTN q2924651 NCBI GI BLAST score 243 E value 1.0e-134 Match length 405 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana] 164309 Seq. No. LIB3177-075-P1-K1-A9 Seq. ID Method BLASTX NCBI GI g132110 543 BLAST score 8.0e-56 E value 104 Match length % identity 98 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana] 164310 Seq. No. Seq. ID LIB3177-075-P1-K1-B1 Method BLASTX NCBI GI q4539335 542 BLAST score 4.0e-58 E value Match length 138 % identity 76 NCBI Description (AL035539) putative protein [Arabidopsis thaliana] 164311 Seq. No. Seq. ID LIB3177-075-P1-K1-B11 Method BLASTX NCBI GI q4741952 BLAST score 667 E value 3.0e-70Match length 126 75 % identity

Seq. No. 164312

Seq. ID LIB3177-075-P1-K1-B12

21985

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]



Method BLASTX NCBI GI g120667 702 BLAST score E value 2.0e-74 Match length 144 % identity 97 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] Seq. No. 164313 Seq. ID LIB3177-075-P1-K1-B2 Method BLASTX NCBI GI g2062164 BLAST score 252 1.0e-21 E value Match length 47 100 % identity (AC001645) jasmonate inducible protein isolog [Arabidopsis NCBI Description thaliana] Seq. No. 164314 Seq. ID LIB3177-075-P1-K1-B3 Method BLASTX NCBI GI g4204285 BLAST score 691 4.0e-73 E value Match length 138 96 % identity NCBI Description (AC003027) lcl prt seq No definition line found [Arabidopsis thaliana] Seq. No. 164315 LIB3177-075-P1-K1-B5 Seq. ID Method BLASTX NCBI GI g115492 BLAST score 174 E value 2.0e-12 Match length 145 % identity 31 NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831) calmodulin-related protein [Petunia hybrida] Seq. No. 164316 Seq. ID LIB3177-075-P1-K1-B6 Method BLASTX NCBI GI q166867 BLAST score 599 E value 3.0e-62

Match length 140 % identity 80

NCBI Description (J05216) ribosomal protein S11 (probable start codon at bp

67) [Arabidopsis thaliana]

E value

Match length

% identity

4.0e-78

142

99



```
164317
Seq. No.
Seq. ID
                  LIB3177-075-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2829899
                  134
BLAST score
                  8.0e-08
E value
                  118
Match length
                  53
% identity
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp AJ001449 2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
                  164318
Seq. No.
                  LIB3177-075-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132102
                  437
BLAST score
                  2.0e-43
E value
                  95
Match length
                  92
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
                  164319
Seq. No.
                  LIB3177-075-P1-K1-C1
Seq. ID
Method
                  BLASTN
                  g4522002
NCBI GI
BLAST score
                  231
E value
                  1.0e-127
Match length
                   418
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T23K3 genomic
                   sequence, complete sequence
                  164320
Seq. No.
                  LIB3177-075-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2880049
BLAST score
                   628
                   8.0e-66
E value
Match length
                   122
% identity
                   99
NCBI Description
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
                   164321
Seq. No.
                   LIB3177-075-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g115767
BLAST score
                   734
```



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164322

Seq. ID LIB3177-075-P1-K1-C3

Method BLASTX
NCBI GI g231660
BLAST score 62
E value 4.0e-30
Match length 139
% identity 49

NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 164323

Seq. ID LIB3177-075-P1-K1-C4

Method BLASTX
NCBI GI g2245032
BLAST score 173
E value 2.0e-12
Match length 73
% identity 52

NCBI Description (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]

Seq. No. 164324

Seq. ID LIB3177-075-P1-K1-C5

Method BLASTX
NCBI GI g2129569
BLAST score 387
E value 3.0e-66
Match length 130
% identity 98

NCBI Description cytosolic cyclophilin ROC3 - Arabidopsis thaliana

>gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis
thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825)

cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]

Seq. No. 164325

Seq. ID LIB3177-075-P1-K1-C6

Method BLASTX
NCBI GI g2829918
BLAST score 532
E value 2.0e-54
Match length 104
% identity 99

NCBI Description (AC002291) similar to "tub" protein gp U82468 2072162

[Arabidopsis thaliana]

Seq. No. 164326

Seq. ID LIB3177-075-P1-K1-C7

MethodBLASTXNCBI GIg4455250BLAST score148

```
E value
                  1.0e-09
Match length
                  64
% identity
                  48
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164327
                  LIB3177-075-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170089
BLAST score
                  101
E value
                  7.0e-29
Match length
                  74
% identity
                  95
NCBI Description
                  GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                  >gi_481822_pir__S39542 probable glutathione transferase (EC
                  2.5.1.18) (clone ERD13) - Arabidopsis thaliana
                  >gi 497789 dbj BAA04554_ (D17673) glutathione S-transferase
                  [Arabidopsis thaliana] >gi 3201614 (AC004669) glutathione
                  S-transferase [Arabidopsis thaliana]
Seq. No.
                  164328
Seq. ID
                  LIB3177-075-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  633
E value
                  6.0e-66
Match length
                  124
% identity
                  97
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
```

164329 Seq. No.

LIB3177-075-P1-K1-D1 Seq. ID

Method BLASTN NCBI GI q3128142 BLAST score 372 0.0e + 00E value Match length 418 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No. 164330

Seq. ID LIB3177-075-P1-K1-D11

Method BLASTX NCBI GI g132074 BLAST score 697 E value 9.0e-74Match length 129 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (\overline{EC} 4. $\overline{1.1.39}$) small chain

Al precursor - Arabidopsis thaliana



```
Seq. No.
                  164331
Seq. ID
                  LIB3177-075-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g4063737
BLAST score
                  133
E value
                  1.0e-68
Match length
                  281
% identity
                  87
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164332
                  LIB3177-075-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345655
BLAST score
                  358
                  4.0e-34
E value
Match length
                  66
% identity
                  100
NCBI Description
                  CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD)
                  >gi 757535 emb CAA83508 (Z31715) cinnamyl alcohol
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  164333
                  LIB3177-075-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2465923
BLAST score
                  350
E value
                  4.0e-33
Match length
                  105
% identity
                  66
NCBI Description
                  (AF024648) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana]
Seq. No.
                  164334
Seq. ID
                  LIB3177-075-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2760834
BLAST score
                  436
E value
                  3.0e-43
Match length
                  82
                  100
% identity
NCBI Description
                  (AC003105) putative nitrate transporter [Arabidopsis
                  thaliana]
Seq. No.
                  164335
Seq. ID
                  LIB3177-075-P1-K1-D6
Method
                  BLASTX
```

Method BLASTX
NCBI GI 9480450
BLAST score 450
E value 8.0e-45
Match length 102
% identity 89

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]



```
Seq. No.
                   164336
Seq. ID
                   LIB3177-075-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q3319921
BLAST score
                   276
                   2.0e-24
E value
Match length
                   99
                   59
% identity
NCBI Description
                   (AJ223388) Hev b 3 [Hevea brasiliensis]
                   >gi 3319923 emb CAA11304 (AJ223389) Hev b 3 [Hevea
                   brasiliensis] >gi 3319925 emb CAA11305 (AJ223390) Hev b 3
                   [Hevea brasiliensis] >gi \overline{3}818\overline{4}75 (AF05\overline{1}317) small rubber
                   particle protein [Hevea brasiliensis]
Seq. No.
                   164337
Seq. ID
                   LIB3177-075-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q1709825
BLAST score
                   568
E value
                   1.0e-58
Match length
                   130
% identity
                   88
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                   164338
                   LIB3177-075-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169201
BLAST score
                   575
E value
                   2.0e-59
                   139
Match length
% identity
                   85
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                   >gi_421830_pir S33707 DRT112 protein - Arabidopsis
                   thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                   164339
                   LIB3177-075-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2739010
BLAST score
                   286
E value
                   1.0e-25
Match length
                   97
% identity
                   53
NCBI Description (AF022464) CYP77A3p [Glycine max]
Seq. No.
                   164340
Seq. ID
                   LIB3177-075-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   q4559344
BLAST score
                   275
E value
                   1.0e-153
Match length
                   345
% identity
```

21991

NCBI Description Arabidopsis thaliana chromosome II BAC F27C12 genomic

sequence, complete sequence



Seq. No. 164341 Seq. ID LIB3177-075-P1-K1-E2 Method BLASTX NCBI GI q1703129 BLAST score 483 E value 1.0e-48 Match length 110 % identity 85 NCBI Description ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana] Seq. No. 164342 Seq. ID LIB3177-075-P1-K1-E3 Method BLASTX NCBI GI q4538963 BLAST score 547 E value 3.0e-56 Match length 134 % identity 63 NCBI Description (AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] Seq. No. 164343 Seq. ID LIB3177-075-P1-K1-E4 Method BLASTX NCBI GI q4218123 BLAST score 437 E value 3.0e-43Match length 139 % identity NCBI Description (AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana] Seq. No. 164344 Seq. ID LIB3177-075-P1-K1-E5 Method BLASTX NCBI GI g115470 BLAST score 767 E value 5.0e-82 Match length 147 % identity 99 NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__\$28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana] 164345

Seq. No.

Seq. ID LIB3177-075-P1-K1-E7

Method BLASTX NCBI GI g115767 BLAST score 585 E value 1.0e-60 Match length 111



```
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372_emb CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164346
Seq. ID
                  LIB3177-075-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3128168
BLAST score
                  170
E value
                  5.0e-12
                  65
Match length
                  52
% identity
NCBI Description
                  (AC004521) putative carboxyl-terminal peptidase
                  [Arabidopsis thaliana]
Seq. No.
                  164347
Seq. ID
                  LIB3177-075-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  619
E value
                  1.0e-64
Match length
                  118
% identity
                  99
NCBI Description
                 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  164348
Seq. ID
                  LIB3177-075-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g3702735
BLAST score
                  329
E value
                  0.0e + 00
Match length
                  420
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164349
Seq. ID
                  LIB3177-075-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4376158
BLAST score
                  626
E value
                  2.0e-65
Match length
                  128
```

% identity 96

(X98873) aspartate kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 164350

Seq. ID LIB3177-075-P1-K1-F2

Method BLASTX



NCBI GI g4510345 BLAST score 395 E value 2.0e-38 Match length 74 % identity 100

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 164351

Seq. ID LIB3177-075-P1-K1-F3

Method BLASTN
NCBI GI g2696018
BLAST score 75
E value 6.0e-34
Match length 273
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 164352

Seq. ID LIB3177-075-P1-K1-F4

Method BLASTX
NCBI GI g2879811
BLAST score 358
E value 4.0e-34
Match length 88
% identity 78

NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No. 164353

Seq. ID LIB3177-075-P1-K1-F6

Method BLASTX
NCBI GI g1076287
BLAST score 400
E value 5.0e-39
Match length 87
% identity 90

NCBI Description amine acid permease - Arabidopsis thaliana

>gi_510236_emb_CAA50672_ (X71787) amine acid permease

[Arabidopsis thaliana]

Seq. No. 164354

Seq. ID LIB3177-075-P1-K1-F8

Method BLASTN
NCBI GI g2894557
BLAST score 54
E value 1.0e-21
Match length 141
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T805

(ESSAII project)

Seq. No. 164355

Seq. ID LIB3177-075-P1-K1-G1

Method BLASTX
NCBI GI g2213585
BLAST score 745
E value 2.0e-79



Match length 140 % identity 100

NCBI Description (AC000348) T7N9.5 [Arabidopsis thaliana]

Seq. No. 164356

Seq. ID LIB3177-075-P1-K1-G10

Method BLASTX
NCBI GI g4587542
BLAST score 706
E value 7.0e-75
Match length 135
% identity 99

NCBI Description (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase

with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No. 164357

Seq. ID LIB3177-075-P1-K1-G11

Method BLASTX
NCBI GI g2245093
BLAST score 620
E value 9.0e-65
Match length 137
% identity 90

NCBI Description (Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No. 164358

Seq. ID LIB3177-075-P1-K1-G12

Method BLASTX
NCBI GI g4586057
BLAST score 589
E value 4.0e-61
Match length 112
% identity 98

NCBI Description (AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No. 164359

Seq. ID LIB3177-075-P1-K1-G3

Method BLASTN
NCBI GI g3193305
BLAST score 390
E value 0.0e+00
Match length 406
% identity 99

NCBI Description Arabidopsis thaliana BAC F3D13

Seq. No. 164360

Seq. ID LIB3177-075-P1-K1-G4

Method BLASTX
NCBI GI g3953473
BLAST score 659
E value 3.0e-69
Match length 133
% identity 100

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 164361



```
Seq. ID
                  LIB3177-075-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q99736
BLAST score
                  118
E value
                  2.0e-64
Match length
                  129
                  98
% identity
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                  Arabidopsis thaliana >gi 16187 emb CAA46814 (X66016)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                  164362
Seq. ID
                  LIB3177-075-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g132090
BLAST score
                  719
E value
                  2.0e-76
Match length
                  132
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B1 precursor - Arabidopsis thaliana >gi 16193 emb CAA32700
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  164363
Seq. ID
                  LIB3177-075-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3158376
BLAST score
                  371
E value
                  1.0e-35
Match length
                  113
% identity
                  65
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  164364
                  LIB3177-075-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193289
BLAST score
                  108
                  2.0e-57
E value
Match length
                  144
% identity
                  85
NCBI Description
                  (AF069298) similar to several small proteins (~100 aa) that
                  are induced by heat, auxin, ethylene and wounding such as
                  Phaseolus aureus indole-3-acetic acid induced protein ARG
                  (SW:32292) [Arabidopsis thaliana]
Seq. No.
                  164365
Seq. ID
                  LIB3177-075-P1-K1-G9
```

Method BLASTN NCBI GI g4490291 BLAST score 198 1.0e-107 E value Match length 330 % identity 96



NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

164366 Seq. No.

Seq. ID LIB3177-075-P1-K1-H1

Method BLASTN NCBI GI g2264304 BLAST score 229 E value 1.0e-126 Match length 356 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBG8, complete sequence [Arabidopsis thaliana]

164367 Seq. No.

Seq. ID LIB3177-075-P1-K1-H10

Method BLASTX g4538963 NCBI GI BLAST score 581 E value 2.0e-60 Match length 111 74 % identity

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 164368

Seq. ID LIB3177-075-P1-K1-H11

Method BLASTX NCBI GI q132110 BLAST score 241 E value 1.0e-20 Match length 65

77 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164369

Seq. ID LIB3177-075-P1-K1-H12

Method BLASTX NCBI GI q115783 BLAST score 648 E value 5.0e-68 Match length 121 100 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

> (CAB-140) (LHCP) >qi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

164370 Seq. No.

Seq. ID LIB3177-075-P1-K1-H2

BLASTX Method



```
NCBI GI
                  q4185509
BLAST score
                  569
E value
                  8.0e-59
Match length
                  115
                  97
% identity
NCBI Description
                  (AF102821) actin depolymerizing factor 3 [Arabidopsis
                  thaliana]
Seq. No.
                  164371
Seq. ID
                  LIB3177-075-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g4756963
                  313
BLAST score
                  1.0e-176
E value
Match length
                  383
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
Seq. No.
                  164372
Seq. ID
                  LIB3177-075-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g4589410
BLAST score
                  426
E value
                  0.0e + 00
Match length
                  448
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2015, complete sequence
Seq. No.
                  164373
Seq. ID
                  LIB3177-075-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3286693
BLAST score
                  600
E value
                  2.0e-62
Match length
                  122
                  99
% identity
NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                  (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  164374
Seq. ID
                  LIB3177-075-P1-K1-H6
Method
                  BLASTX
                  g2347192
                  199
                  2.0e-15
```

NCBI GI BLAST score E value Match length 49 % identity 84

NCBI Description (AC002338) spliceosomal protein U2B isolog [Arabidopsis

thaliana]

Seq. No. 164375

Seq. ID LIB3177-075-P1-K1-H8

Method BLASTX q4510345 NCBI GI BLAST score 218



E value 1.0e-17 Match length 41 % identity 90

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 164376

Seq. ID LIB3177-075-P1-K1-H9

Method BLASTX
NCBI GI g282865
BLAST score 360
E value 2.0e-34
Match length 83
% identity 82

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]

>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164377

Seq. ID LIB3177-076-P1-K1-A1

Method BLASTX
NCBI GI g116392
BLAST score 622
E value 4.0e-65
Match length 120
% identity 99

NCBI Description CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE)

>gi_66543_pir__SYMUCN naringenin-chalcone synthase (EC
2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308)

chalcone synthase [Arabidopsis thaliana]

Seq. No. 164378

Seq. ID LIB3177-076-P1-K1-A10

Method BLASTX
NCBI GI g4585978
BLAST score 766
E value 7.0e-82
Match length 150
% identity 97

NCBI Description (AC005287) NADP specific isocitrate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 164379

Seq. ID LIB3177-076-P1-K1-A11

Method BLASTX
NCBI GI g2130028
BLAST score 352
E value 3.0e-33
Match length 86
% identity 73

NCBI Description B12D protein - barley >gi_471319_emb_CAA54065.1 (X76604)

HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805)

B12Dg1 [Hordeum vulgare]

Seq. No. 164380

NCBI Description

```
Total V
```

```
LIB3177-076-P1-K1-A12
Seq. ID
                   BLASTN
Method
                   q4490701
NCBI GI
BLAST score
                   131
E value
                   2.0e-67
Match length
                   422
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
NCBI Description
                   (ESSA project)
Seq. No.
                   164381
                   LIB3177-076-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1619321
BLAST score
                   176
                   3.0e-13
E value
                   52
Match length
                   65
% identity
NCBI Description (Y07563) hin1 [Nicotiana tabacum]
                   164382
Seq. No.
                   LIB3177-076-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2924520
BLAST score
                   596
E value
                   5.0e-62
Match length
                   113
                   99
% identity
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   164383
Seq. No.
                   LIB3177-076-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132110
BLAST score
                   630
                   6.0e-66
E value
Match length
                   118
                   98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi 68060 pir RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{\text{1.1}}.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
                   164384
Seq. No.
Seq. ID
                   LIB3177-076-P1-K1-A5
                   BLASTX
Method
NCBI GI
                   q117238
BLAST score
                   691
E value
                   5.0e-73
Match length
                   138
                   98
% identity
```

MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN

CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)

>gi_81656_pir__S12785 protein ch-42 precursor, chloroplast



- Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No. 164385

Seq. ID LIB3177-076-P1-K1-A6

Method BLASTX
NCBI GI g137465
BLAST score 763
E value 2.0e-81
Match length 150
% identity 99

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)

(V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain -

Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 164386

Seq. ID LIB3177-076-P1-K1-A7

Method BLASTX
NCBI GI g1169278
BLAST score 305
E value 6.0e-28
Match length 75
% identity 84

NCBI Description DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 164387

Seq. ID LIB3177-076-P1-K1-A8

Method BLASTX
NCBI GI g115385
BLAST score 574
E value 2.0e-59
Match length 115
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164388

Seq. ID LIB3177-076-P1-K1-A9

Method BLASTX
NCBI GI g2494610
BLAST score 327
E value 2.0e-30
Match length 129
% identity 57

NCBI Description CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR

>gi_1079732 (U39877) cpFtsZ [Arabidopsis thaliana]

Seq. No. 164389



```
Seq. ID
                   LIB3177-076-P1-K1-B1
 Method
                   BLASTX
NCBI GI
                   g543751
BLAST score
                   633
E value
                   3.0e-66
Match length
                   120
 % identity
                   99
NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
                   (ETHYLENE-FORMING ENZYME) (EFE) >gi_541861_pir__JT0755
                   ethylene-forming enzyme - Arabidopsis thaliana
                   >gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   164390
Seq. ID
                   LIB3177-076-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2493122
BLAST score
                   251
E value
                   1.0e-21
Match length
                   78
% identity
                   69
NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                   SUBUNIT) (TONOPLAST ATPASE 70 KD SUBUNIT) (BN59)
                   >gi_1362024_pir__S57790 H+-transporting ATPase (EC
                   3.6.1.35), vacuolar, 70K chain (clone BN59) - rape
                  >gi 558479 (U15604) tonoplast ATPase 70 kDa subunit
                   [Brassica napus]
Seq. No.
                  164391
Seq. ID
                  LIB3177-076-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4741954
BLAST score
                  588
E value
                  5.0e-61
Match length
                  114
% identity
                  100
NCBI Description (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                  164392
Seq. ID
                  LIB3177-076-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1710549
BLAST score
                  265
E value
                  2.0e-23
Match length
                  49
% identity
                  98
NCBI Description 60S RIBOSOMAL PROTEIN L39
Seq. No.
                  164393
Seq. ID
                  LIB3177-076-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  524
E value
                  1.0e-53
Match length
                  101
% identity
                  99
```

22002

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. ID

Method

NCBI GI



```
Seq. No.
                   164394
Seq. ID
                   LIB3177-076-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g3451065
BLAST score
                   530
E value
                   3.0e-54
Match length
                   114
% identity
                   91
NCBI Description (AL031326) water channel - like protein [Arabidopsis
                   thalianal
Seq. No.
                   164395
Seq. ID
                  LIB3177-076-P1-K1-B4
Method
                  BLASTX
NCBI GI
                   g4204265
BLAST score
                  173
E value
                  2.0e-12
Match length
                  123
% identity
                  34
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  164396
Seq. ID
                  LIB3177-076-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4522012
BLAST score
                  479
E value
                  3.0e-48
Match length
                  153
% identity
                  58
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164397
Seq. ID
                  LIB3177-076-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3702315
BLAST score
                  323
E value
                  0.0e+00
Match length
                  429
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T3F17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164398
Seq. ID
                  LIB3177-076-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q4741948
BLAST score
                  519
E value
                  2.0e-58
Match length
                  122
% identity
                  96
NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164399
```

22003

LIB3177-076-P1-K1-B8

BLASTN

g3985958



BLAST score 317 E value 1.0e-178 Match length 417 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 164400

Seq. ID LIB3177-076-P1-K1-B9

Method BLASTX
NCBI GI g2662375
BLAST score 216
E value 2.0e-17
Match length 115
% identity 39

NCBI Description (D89060) oligosaccharyltransferase [Homo sapiens]

Seq. No. 164401

Seq. ID LIB3177-076-P1-K1-C1

Method BLASTX
NCBI GI g595768
BLAST score 146
E value 4.0e-09
Match length 47
% identity 62

NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]

Seq. No. 164402

Seq. ID LIB3177-076-P1-K1-C10

Method BLASTX
NCBI GI g2119846
BLAST score 708
E value 3.0e-76
Match length 145
% identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164403

Seq. ID LIB3177-076-P1-K1-C11

Method BLASTX
NCBI GI g132074
BLAST score 729
E value 2.0e-77
Match length 133
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 164404



```
Seq. ID
                   LIB3177-076-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g2583125
BLAST score
                   338
E value
                   1.0e-31
Match length
                   113
% identity
                   61
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
                   thaliana]
Seq. No.
                   164405
Seq. ID
                   LIB3177-076-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2832625
BLAST score
                   299
E value
                   3.0e-27
Match length
                   69
% identity
                   81
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   164406
Seq. ID
                   LIB3177-076-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q132110
BLAST score
                   749
E value
                   8.0e-80
Match length
                   138
% identity
                   99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1.39}) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164407
Seq. ID
                   LIB3177-076-P1-K1-C5
Method
                  BLASTN
NCBI GI
                   g3176694
BLAST score
                  279
E value
                   1.0e-155
Match length
                   406
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164408
Seq. ID
                  LIB3177-076-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4204285
BLAST score
                  440
```

E value 1.0e-43 Match length 149 % identity 56

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]



```
Seq. No.
                   164409
Seq. ID
                   LIB3177-076-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2583134
BLAST score
                   234
E value
                   1.0e-19
Match length
                   44
% identity
                   100
NCBI Description (AC002387) putative proline-rich protein [Arabidopsis
                   thaliana]
Seq. No.
                   164410
Seq. ID
                  LIB3177-076-P1-K1-C8
Method
                  BLASTN
NCBI GI
                   g4006885
BLAST score
                  143
E value
                   1.0e-74
Match length
                  415
% identity
                   96
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No
Seq. No.
                  164411
Seq. ID
                  LIB3177-076-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4741950
BLAST score
                  748
E value
                  9.0e-80
Match length
                  140
% identity
                  100
NCBI Description (AF134125) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164412
Seq. ID
                  LIB3177-076-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2829896
BLAST score
                  283
E value
                  3.0e-25
Match length
                  87
% identity
                  62
NCBI Description (AC002311) highly similar to auxin-regulated protein GH3,
                  gp_X60033_18591 [Arabidopsis thaliana]
Seq. No.
                  164413
Seq. ID
                  LIB3177-076-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4539316
BLAST score
                  671
                  1.0e-70
E value
Match length
                  138
% identity
                  100
NCBI Description (AL035679) putative fructose-bisphosphate aldolase
                  [Arabidopsis thaliana]
```

Seq. No. 164414

Seq. ID LIB3177-076-P1-K1-D2

Method BLASTX



NCBI GI g2245079 BLAST score 295 E value 1.0e-26 Match length 104 % identity 58

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 164415

Seq. ID LIB3177-076-P1-K1-D4

Method BLASTN
NCBI GI g4585952
BLAST score 63
E value 5.0e-27
Match length 157
% identity 90

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,

complete sequence

Seq. No. 164416

Seq. ID LIB3177-076-P1-K1-D5

Method BLASTX
NCBI GI g3219858
BLAST score 601
E value 2.0e-62
Match length 116
% identity 100

NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE

>gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II

13.6 kDa subunit [Arabidopsis thaliana]

>gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA

polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No. 164417

Seq. ID LIB3177-076-P1-K1-D6

Method BLASTX
NCBI GI g2252828
BLAST score 374
E value 2.0e-48
Match length 123
% identity 87

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 164418

Seq. ID LIB3177-076-P1-K1-D7

Method BLASTX
NCBI GI 94741960
BLAST score 517
E value 1.0e-52
Match length 118
% identity 85

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 164419

Seq. ID LIB3177-076-P1-K1-D8

Method BLASTX NCBI GI g687677



```
BLAST score
E value
                    3.0e-43
Match length
                    88
% identity
                    99
NCBI Description (U19925) unknown [Arabidopsis thaliana]
Seq. No.
                   164420
Seq. ID
                   LIB3177-076-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g1175012
BLAST score
                   521
E value
                   3.0e-53
Match length
                   112
% identity
                   91
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
                   B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                   protein TMP-B [Arabidopsis thaliana]
Seq. No.
                   164421
Seq. ID
                   LIB3177-076-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g4056502
BLAST score
                   618
E value
                   2.0e-64
Match length
                   129
% identity
                   92
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                   164422
Seq. ID
                   LIB3177-076-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g541858
BLAST score
                   756
E value
                   1.0e-80
Match length
                   144
% identity
                   99
NCBI Description endoxyloglucan transferase - Arabidopsis thaliana
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                   164423
                   LIB3177-076-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2832642
                   187
                   6.0e-14
                   96
% identity
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]
```

NCBI GI BLAST score E value Match length

Seq. No. 164424

Seq. ID LIB3177-076-P1-K1-E2

Method BLASTX NCBI GI g2078350 BLAST score 264 E value 5.0e-23

% identity



```
Match length
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   164425
Seq. ID
                   LIB3177-076-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g3176694
BLAST score
                   274
E value
                   1.0e-153
Match length
                   403
% identity
                   99
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164426
Seq. ID
                   LIB3177-076-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4581146
BLAST score
                   152
E value
                   6.0e-10
Match length
                   31
% identity
                   94
NCBI Description
                  (AC006919) putative fructose-bisphosphate aldolase,
                   cytoplasmic [Arabidopsis thaliana]
Seq. No.
                   164427
Seq. ID
                   LIB3177-076-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g2245057
BLAST score
                   409
E value
                   3.0e-40
Match length
                   75
                   100
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   164428
Seq. ID
                  LIB3177-076-P1-K1-E8
Method
                  BLASTX
NCBI GI
                   g4240116
BLAST score
                   532
E value
                  2.0e-54
Match length
                  124
% identity
                   84
                  (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                  thaliana] >gi 4240118_dbj_BAA74838_ (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                  164429
Seq. ID
                  LIB3177-076-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q132659
BLAST score
                  372
E value
                  1.0e-35
Match length
                  82
```

22009

NCBI Description 50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)



>gi_81483_pir_ A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi_170133 (J04461) ribosomal protein L13 [Spinacia oleracea]

Seq. No. 164430

Seq. ID LIB3177-076-P1-K1-F10

Method BLASTX NCBI GI g2129578 BLAST score 315 E value 3.0e-29 Match length 62 % identity 97

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 164431

Seq. ID LIB3177-076-P1-K1-F11

Method BLASTX NCBI GI g115767 BLAST score 651 E value 2.0e-68 Match length 124 % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372 emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164432

Seq. ID LIB3177-076-P1-K1-F12

Method BLASTN NCBI GI g3212846 BLAST score 137 E value 5.0e-71 Match length 364 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164433

Seq. ID LIB3177-076-P1-K1-F2

Method BLASTN NCBI GI g2618677 BLAST score 101 E value 2.0e-49 Match length 510 % identity 47

NCBI Description Arabidopsis thaliana BAC F21B7 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No. 164434



Seq. ID LIB3177-076-P1-K1-F3 Method BLASTX NCBI GI q1169201 BLAST score 611 E value 1.0e-63 Match length 150 % identity 83 NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana] Seq. No. 164435 Seq. ID LIB3177-076-P1-K1-F4 Method BLASTX NCBI GI q3850579 BLAST score 554 E value 4.0e-57 Match length 124 % identity 85 NCBI Description (AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an Seq. No. 164436 Seq. ID LIB3177-076-P1-K1-F5 Method BLASTX NCBI GI g2500430 BLAST score 655 E value 7.0e-69 Match length 127 % identity 100 NCBI Description 40S RIBOSOMAL PROTEIN S16 Seq. No. 164437 Seq. ID LIB3177-076-P1-K1-F6 Method BLASTX NCBI GI g4006883 BLAST score 453 E value 3.0e-45Match length 111 % identity NCBI Description (Z99707) cysteine proteinase [Arabidopsis thaliana] Seq. No. 164438 Seq. ID LIB3177-076-P1-K1-F7 Method BLASTX q421826 633 3.0e-66

NCBI GI BLAST score E value Match length 143 % identity 83

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis

thaliana1



```
Seq. No.
                   164439
Seq. ID
                   LIB3177-076-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g4218123
BLAST score
                   332
E value
                   3.0e-34
Match length
                   136
% identity
NCBI Description
                   (AL035353) photosystem I subunit PSI-E-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   164440
Seq. ID
                   LIB3177-076-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q1568480
BLAST score
                   648
E value
                   5.0e-68
Match length
                   150
% identity
NCBI Description (Z71703) cdc2-like protein kinase [Beta vulgaris]
Seq. No.
                   164441
Seq. ID
                   LIB3177-076-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q4454032
BLAST score
                   302
E value
                   2.0e-31
Match length
                   118
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                   164442
Seq. ID
                  LIB3177-076-P1-K1-G11
Method
                  BLASTX
NCBI GI
                   g625977
BLAST score
                   609
E value
                   1.0e-63
Match length
                  118
% identity
                   100
NCBI Description p40 protein homolog - Arabidopsis thaliana >gi_402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  164443
Seq. ID
                  LIB3177-076-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1175013
BLAST score
                  514
                  2.0e-52
                  113
% identity
                  88
```

E value Match length

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542 pir S44084 plasma membrane intrinsic protein 2a - Arabidopsis Thaliana

>gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic

protein 2a [Arabidopsis thaliana]

Seq. No. 164444



```
Seq. ID
                    LIB3177-076-P1-K1-G2
Method
                    BLASTX
NCBI GI
                    q3337361
BLAST score
                    338
E value
                    1.0e-31
Match length
                    146
% identity
                    50
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                    LIB3177-076-P1-K1-G3
Method
                    BLASTX
NCBI GI
                    g4454036
BLAST score
                    729
E value
                    1.0e-77
Match length
                    133
% identity
                    99
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                    thaliana]
Seq. No.
                    164446
Seq. ID
                    LIB3177-076-P1-K1-G4
Method
                    BLASTN
NCBI GI
                    g3241922
BLAST score
                   19
E value
                    1.1e+00
Match length
                    324
% identity
                    73
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164447
Seq. ID
                   LIB3177-076-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q4337175
BLAST score
                   568
E value
                   9.0e-59
Match length
                   111
% identity
                   100
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T444439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   164448
Seq. ID
                   LIB3177-076-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   q336917
BLAST score
                   51
E value
                   1.0e-19
Match length
                   135
% identity
                   90
NCBI Description Epifagus virginiana chloroplast complete genome
Seq. No.
                   164449
```

Seq. ID LIB3177-076-P1-K1-G7

Method BLASTX



NCBI GI g282865 BLAST score 670 E value 1.0e-70 Match length 133 % identity 72

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164450

Seq. ID LIB3177-076-P1-K1-G8

Method BLASTX
NCBI GI g2213583
BLAST score 319
E value 1.0e-29
Match length 125
% identity 53

NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No. 164451

Seq. ID LIB3177-076-P1-K1-G9

Method BLASTN
NCBI GI g2264313
BLAST score 160
E value 4.0e-85
Match length 160
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOP10, complete sequence [Arabidopsis thaliana]

Seq. No. 164452

Seq. ID LIB3177-076-P1-K1-H1

Method BLASTX
NCBI GI g2062161
BLAST score 735
E value 3.0e-78
Match length 139
% identity 50

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 164453

Seq. ID LIB3177-076-P1-K1-H10

Method BLASTN
NCBI GI 9790582
BLAST score 377
E value 0.0e+00
Match length 381
% identity 100

NCBI Description Arabidopsis thaliana putative pathogenesis-related protein

(ATOZI1) mRNA, complete cds

Seq. No. 164454

Seq. ID LIB3177-076-P1-K1-H11



Method BLASTN NCBI GI q2618603 BLAST score 288 E value 1.0e-161 Match length 296 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No. 164455

Seq. ID LIB3177-076-P1-K1-H12 Method BLASTX NCBI GI q1843527 BLAST score 302 E value 1.0e-27 Match length 103 % identity

NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 164456

Seq. ID LIB3177-076-P1-K1-H3

40

Method BLASTX NCBI GI q2499973 BLAST score 226 E value 1.0e-18 Match length 103 % identity 52

NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II

[Arabidopsis thaliana]

Seq. No. 164457

Seq. ID LIB3177-076-P1-K1-H4

Method BLASTN NCBI GI g2351067 BLAST score 232 E value 1.0e-128 Match length 360 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No. 164458

Seq. ID LIB3177-076-P1-K1-H5

Method BLASTX NCBI GI g2501021 BLAST score 162 E value 2.0e-11 Match length 38 % identity 82

NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)

>gi 1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase

[Synechocystis sp.]

Seq. No. 164459

Seq. ID LIB3177-076-P1-K1-H6

Method BLASTX



```
NCBI GI
                   g3915826
BLAST score
                   461
E value
                  3.0e-46
Match length
                  103
% identity
                  84
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  164460
Seq. ID
                  LIB3177-076-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  712
E value
                  2.0e-75
Match length
                  134
% identity
                  76
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164461
Seq. ID
                  LIB3177-076-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g3046847
BLAST score
                  178
E value
                  1.0e-95
Match length
                  316
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
                  K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164462
Seq. ID
                  LIB3177-077-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g3688799
BLAST score
                  492
                  7.0e-50
E value
Match length
                  99
% identity
                  99
NCBI Description (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  164463
Seq. ID
                  LIB3177-077-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g132090
BLAST score
                  756
E value
                  1.0e-80
Match length
                  139
```

% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR

(RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164464

Seq. ID LIB3177-077-P1-K1-A12

Method BLASTX



NCBI GI q1172873 BLAST score 417 E value 4.0e-41 Match length 95 % identity 89

NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857 pir JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619 dbj BAA02374

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 164465

Seq. ID LIB3177-077-P1-K1-A2

Method BLASTX NCBI GI g1402908 BLAST score 756 E value 1.0e-80 Match length 146 % identity 99

NCBI Description (X98315) peroxidase [Arabidopsis thaliana]

>gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)

peroxidase [Arabidopsis thaliana]

Seq. No. 164466

Seq. ID LIB3177-077-P1-K1-A3

Method BLASTX NCBI GI q2130096 BLAST score 232 E value 3.0e-19 Match length 115 % identity 37

NCBI Description cytochrome P450tyr - sorghum >gi 984543 (U32624) cytochrome

P-450 [Sorghum bicolor]

Seq. No. 164467

Seq. ID LIB3177-077-P1-K1-A4

Method BLASTN NCBI GI q4220635 BLAST score 283 E value 1.0e-158 Match length 283 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 164468

Seq. ID LIB3177-077-P1-K1-A5

Method BLASTX NCBI GI q81600 BLAST score 645 E value 1.0e-67 Match length 144 % identity 92

NCBI Description chaperonin 60 beta (clone bX) - Arabidopsis thaliana

(fragment)

Seq. No. 164469



```
Seq. ID
                   LIB3177-077-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q2738248
BLAST score
                   760
E value
                   4.0e-81
Match length
                   153
% identity
                   97
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   164470
Seq. ID
                   LIB3177-077-P1-K1-A7
Method
                   BLASTN
NCBI GI
                   q2979540
BLAST score
                   99
E value
                   3.0e-48
Match length
                   457
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F17K2 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164471
Seq. ID
                  LIB3177-077-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  q4586019
BLAST score
                  233
E value
                   1.0e-128
Match length
                  233
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T3P4 genomic
                  sequence, complete sequence
Seq. No.
                  164472
Seq. ID
                  LIB3177-077-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3169169
BLAST score
                  411
E value
                  0.0e+00
Match length
                  443
% identity
                  80
NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164473
Seq. ID
                  LIB3177-077-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4454037
BLAST score
                  435
E value
                  3.0e-43
Match length
                  84
% identity
                  95
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
```

Seq. No. 164474

Seq. ID LIB3177-077-P1-K1-B11

Method BLASTX

% identity

97



```
NCBI GI
                   q464986
BLAST score
                   696
E value
                   1.0e-73
Match length
                   129
% identity
                   100
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   164475
Seq. ID
                   LIB3177-077-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4165550
BLAST score
                   686
E value
                   2.0e-72
Match length
                   143
% identity
                   91
NCBI Description (AJ004915) apgm [Malus domestica]
Seq. No.
                   164476
Seq. ID
                   LIB3177-077-P1-K1-B2
Method
                   BLASTN
NCBI GI
                   g4455339
BLAST score
                   305
E value
                   1.0e-171
Match length
                   305
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
                   (ESSAII project)
Seq. No.
                   164477
Seq. ID
                   LIB3177-077-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2117612
BLAST score
                   869
E value
                   7.0e - 94
Match length
                   157
% identity
                   100
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                   164478
Seq. ID
                  LIB3177-077-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   g3883125
BLAST score
                  232
E value
                   1.0e-128
Match length
                  263
```

NCBI Description Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA,

Seq. No.

Seq. ID

164484

LIB3177-077-P1-K1-C10



complete cds

```
Seq. No.
                   164479
                   LIB3177-077-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g16225
BLAST score
                   628
E value
                   1.0e-65
Match length
                   123
% identity
                   65
NCBI Description (Z12023) calmodulin [Arabidopsis thaliana]
Seq. No.
                   164480
Seq. ID
                  LIB3177-077-P1-K1-B7
Method
                   BLASTX
                   q4056457
NCBI GI
BLAST score
                   472
                   2.0e-47
E value
Match length
                   130
% identity
                   71
NCBI Description (AC005990) ESTs gb_234051 and gb_F13722 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  164481
Seq. ID
                  LIB3177-077-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g3298610
BLAST score
                  145
E value
                   4.0e-76
Match length
                  157
% identity
                  98
NCBI Description Arabidopsis thaliana BAC T2H3
Seq. No.
                  164482
Seq. ID
                  LIB3177-077-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2558662
BLAST score
                  143
E value
                  6.0e-09
Match length
                  115
% identity
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                  164483
Seq. ID
                  LIB3177-077-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1173104
BLAST score
                  738
E value
                  1.0e-78
Match length
                  150
% identity
                  90
NCBI Description RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
                  [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
```



```
Method
                   BLASTX
NCBI GI
                   g3298443
BLAST score
                   311
E value
                   2.0e-28
Match length
                   84
 % identity
                   69
                  (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   164485
Seq. ID
                   LIB3177-077-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q461532
BLAST score
                   236
E value
                   9.0e-20
Match length
                   64
% identity
                   66
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1362500 pir D49993
                   ADP-ribosylation factor - Ajellomyces capsulata >gi 407693
                   (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
Seq. No.
                   164486
Seq. ID
                   LIB3177-077-P1-K1-C2
Method
                   BLASTX
«NCBI GI
                   q4115337
BLAST score
                   764
E value
                   1.0e-81
Match length
                   154
% identity
                   18
NCBI Description (L81141) ubiquitin [Pisum sativum]
Seq. No.
                   164487
Seq. ID
                   LIB3177-077-P1-K1-C3
Method
                  BLASTN
NCBI GI
                   g3985954
BLAST score
                   398
E value
                   0.0e+00
Match length
                   457
% identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRG21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164488
Seq. ID
                  LIB3177-077-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q3985958
BLAST score
                  317
E value
                  1.0e-178
Match length
                   454
% identity
                   95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                  164489
```

Seq. No.

Seq. ID LIB3177-077-P1-K1-C5

Method BLASTX NCBI GI g135860



BLAST score 565 E value 2.0e-58 Match length 123 % identity 63

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic

protein gamma - Arabidopsīs thaliana

>gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic

protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129 prf_1908432B tonoplast intrinsic protein gamma

[Arabidopsis thaliana]

Seq. No. 164490

Seq. ID LIB3177-077-P1-K1-C6

Method BLASTX
NCBI GI g4455364
BLAST score 255
E value 6.0e-22
Match length 56
% identity 82

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana

- Seq. No. 164491

Seq. ID LIB3177-077-P1-K1-C7

Method BLASTN
NCBI GI g3449334
BLAST score 310
E value 1.0e-174
Match length 394
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYH9, complete sequence [Arabidopsis thaliana]

Seq. No. 164492

Seq. ID LIB3177-077-P1-K1-C8

Method BLASTX
NCBI GI g282865
BLAST score 659
E value 3.0e-69
Match length 131
% identity 72

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1 (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164493

Seq. ID LIB3177-077-P1-K1-C9

Method BLASTN
NCBI GI g2618602
BLAST score 216
E value 1.0e-118
Match length 412



% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 164494

Seq. ID LIB3177-077-P1-K1-D10

Method BLASTX
NCBI GI g2119846
BLAST score 763
E value 2.0e-81
Match length 145
% identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164495

Seq. ID LIB3177-077-P1-K1-D11

Method BLASTX
NCBI GI g267083
BLAST score 560
E value 1.0e-57
Match length 107
% identity 100

NCBI Description TUBULIN BETA-9 CHAIN >gi_320190 pir JQ1593 tubulin beta-9

chain - Arabidopsis thaliana $>gi_1 = 16\overline{69}10$ (M84706) beta-9

tubulin [Arabidopsis thaliana]

Seq. No. 164496

Seq. ID LIB3177-077-P1-K1-D12

Method BLASTN
NCBI GI g4417264
BLAST score 45
E value 5.0e-16
Match length 123
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F7D8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164497

Seq. ID LIB3177-077-P1-K1-D2

Method BLASTX
NCBI GI g2911055
BLAST score 577
E value 2.0e-67
Match length 156

% identity 87

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 164498

Seq. ID LIB3177-077-P1-K1-D3

Method BLASTX NCBI GI g166835



BLAST score 303 E value 8.0e-28 Match length 85 % identity 74

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi 2642170 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 164499

Seq. ID LIB3177-077-P1-K1-D4

Method BLASTX
NCBI GI g2055273
BLAST score 344
E value 2.0e-32
Match length 66
% identity 100

NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No. 164500

Seq. ID LIB3177-077-P1-K1-D5

Method BLASTX
NCBI GI g464720
BLAST score 251
E value 2.0e-21
Match length 50
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S28 >gi_409184 (L09755) ribosomal

protein S28 [Arabidopsis thaliana]

Seq. No. 164501

Seq. ID LIB3177-077-P1-K1-D7

Method BLASTX
NCBI GI g132110
BLAST score 666
E value 4.0e-70
Match length 122
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164502

Seq. ID LIB3177-077-P1-K1-D8

Method BLASTX
NCBI GI g4585882
BLAST score 570
E value 6.0e-59
Match length 112
% identity 99

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 164503

Seq. ID LIB3177-077-P1-K1-D9



```
Method
                   BLASTN
NCBI GI
                   g4510360
BLAST score
                   292
E value
                   1.0e-163
Match length
                  340
% identity
                   96
NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  164504
Seq. ID
                  LIB3177-077-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q544425
BLAST score
                  424
E value
                  7.0e-42
Match length
                  82
% identity
                  100
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
                  >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi_166658
                   (L04171) ORF [Arabidopsis thaliana] >gi 166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  164505
Seq. ID
                  LIB3177-077-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  709
E value
                  4.0e-75
Match length
                  131
% identity
                  77
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164506
Seq. ID
                  LIB3177-077-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  q3702735
BLAST score
                  129
E value
                  1.0e-66
Match length
                  164
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164507
Seq. ID
                  LIB3177-077-P1-K1-E12
Method
                  BLASTX
                  g416758
                  780
                  2.0e-83
```

NCBI GI BLAST score E value Match length 146 % identity 99

SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130) NCBI Description carboxypeptidase Y-like protein [Arabidopsis thaliana]

>gi_445120 prf 1908426A carboxypeptidase Y [Arabidopsis

thaliana]

E value

Match length

% identity

5.0e-11

53

60



```
Seq. No.
                   164508
Seq. ID
                   LIB3177-077-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g4220514
BLAST score
                   438
E value
                   2.0e-43
Match length
                   119
% identity
                   70
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   164509
Seq. ID
                   LIB3177-077-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   q4220638
BLAST score
                   50
E value
                   2.0e-19
Match length
                   173
% identity
                   89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164510
Seq. ID
                   LIB3177-077-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   678
E value
                   1.0e-71
Match length
                   131
% identity
                   98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                   a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164511
Seq. ID
                   LIB3177-077-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g166702
BLAST score
                   663
E value
                   9.0e-70
Match length
                   149
% identity
                   87
NCBI Description (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit
                   [Arabidopsis thaliana]
Seq. No.
                   164512
Seq. ID
                   LIB3177-077-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4493904
BLAST score
                   157
```



NCBI Description (AL034558) predicted using hexExon; MAL3P2.26 (PFC0285c), T-complex protein beta subunit, len: 541 aa; Similarity to T-complex proteins beta subunits. C.elegans T-complex protein beta subunit (SW:TCPB CAEEL) BLAST Score: 1527 Seq. No. 164513 Seq. ID LIB3177-077-P1-K1-E7 Method BLASTN NCBI GI g4490324 BLAST score 116 E value 8.0e-59 Match length 124 % identity 75 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project) Seq. No. 164514 Seq. ID LIB3177-077-P1-K1-E8 Method BLASTX NCBI GI g1542941 BLAST score 198 E value 2.0e-15 Match length 52 % identity 81 NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus satīvus] Seq. No. 164515 Seq. ID LIB3177-077-P1-K1-E9 Method BLASTX NCBI GI g294666 BLAST score 227 E value 1.0e-18 Match length 122 % identity 43 NCBI Description (L13241) beta-ketoacyl-ACP synthase [Ricinus communis] Seq. No. 164516 Seq. ID LIB3177-077-P1-K1-F1 Method BLASTX NCBI GI q2062157 BLAST score 303 E value 4.0e-58 Match length 120 % identity 34 NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana] Seq. No. 164517 LIB3177-077-P1-K1-F10

Seq. ID

Method BLASTX NCBI GI g2829899 BLAST score 593 E value 1.0e-61 Match length 117 % identity

NCBI Description (AC002311) similar to ripening-induced protein, $gp_AJ001449_2465015$ and major#latex protein,





gp X91961 1107495 [Arabidopsis thaliana]

 Seq. No.
 164518

 Seq. ID
 LIB3177-077-P1-K1-F11

 Method
 BLASTX

 NCBI GI
 q4454037

 NCBI GI
 g4454037

 BLAST score
 599

 E value
 3.0e-62

 Match length
 112

 % identity
 99

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 164519

Seq. ID LIB3177-077-P1-K1-F12

Method BLASTX
NCBI GI g4538963
BLAST score 565
E value 3.0e-58
Match length 137
% identity 64

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129 1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 164520

Seq. ID LIB3177-077-P1-K1-F2

Method BLASTX
NCBI GI 94454473
BLAST score 365
E value 8.0e-35
Match length 123
% identity 60

NCBI Description (AC006234) putative beta-expansin protein [Arabidopsis

thaliana]

Seq. No. 164521

Seq. ID LIB3177-077-P1-K1-F3 -

Method BLASTX
NCBI GI g1702987
BLAST score 592
E value 6.0e-66
Match length 136
% identity 96

NCBI Description 14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14

protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis

thaliana]

Seq. No. 164522

Seq. ID LIB3177-077-P1-K1-F5

Method BLASTX
NCBI GI g115385
BLAST score 577
E value 1.0e-59
Match length 111
% identity 100



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 164523 Seq. ID LIB3177-077-P1-K1-F6 Method BLASTX NCBI GI g132074 BLAST score 709 E value 1.0e-78 Match length 142 % identity 91 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana Seq. No. 164524 Seq. ID LIB3177-077-P1-K1-F8 Method BLASTN NCBI GI g3269280 BLAST score 144 E value 4.0e-75 Match length 311 % identity 97 NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project) Seq. No. 164525 Seq. ID LIB3177-077-P1-K1-F9 Method BLASTN NCBI GI g3851669 BLAST score 126 E value 2.0e-64 Match length 134 % identity 99 NCBI Description Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid protein, complete cds Seq. No. 164526 Seq. ID LIB3177-077-P1-K1-G1 BLASTN

Method NCBI GI g4262221 BLAST score 36 E value 1.0e-10 Match length 242 % identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164527

Seq. ID LIB3177-077-P1-K1-G10

Method BLASTX NCBI GI q115385 BLAST score 704 E value 1.0e-74 Match length 135



% identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 164528 Seq. ID LIB3177-077-P1-K1-G11 Method BLASTX NCBI GI q1076668 BLAST score 511 E value 4.0e-52 Match length 109 % identity 87 NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823 (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No. 164529 Seq. ID LIB3177-077-P1-K1-G12 Method BLASTX

NCBI GI q133938 BLAST score 560 E value 1.0e-57 Match length 144 % identity 77

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70866 pir R3SP3

ribosomal protein S3 - spinach chloroplast

>gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3

[Spinacia oleracea]

Seq. No. 164530

Seq. ID LIB3177-077-P1-K1-G2

Method BLASTX NCBI GI g2832241 BLAST score 721 E value 1.0e-76 Match length 151 % identity 93

NCBI Description (AF030864) nonphototropic hypocotyl 1 [Arabidopsis

thaliana]

Seq. No. 164531

Seq. ID LIB3177-077-P1-K1-G3

Method BLASTX NCBI GI g115385 BLAST score 548 E value 2.0e-56 Match length 105 % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164532

Seq. ID LIB3177-077-P1-K1-G4

Method BLASTX NCBI GI q1076413



BLAST score E value 1.0e-80 Match length 149 % identity 100

serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis NCBI Description thaliana >gi_2146776_pir S67482 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_608577 (L34076)

serine acetyltransferase [Arabidopsis thaliana]

>gi_608677_emb_CAA84371_ (Z34888) serine acetyltransferase
[Arabidopsis thaliana] >gi_1093493_prf__2104212A Ser

acetyltransferase [Arabidopsis thaliana]

Seq. No. 164533

Seq. ID LIB3177-077-P1-K1-G5

Method BLASTN NCBI GI g4454447 BLAST score 328 E value 0.0e+00Match length 344 99 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164534

Seq. ID LIB3177-077-P1-K1-G6

Method BLASTX NCBI GI q3878874 BLAST score 196 E value 5.0e-15 Match length 140 % identity 34

NCBI Description (Z69793) R03A10.3 [Caenorhabditis elegans]

Seq. No. 164535

Seq. ID LIB3177-077-P1-K1-G7

BLASTN Method NCBI GI q166781 BLAST score 97 E value 2.0e-47 Match length 160 % identity 90

NCBI Description A.thaliana nitrate reductase mRNA, complete cds

Seq. No. 164536

Seq. ID LIB3177-077-P1-K1-G8

Method BLASTX NCBI GI q3885511 BLAST score 393 E value 3.0e-38 Match length 99 % identity 81

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 164537

Seq. ID LIB3177-077-P1-K1-G9

Method BLASTX

Match length

% identity

69

57



```
NCBI GI
                   q3169185
BLAST score
                   245
E value
                   8.0e-21
Match length
                   62
                   76
% identity
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164538
Seq. ID
                   LIB3177-077-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g4415930
BLAST score
                   572
E value
                   4.0e-59
Match length
                   134
% identity
                   81
NCBI Description
                   (AC006418) unknown protein [Arabidopsis thaliana]
                   >gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   164539
Seq. ID
                   LIB3177-077-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q3860315
BLAST score
                   310
E value
                   2.0e-28
Match length
                   68
% identity
NCBI Description (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
Seq. No.
                   164540
Seq. ID
                   LIB3177-077-P1-K1-H7
Method
                  BLASTX
NCBI GI
                   g4417280
BLAST score
                   697
E value
                   1.0e-73
Match length
                  154
% identity
                   92
NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.
                  164541
Seq. ID
                  LIB3177-077-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4538979
BLAST score
                  170
E value
                  6.0e-12
                  90
Match length
% identity
                  56
NCBI Description (AL049487) putative protein [Arabidopsis thaliana]
Seq. No.
                  164542
Seq. ID
                  LIB3177-077-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  98
E value
                  2.0e-11
```



```
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   164543
Seq. ID
                   LIB3177-078-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2062164
BLAST score
                   708
E value
                   5.0e-75
Match length
                   150
% identity
                   58
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164544
Seq. ID
                   LIB3177-078-P1-K1-A10
Method
                  BLASTX
NCBI GI
                   g2117612
BLAST score
                  821
E value
                   3.0e-88
Match length
                  149
% identity
                  100
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                  164545
Seq. ID
                  LIB3177-078-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4160280
BLAST score
                  402
E value
                  3.0e-39
Match length
                  135
% identity
                  54
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                  164546
Seq. ID
                  LIB3177-078-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  153
E value
                  4.0e-10
Match length
                  45
% identity
                  69
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  164547
                  LIB3177-078-P1-K1-A3
Method
                  BLASTX
```

Seq. ID

NCBI GI g1621268 BLAST score 475 E value 9.0e-48 Match length 127 % identity 68

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 164548

Seq. ID LIB3177-078-P1-K1-A4

Method BLASTX



NCBI GI g421826 BLAST score 393 E value 4.0e-38 Match length 76 % identity 100

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thalianal

Seq. No. 164549

Seq. ID LIB3177-078-P1-K1-A5

Method BLASTX
NCBI GI 94522012
BLAST score 115
E value 2.0e-05
Match length 150
% identity 43

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 164550

Seq. ID LIB3177-078-P1-K1-A7

Method BLASTX
NCBI GI g4586047
BLAST score 470
E value 3.0e-47
Match length 110
% identity 81

NCBI Description (AC007020) putative ferritin protein [Arabidopsis thaliana]

>gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279)
hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No. 164551

Seq. ID LIB3177-078-P1-K1-A8

Method BLASTX
NCBI GI g132074
BLAST score 728
E value 2.0e-77
Match length 135
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 164552

Seq. ID LIB3177-078-P1-K1-A9

Method BLASTX
NCBI GI g4725950
BLAST score 218
E value 1.0e-17
Match length 126
% identity 44

NCBI Description (AL049730) putative Phospholipase D [Arabidopsis thaliana]

>gi_4725951_emb_CAB41722.1_ (AL049730) putative

proline-rich protein [Arabidopsis thaliana]

Seq. No. 164553



Seq. ID LIB3177-078-P1-K1-B1 Method BLASTX NCBI GI q3337356 BLAST score 613 E value 7.0e-64 Match length 136 % identity 90 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana] Seq. No. 164554 Seq. ID LIB3177-078-P1-K1-B10 Method BLASTX NCBI GI g3335340 BLAST score 590 E value 3.0e-61 Match length 138 % identity 80 NCBI Description (AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana] Seq. No. 164555 Seq. ID LIB3177-078-P1-K1-B12 Method BLASTX NCBI GI q2335106 BLAST score 142 E value 1.0e-08 Match length 130 % identity NCBI Description (AC002339) salt inducible protein-like [Arabidopsis thalianal Seq. No. 164556 Seq. ID LIB3177-078-P1-K1-B2 Method BLASTX NCBI GI g3337356 BLAST score 359 E value 4.0e-34 84 Match length 89 % identity NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana] Seq. No. 164557 Seq. ID LIB3177-078-P1-K1-B3 Method BLASTN NCBI GI g2828186 BLAST score 73

9.0e-33 E value Match length 256 % identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                   LIB3177-078-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q1931647
BLAST score
                   625
E value
                   2.0e-65
Match length
                   138
% identity
                   88
NCBI Description (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
Seq. No.
                   164559
Seq. ID
                   LIB3177-078-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   q1550740
BLAST score
                   611
E value
                   1.0e-63
Match length
                   119
% identity
                   99
NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
Seq. No.
                   164560
Seq. ID
                   LIB3177-078-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q4530591
BLAST score
                   690
E value
                   6.0e-73
Match length
                   138
% identity
                   100
NCBI Description
                  (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
                   >gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1
                   [Arabidopsis thaliana]
Seq. No.
                   164561
Seq. ID
                   LIB3177-078-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   736
E value
                   2.0e-78
Match length
                   141
% identity
                   99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603 pir A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164562
Seq. ID
                   LIB3177-078-P1-K1-B8
Method
                   BLASTN
```

NCBI GI q2477521 BLAST score 360 E value 0.0e + 00Match length 452 % identity 14



```
NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164563
Seq. ID
                  LIB3177-078-P1-K1-B9
Method
                  BLASTX
NCBI GI
                   g2506496
BLAST score
                   679
E value
                   1.0e-71
Match length
                   130
% identity
                   100
                  GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)
NCBI Description
                  >gi_1890156_emb_CAA72413_ (Y11727) gluthatione
                  S-transferase [Arabidopsis thaliana]
Seq. No.
                  164564
Seq. ID
                  LIB3177-078-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  q3510336
BLAST score
                  140
E value
                   3.0e-73
Match length
                  144
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164565
Seq. ID
                  LIB3177-078-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2264318
BLAST score
                  130
E value
                  4.0e-67
Match length
                  138
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164566
Seq. ID
                  LIB3177-078-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  601
E value
                  1.0e-62
Match length
                  117
% identity
                  73
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
```

Seq. ID LIB3177-078-P1-K1-C2

Method BLASTN NCBI GI g4468103 BLAST score 239 E value 1.0e-132

Match length 239 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)



```
Seq. No.
                   164568
Seq. ID
                   LIB3177-078-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q1703108
BLAST score
                   349
E value
                   4.0e-33
Match length
                   68
% identity
                   100
NCBI Description
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
                   thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   164569
Seq. No.
Seq. ID
                   LIB3177-078-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   g3659491
BLAST score
                   416
E value
                   0.0e+00
Match length
                   458
% identity
                   99
NCBI Description
                   Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164570
Seq. ID
                   LIB3177-078-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q4741940
BLAST score
                   595
E value
                   9.0e-62
Match length
                   110
% identity
                   67
NCBI Description (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                   164571
Seq. ID
                   LIB3177-078-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g399013
BLAST score
                   656
E value
                   6.0e-69
Match length
                   149
% identity
                   83
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                   >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                   thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]
                   >gi 445607_prf__1909354A adenylate translocator
```

Seq. ID LIB3177-078-P1-K1-C7

[Arabidopsis thaliana]

Method BLASTN NCBI GI g166833 BLAST score 43



```
E value
                   1.0e-15
Match length
                   82
% identity
                   100
NCBI Description Arabidopisis thaliana ribulose bisphosphate
                  carboxylase/oxygenase activase (rca) gene, complete cds
Seq. No.
                  164573
Seq. ID
                  LIB3177-078-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3420055
BLAST score
                  644
E value
                  1.0e-67
Match length
                  124
% identity
                  100
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  164574
Seq. ID
                  LIB3177-078-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4689366
BLAST score
                  381
E value
                  1.0e-36
Match length
                  139
% identity
                  55
NCBI Description (AF134155) RING finger protein [Arabidopsis thaliana]
Seq. No.
                  164575
Seq. ID
                  LIB3177-078-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4006858
BLAST score
                  232
E value
                  2.0e-19
Match length
                  62
% identity
                  63
NCBI Description (Z99707) cold acclimation protein homolog [Arabidopsis
                  thalianal
Seq. No.
                  164576
Seq. ID
                  LIB3177-078-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                  586
E value
                  7.0e-61
Match length
                  124
% identity
                  96
NCBI Description (U97200) cobalamin-independent methionine synthase
                  [Arabidopsis thaliana]
Seq. No.
                  164577
Seq. ID
                  LIB3177-078-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3660471
BLAST score
                  440
E value
                  1.0e-43
Match length
                  121
% identity
```

22039

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

Match length

% identity

145

54



subunit [Arabidopsis thaliana]

```
Seq. No.
                   164578
Seq. ID
                  LIB3177-078-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  587
E value
                   5.0e-61
Match length
                  109
% identity
                   99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  164579
Seq. No.
                  LIB3177-078-P1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4678340
BLAST score
                  253
E value
                  1.0e-140
Match length
                  368
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11
                  (ESSA project)
                  164580
Seq. No.
Seq. ID
                  LIB3177-078-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  546
E value
                  5.0e-56
Match length
                  144
% identity
                  74
NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                  164581
Seq. ID
                  LIB3177-078-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2281115
BLAST score
                  691
E value
                  5.0e-73
Match length
                  153
% identity
                  90
NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis
                  thaliana]
Seq. No.
                  164582
Seq. ID
                  LIB3177-078-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  479
E value
                  3.0e-48
```

22040

NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTN

q3702730



```
Seq. No.
                   164583
Seq. ID
                   LIB3177-078-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g3688799
BLAST score
                   666
E value
                   4.0e-70
Match length
                   133
% identity
                   99
NCBI Description
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                   thaliana]
Seq. No.
                   164584
Seq. ID
                   LIB3177-078-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   g3420042
BLAST score
                   136
E value
                   2.0e-70
Match length
                   420
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164585
Seq. ID
                   LIB3177-078-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q1621539
BLAST score
                   529
E value
                   4.0e-60
Match length
                   126
% identity
                   45
NCBI Description (U28415) annexin-like protein [Arabidopsis thaliana]
Seq. No.
                   164586
Seq. ID
                  LIB3177-078-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3402716
BLAST score
                  218
E value
                  1.0e-17
Match length
                  114
% identity
                   47
NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164587
Seq. ID
                  LIB3177-078-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  q3288823
BLAST score
                  639
E value
                  6.0e-67
Match length
                  127
% identity
                  100
NCBI Description (AF063852) FUS5 [Arabidopsis thaliana]
Seq. No.
                  164588
                  LIB3177-078-P1-K1-E12
Seq. ID
```



```
BLAST score
                   90
E value
                   4.0e-43
Match length
                   97
                   99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164589
Seq. ID
                  LIB3177-078-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                  683
                  4.0e-72
E value
Match length
                  128
                  100
% identity
NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana]
                  164590
Seq. No.
                  LIB3177-078-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g516248
BLAST score
                  85
E value
                  5.0e-40
Match length
                  92
% identity
                  99
NCBI Description A.thaliana gene for porphobilinogen deaminase
Seq. No.
                  164591
                  LIB3177-078-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1514639
BLAST score
                  726
E value
                  4.0e-77
Match length
                  150
% identity
NCBI Description (X85181) alpha-glucan phosphorylase [Spinacia oleracea]
Seq. No.
                  164592
Seq. ID
                  LIB3177-078-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g4733953
BLAST score
                  326
E value
                  0.0e+00
Match length
                  350
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                  sequence, complete sequence
Seq. No.
                  164593
Seq. ID
                  LIB3177-078-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  72
E value
                  3.0e-32
Match length
                  154
% identity
                  94
```

22042

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10



(ESSA project)

```
Seq. No.
                  164594
Seq. ID
                  LIB3177-078-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  q1279569
BLAST score
                  86
E value
                  2.0e-40
Match length
                  260
                  90
% identity
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
Seq. No.
                  164595
Seq. ID
                  LIB3177-078-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g416652
BLAST score
                  415
E value
                  1.0e-40
Match length
                  136
% identity
                  59
NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
                  PCNT107) >gi_19793_emb_CAA39707_ (X56266) auxin-induced
                  protein [Nicotiana tabacum]
Seq. No.
                  164596
Seq. ID
                  LIB3177-078-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q1071912
BLAST score
                  649
E value
                  4.0e-68
Match length
                  138
% identity
                  94
NCBI Description cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis
                  thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine
                  synthase [Arabidopsis thaliana]
Seq. No.
                  164597
Seq. ID
                  LIB3177-078-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  637
E value
                  1.0e-66
Match length
                  128
% identity
                  97
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 2505871 emb_CAA72909_ (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb T21121, gb_Z17755, gb_\overline{R}64776 and
```

gb R30430 come from this gene. [Arabidopsis thaliana]



164598

>gi_4538910_emb_CAB39647.1 (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. Seq. ID LIB3177-078-P1-K1-F2 Method BLASTN NCBI GI g4454447 BLAST score 368 E value 0.0e+00Match length 455

98 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164599 LIB3177-078-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI g4835235 BLAST score 241 E value 2.0e-20 Match length 103 % identity 49

NCBI Description (AL049862) putative protein [Arabidopsis thaliana]

Seq. No. 164600

Seq. ID LIB3177-078-P1-K1-F5

Method BLASTX NCBI GI g132110 BLAST score 657 E value 4.0e-69 Match length 122 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164601

Seq. ID LIB3177-078-P1-K1-F6

Method BLASTX NCBI GI g4490330 BLAST score 773 E value 1.0e-82 Match length 151 % identity

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis

thaliana

Seq. No. 164602

Seq. ID LIB3177-078-P1-K1-F7

Method BLASTX NCBI GI g4741962 BLAST score 478 E value 4.0e-48 Match length 132



% identity 57

NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No. 164603

Seq. ID LIB3177-078-P1-K1-F8

Method BLASTX
NCBI GI g3063697
BLAST score 812
E value 3.0e-87
Match length 151
% identity 99

NCBI Description (AL022537) putative myb-protein (partial) [Arabidopsis

thaliana]

Seq. No. 164604

Seq. ID LIB3177-078-P1-K1-F9

Method BLASTX
NCBI GI g3776001
BLAST score 638
E value 8.0e-67
Match length 128
% identity 95

NCBI Description (AJ010464) RNA helicase [Arabidopsis thaliana]

Seq. No. 164605

Seq. ID LIB3177-078-P1-K1-G1

Method BLASTX
NCBI GI g2119846
BLAST score 752
E value 3.0e-80
Match length 143
% identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164606

Seq. ID LIB3177-078-P1-K1-G11

Method BLASTX
NCBI GI g4587541
BLAST score 700
E value 4.0e-74
Match length 137
% identity 99

NCBI Description (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase

with GDSL-motif family. ESTs gb_T44453, gb_T04815,

gb_T45993, gb_R30138, gb_AI0995 $\overline{7}$ 0 and gb_T $\overline{2}$ 2281 come from

this gene. [Arabidopsis thaliana]

Seq. No. 164607

Seq. ID LIB3177-078-P1-K1-G12

Method BLASTX NCBI GI g1362002



```
BLAST score
                   278
E value
                   4.0e-25
                   58
Match length
% identity
                   95
NCBI Description
                  protein kinase 1 - Arabidopsis thaliana >qi 166817 (L05561)
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  164608
                  LIB3177-078-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128205
BLAST score
                  687
E value
                  1.0e-72
Match length
                  151
                  89
% identity
NCBI Description (AC004077) putative pyruvate dehydrogenase complex E1 beta
                  subunit [Arabidopsis thaliana]
Seq. No.
                  164609
Seq. ID
                  LIB3177-078-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g3201608
BLAST score
                  218
E value
                  1.0e-119
Match length
                  448
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F7F1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164610
Seq. ID
                  LIB3177-078-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4455210
BLAST score
                  348
E value
                  7.0e - 33
Match length
                  77
% identity
NCBI Description
                  (AL035440) putative aspartate-tRNA ligase [Arabidopsis
                  thaliana]
Seq. No.
                  164611
Seq. ID
                  LIB3177-078-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g3201608
BLAST score
                  40
E value
                  3.0e-13
Match length
                  76
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB3177-078-P1-K1-G6

Method BLASTN
NCBI GI g3540210
BLAST score 91

E value 8.0e-44



Match length 155 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164613

LIB3177-078-P1-K1-G7 Seq. ID

Method BLASTX NCBI GI q282865 BLAST score 666 E value 4.0e-70 Match length 132 72 % identity

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi 166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164614

Seq. ID LIB3177-078-P1-K1-G8

Method BLASTX NCBI GI g2244750 BLAST score 733 E value 5.0e-78 Match length 150 % identity

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 164615

Seq. ID LIB3177-078-P1-K1-G9

Method BLASTX NCBI GI q2506443 BLAST score 364 E value 4.0e-35 75 Match length % identity 99

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi_2117520_pir__JQ1285
glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi_1402885_emb_CAA66816_ (X98130)
glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No. 164616

Seq. ID LIB3177-078-P1-K1-H1

Method BLASTX NCBI GI g2317729 BLAST score 694 E value 2.0e-73 Match length 130

NCBI Description



```
% identity
NCBI Description
                   (AF013627) reversibly glycosylated polypeptide-1
                   [Arabidopsis thaliana]
                   164617
Seq. No.
Seq. ID
                   LIB3177-078-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2191138
BLAST score
                   391
E value
                   4.0e-38
Match length
                   80
% identity
                   99
NCBI Description
                  (AF007269) A IG002N01.18 gene product [Arabidopsis
                   thalianal
                   164618
Seq. No.
                   LIB3177-078-P1-K1-H11
Seq. ID
Method
                   BLASTX
                   g3461817
NCBI GI
BLAST score
                   301
E value
                   2.0e-27
Match length
                   134
% identity
                   45
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164619
Seq. ID
                   LIB3177-078-P1-K1-H12
Method
                  BLASTX
NCBI GI
                   q4582468
BLAST score
                   570
E value
                   7.0e-59
Match length
                   118
% identity
                   98
NCBI Description
                  (AC007071) putative 40S ribosomal protein; contains
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   164620
Seq. ID
                   LIB3177-078-P1-K1-H2
Method
                  BLASTX
NCBI GI
                   q4584541
BLAST score
                   592
E value
                   2.0e-61
Match length
                   115
% identity
                   100
NCBI Description (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  164621
Seq. ID
                  LIB3177-078-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3249086
BLAST score
                  217
E value
                  2.0e-17
Match length
                  148
% identity
                  66
```

22048

(AC004473) Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) gb AF006086 from Homo

% identity

100





```
sapiens. EST gb Z37222 comes [Arabidopsis thaliana]
```

Seq. No. 164622 Seq. ID LIB3177-078-P1-K1-H4 Method BLASTX NCBI GI g2062164 BLAST score 528 E value 4.0e-54Match length 101 % identity 99 (AC001645) jasmonate inducible protein isolog [Arabidopsis NCBI Description thalianal Seq. No. 164623 Seq. ID LIB3177-078-P1-K1-H5 Method BLASTX NCBI GI q4262174 BLAST score 774 E value 8.0e-83 Match length 144% identity 99 NCBI Description (AC005508) 9058 [Arabidopsis thaliana] Seq. No. 164624 Seq. ID LIB3177-078-P1-K1-H6 Method BLASTX NCBI GI q1173218 BLAST score 494 E value 6.0e-50 Match length 109 % identity 90 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] Seq. No. 164625 Seq. ID LIB3177-078-P1-K1-H8 Method BLASTX NCBI GI q3261659 BLAST score 119 E value 9.0e-10 90 Match length % identity 42 NCBI Description (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis] Seq. No. 164626 LIB3177-079-P1-K1-A1 Seq. ID Method BLASTN NCBI GI q4581084 BLAST score 278 E value 1.0e-155 Match length 360

22049

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence



Seq. ID LIB3177-079-P1-K1-A10

Method BLASTX NCBI GI q2104677 BLAST score 232 E value 3.0e-19 Match length 111 % identity 49

NCBI Description (X97904) transcription factor [Vicia faba]

Seq. No. 164628

Seq. ID LIB3177-079-P1-K1-A11

Method BLASTX NCBI GI g1170203 BLAST score 335 E value 2.0e-31 Match length 93 72 % identity

NCBI Description GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi 454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No. 164629

Seq. ID LIB3177-079-P1-K1-A12

Method BLASTX NCBI GI g3776029 BLAST score 771 E value 2.0e-82 Match length 151 % identity 100

NCBI Description (AJ010476) RNA helicase [Arabidopsis thaliana]

Seq. No. 164630

Seq. ID LIB3177-079-P1-K1-A2

Method BLASTN NCBI GI g857373 BLAST score 233 E value 1.0e-128 Match length 314

100 % identity

NCBI Description Arabidopsis thaliana mRNA for phosphoinositide specific

phospholipase C, complete cds

Seq. No. 164631

Seq. ID LIB3177-079-P1-K1-A4

Method BLASTN NCBI GI g4454004 BLAST score 245 E value 1.0e-135 Match length 285 % identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 164632

Seq. ID LIB3177-079-P1-K1-A5

Method BLASTX NCBI GI q1495269



```
BLAST score
                   388
E value
                   1.0e-37
Match length
                  112
% identity
                  71
NCBI Description
                  (X97829) product similar to ccr protein, Citrus paradisi;
                  PIR: S52663 [Arabidopsis thaliana]
                  >gi 1550735 emb CAA66824 (X98130) unknown [Arabidopsis
                  thaliana]
                  164633
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g232031
BLAST score
                  332
E value
                  4.0e-31
Match length
                  115
                  54
% identity
NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224
                  translation elongation factor eEF-1 beta chain - rice
                  >gi_218161_dbj_BAA02253 (D12821) elongation factor 1 beta'
                  [Oryza sativa]
Seq. No.
                  164634
Seq. ID
                  LIB3177-079-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g166695
BLAST score
                  43
E value
                  2.0e-15
Match length
                  51
% identity
NCBI Description Arabidopsis thaliana recombination and DNA-damage
                  resistance protein (DRT112) mRNA, complete cds
Seq. No.
                  164635
Seq. ID
                  LIB3177-079-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q4262180
BLAST score
                  511
E value
                  4.0e-52
Match length
                  99
% identity
                  94
NCBI Description (AC005508) 29621 [Arabidopsis thaliana]
Seq. No.
                  164636
Seq. ID
                  LIB3177-079-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3047117
BLAST score
                  440
E value
                  8.0e-44
Match length
                  117
                  74
% identity
NCBI Description
                  (AF058919) similar to ATP-dependent RNA helicases
```

Seq. ID LIB3177-079-P1-K1-B11

[Arabidopsis thaliana]

Method BLASTX



NCBI GI g4741960 BLAST score 507 E value 2.0e-51Match length 116 % identity NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana] 164638 Seq. No. Seq. ID LIB3177-079-P1-K1-B12 Method BLASTX NCBI GI g1402908 BLAST score 670 E value 1.0e-70 Match length 129 % identity 100 NCBI Description (X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana] Seq. No. 164639 LIB3177-079-P1-K1-B2 Seq. ID Method BLASTX NCBI GI g1708577 BLAST score 293 1.0e-26 E value Match length 68 % identity 68 TRYPSIN INHIBITOR 2 PRECURSOR (MTI-2) NCBI Description >gi_2129818_pir__S65661 trypsin inhibitor 2 - white mustard >gi_1054853 emb_CAA58994 (X84208) trypsin inhibitor 2 [Sinapis alba] >gi_2791356 emb CAA76116 (Y16190) trypsin inhibitor 2 [Sinapis alba] Seq. No. 164640 Seq. ID LIB3177-079-P1-K1-B3 Method BLASTX NCBI GI g3261659 BLAST score 166 E value 1.0e-11 Match length 66 % identity 48 NCBI Description (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis] Seq. No. 164641 Seq. ID LIB3177-079-P1-K1-B4 Method BLASTN

NCBI GI g3236479 BLAST score 137 E value 5.0e-71 Match length 365 97 % identity

NCBI Description Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8

cM, complete sequence

Seq. No. 164642

NCBI Description



Seq. ID LIB3177-079-P1-K1-B5 Method BLASTX g1170089 NCBI GI BLAST score 656 E value 5.0e-69 Match length 129 100 % identity NCBI Description GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi 481822 pir S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana] Seq. No. 164643 LIB3177-079-P1-K1-B6 Seq. ID Method BLASTX NCBI GI g3176690 736 BLAST score E value 3.0e-78 Match length 155 % identity 99 NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana] Seq. No. 164644 Seq. ID LIB3177-079-P1-K1-B7 Method BLASTX NCBI GI g1402914 BLAST score 463 E value 2.0e-46 Match length 92 % identity 100 NCBI Description (X98318) peroxidase [Arabidopsis thaliana] Seq. No. 164645 Seq. ID LIB3177-079-P1-K1-B8 Method BLASTX NCBI GI q3702323 BLAST score 410 E value 3.0e-40Match length 93 % identity NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] Seq. No. 164646 Seq. ID LIB3177-079-P1-K1-B9 Method BLASTX NCBI GI g2281086 BLAST score 182 E value 1.0e-13 Match length 62 % identity

22053

[Arabidopsis thaliana]

(AC002333) indole-3-acetate beta-glucosyltransferase isolog



```
Seq. No.
                   164647
Seq. ID
                   LIB3177-079-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   q3367500
BLAST score
                  108
E value
                   1.0e-53
Match length
                   398
                   100
% identity
NCBI Description REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
                  TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164648
Seq. ID
                  LIB3177-079-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2980757
BLAST score
                  286
E value
                   1.0e-160
Match length
                   343
                   95
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
                  (ESSAII project)
Seq. No.
                  164649
Seq. ID
                  LIB3177-079-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g3738275
BLAST score
                  384
E value
                  0.0e + 00
Match length
                  384
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164650
Seq. ID
                  LIB3177-079-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  602
E value
                  1.0e-62
Match length
                  110
% identity
                  100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  164651
Seq. ID
                  LIB3177-079-P1-K1-C2
```

Method BLASTX
NCBI GI g4115377
BLAST score 449
E value 7.0e-45
Match length 109
% identity 78

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 164652



```
Seq. ID
                  LIB3177-079-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q2407802
BLAST score
                  359
E value
                   4.0e-34
Match length
                  75
                  97
% identity
NCBI Description
                  (Y12576) histone H2B [Arabidopsis thaliana]
                  164653
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q2160182
BLAST score
                  188
E value
                  4.0e-14
Match length
                  133
% identity
                  38
NCBI Description
                  (AC000132) ESTs gb ATTS1236, gb T43334, gb N97019, gb AA395203
                  come from this gene. [Arabidopsis thaliana]
                  164654
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q2911042
BLAST score
                  579
E value
                  6.0e-60
Match length
                  120
% identity
                  100
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  164655
Seq. ID
                  LIB3177-079-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  421
E value
                  1.0e-41
Match length
                  85
% identity
                  95
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  164656
Seq. ID
                  LIB3177-079-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2708751
BLAST score
                  210
E value
                  8.0e-17
Match length
                  78
% identity
                  58
NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID LIB3177-079-P1-K1-C8

Method BLASTX NCBI GI g2832625



```
BLAST score
                   330
E value
                   7.0e-31
Match length
                   70
% identity
                   86
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   164658
                   LIB3177-079-P1-K1-C9
Seq. ID
Method
                   BLASTN
```

Method BLASTN
NCBI GI g2342673
BLAST score 245
E value 1.0e-135
Match length 249
% identity 100

NCBI Description Sequence of BAC F7G19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 164659 Seq. ID LIB3177-079-P1-K1-D10 Method BLASTN

Method BLASTN
NCBI GI g2815404
BLAST score 158
E value 9.0e-84
Match length 222
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMG4, complete sequence [Arabidopsis thaliana]

Seq. No. 164660

Seq. ID LIB3177-079-P1-K1-D11

Method BLASTX
NCBI GI g282865
BLAST score 508
E value 7.0e-52
Match length 104
% identity 68

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164661

Seq. ID LIB3177-079-P1-K1-D12

Method BLASTN
NCBI GI g2351062
BLAST score 182
E value 8.0e-98
Match length 394
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 164662

Seq. ID LIB3177-079-P1-K1-D2

Method BLASTX



NCBI GI g1621268 BLAST score 149 E value 4.0e-10 Match length 35 % identity 80 (Z81012) unknown [Ricinus communis] NCBI Description Seq. No. 164663 LIB3177-079-P1-K1-D3 Seq. ID Method BLASTX NCBI GI g2739371 BLAST score 571 E value 5.0e-59 Match length 110 % identity 100 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana] 164664 Seq. No. Seq. ID LIB3177-079-P1-K1-D4 Method BLASTX NCBI GI g132102 BLAST score 726 E value 4.0e-77 Match length 140 % identity 97 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4. $\overline{1.1}$.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana] Seq. No. 164665 Seq. ID LIB3177-079-P1-K1-D5 Method BLASTN NCBI GI q2673901 BLAST score 255 E value 1.0e-141 Match length 438 % identity 99 NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 164666 Seq. ID LIB3177-079-P1-K1-D6 Method BLASTX g2244762 478 4.0e-48

NCBI GI BLAST score E value Match length 119 % identity 75

NCBI Description (Z97335) major latex protein [Arabidopsis thaliana]

Seq. No. 164667

Seq. ID LIB3177-079-P1-K1-D7

Method BLASTX NCBI GI g2642215

NCBI Description



```
BLAST score
                   185
E value
                   7.0e-14
Match length
                   34
                  100
% identity
NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]
                  164668
Seq. No.
                  LIB3177-079-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678322
BLAST score
                  530
E value
                  2.0e-54
Match length
                  121
                  87
% identity
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
                  164669
Seq. No.
                  LIB3177-079-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2880049
BLAST score
                  265
E value
                  4.0e-23
Match length
                  102
                   55
% identity
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164670
                  LIB3177-079-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                   385
E value
                   3.0e - 37
Match length
                  81
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  164671
Seq. ID
                  LIB3177-079-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2842490
BLAST score
                  447
E value
                  2.0e-44
Match length
                  120
% identity
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                   164672
Seq. ID
                  LIB3177-079-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q4503523
BLAST score
                  172
E value
                  3.0e-27
Match length
                  154
% identity
                   47
```

22058

(AL022313) EIF3-P66 [Homo sapiens]

UNKNOWN >gi_2351378 (U54558) translation initiation factor eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_

NCBI Description

complete cds



```
164673
Seq. No.
Seq. ID
                   LIB3177-079-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q2191138
BLAST score
                   597
E value
                   5.0e-62
Match length
                   119
% identity
                   99
NCBI Description
                   (AF007269) A_IG002N01.18 gene product [Arabidopsis
                   thaliana]
Seq. No.
                   164674
                   LIB3177-079-P1-K1-E2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2244991
BLAST score
                   309
E value
                   1.0e-173
Match length
                   414
                   100
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   164675
                   LIB3177-079-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4507131
BLAST score
                   329
E value
                   1.0e-30
Match length
                   74
% identity
                   78
                   small nuclear ribonucleoprotein polypeptide F
NCBI Description
                   >gi_1085384_pir__S55053 Sm protein F - human
                   >gi_806564_emb_CAA59688_ (X85372) Sm protein F [Homo
                   sapiens]
Seq. No.
                   164676
Seq. ID
                   LIB3177-079-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   q3033373
BLAST score
                   120
E value
                   8.0e-61
Match length
                   132
% identity
                   82
                   Arabidopsis thaliana chromosome II BAC F19I3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164677
Seq. ID
                   LIB3177-079-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   q3883123
BLAST score
                   181
E value
                   2.0e-97
Match length
                   224
% identity
                   97
```

22059

Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,

Seq. ID

Method

164683

BLASTN

LIB3177-079-P1-K1-F11



```
Seq. No.
                   164678
Seq. ID
                  LIB3177-079-P1-K1-E6
Method
                  BLASTX
NCBI GI
                   q4678328
BLAST score
                   387
E value
                   2.0e-37
Match length
                   128
% identity
                   57
NCBI Description
                   (AL049658) aldehyde dehydrogenase (NAD+)-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   164679
Seq. ID
                  LIB3177-079-P1-K1-E7
Method
                  BLASTN
                   g2275194
NCBI GI
BLAST score
                  73
E value
                   7.0e-33
Match length
                   130
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T08I13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164680
Seq. ID
                  LIB3177-079-P1-K1-E8
Method
                  BLASTN
NCBI GI
                   q16249
BLAST score
                   97
E value
                   2.0e-47
Match length
                  104
% identity
                   98
NCBI Description A.thaliana mRNA for Cu, Zn superoxide dismutase
Seq. No.
                   164681
Seq. ID
                  LIB3177-079-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g3869065
BLAST score
                  273
E value
                  1.0e-152
Match length
                  331
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24M7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164682
Seq. ID
                  LIB3177-079-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g4587681
BLAST score
                  484
E value
                  8.0e-49
                  94
Match length
% identity
                  100
NCBI Description
                 (AC007197) hypothetical protein [Arabidopsis thaliana]
```



NCBI GI g2828186 BLAST score 231 E value 1.0e-127 Match length 442 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 164684

Seq. ID LIB3177-079-P1-K1-F12

Method BLASTX
NCBI GI g4835226
BLAST score 171
E value 3.0e-12
Match length 54
% identity 59

NCBI Description (AL049862) putative protein [Arabidopsis thaliana]

Seq. No. 164685

Seq. ID LIB3177-079-P1-K1-F2

Method BLASTX
NCBI GI 94218123
BLAST score 423
E value 1.0e-41
Match length 136
% identity 65

NCBI Description (AL035353) photosystem I subunit PSI-E-like protein

[Arabidopsis thaliana]

Seq. No. 164686

Seq. ID LIB3177-079-P1-K1-F4

Method BLASTX
NCBI GI g115767
BLAST score 670
E value 1.0e-70
Match length 124
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164687

Seq. ID LIB3177-079-P1-K1-F5

Method BLASTX
NCBI GI g1399275
BLAST score 490
E value 2.0e-49
Match length 108
% identity 85

NCBI Description (U31835) calmodulin-domain protein kinase CDPK isoform 6

[Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6

(calmodulin-domain protein kinase isoform 6) [Arabidopsis

thaliana]

Seq. ID

164693

LIB3177-079-P1-K1-G3



```
Seq. No.
                  164688
Seq. ID
                  LIB3177-079-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g16375
BLAST score
                  75
E value
                  9.0e-35
Match length
                  83
% identity
                  98
NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
                  protein
                  164689
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2492514
BLAST score
                  542
E value
                  1.0e-55
Match length
                  125
% identity
                  86
NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
                  >gi_1483215_emb_CAA68141 (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
                  164690
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  576
E value
                  1.0e-59
Match length
                  141
% identity
                  75
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  164691
Seq. ID
                  LIB3177-079-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q4678705
BLAST score
                  55
E value
                  4.0e-22
Match length
                  225
% identity
                  82
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                  (ESSA project)
Seq. No.
                  164692
Seq. ID
                  LIB3177-079-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  g2244868
BLAST score
                  706
E value
                  7.0e-75
Match length
                  135
% identity
                  100
NCBI Description (Z97337) cytochrome P450 [Arabidopsis thaliana]
```



```
BLASTX
Method
NCBI GI
                  q464621
BLAST score
                  197
                  9.0e-16
E value
Match length
                  46
                  87
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                  [Mesembryanthemum crystallinum]
                  164694
Seq. No.
                  LIB3177-079-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g115767
NCBI GI
BLAST score
                  775
E value
                  7.0e-83
                  147
Match length
% identity
                  100
                 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164695
                  LIB3177-079-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1575754
BLAST score
                  480
E value
                  3.0e-48
Match length
                  129
% identity
                  78
NCBI Description
                  (U70616) ADP glucose pyrophosphorylase small subunit
                  [Arabidopsis thaliana]
                  164696
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g4468801
BLAST score
                  246
E value
                  1.0e-136
Match length
                  363
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                  (ESSA project)
Seq. No.
                  164697
```

LIB3177-079-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI g132074 BLAST score 678 E value 1.0e-71 Match length 125 % identity 99



NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

164698 Seq. No.

Seq. ID LIB3177-079-P1-K1-G9

Method BLASTN NCBI GI g4757409 BLAST score 77 E value 4.0e-35 Match length 432

% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVC8, complete sequence

164699 Seq. No.

Seq. ID LIB3177-079-P1-K1-H1

67

Method BLASTX NCBI GI g3478700 BLAST score 508 E value 9.0e-52 Match length 113 % identity 88

NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]

Seq. No. 164700

Seq. ID LIB3177-079-P1-K1-H10

Method BLASTX NCBI GI g4263791 BLAST score 333 E value 4.0e-31 Match length 61 % identity 100

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thalianal

Seq. No. 164701

Seq. ID LIB3177-079-P1-K1-H11

Method BLASTX NCBI GI q1172977 BLAST score 400 E value 2.0e-39 Match length 87 % identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 164702

Seq. ID LIB3177-079-P1-K1-H12

Method BLASTX NCBI GI g2894596 BLAST score 291 E value 2.0e-38 Match length 118 % identity 67

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  164703
Seq. ID
                  LIB3177-079-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2828267
BLAST score
                  521
E value
                   4.0e-53
Match length
                  127
% identity
                  83
NCBI Description (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
Seq. No.
                  164704
                  LIB3177-079-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2252848
BLAST score
                  151
E value
                  2.0e-79
Match length
                  302
% identity
                  97
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                  164705
Seq. ID
                  LIB3177-079-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g2264310
BLAST score
                  191
E value
                  1.0e-103
Match length
                  392
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164706
Seq. ID
                  LIB3177-079-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3913418
BLAST score
                  633
E value
                  2.0e-66
Match length
                  121
% identity
                  99
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi 1531763 emb CAA69073 (Y07765)
                  S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
Seq. No.
                  164707
Seq. ID
                  LIB3177-079-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3184098
BLAST score
                  416
                  8.0e-41
E value
Match length
                  141
% identity
                  59
```

NCBI Description

Seq. ID LIB3177-079-P1-K1-H8

pombe]

22065

(AL023777) coenzyme a synthetase [Schizosaccharomyces



Method BLASTN
NCBI GI g4467094
BLAST score 312
E value 1.0e-175
Match length 320
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10

(ESSA project)

Seq. No. 164709

Seq. ID LIB3177-080-P1-K1-A1

Method BLASTN
NCBI GI g4519191
BLAST score 120
E value 2.0e-61
Match length 141
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9P8, complete sequence

Seq. No. 164710

Seq. ID LIB3177-080-P1-K1-A10

Method BLASTX
NCBI GI g4417280
BLAST score 521
E value 3.0e-53
Match length 124
% identity 86

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 164711

Seq. ID LIB3177-080-P1-K1-A12

Method BLASTN
NCBI GI g3985934
BLAST score 115
E value 7.0e-58
Match length 309
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 164712

Seq. ID LIB3177-080-P1-K1-A2

Method BLASTX
NCBI GI g4539419
BLAST score 288
E value 1.0e-27
Match length 77
% identity 82

NCBI Description (AL049171) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No. 164713

Seq. ID LIB3177-080-P1-K1-A5

Method BLASTX NCBI GI g4678349 BLAST score 312



E value 6.0e-29 Match length 91

% identity 30

NCBI Description (AL049659) putative protein [Arabidopsis thaliana]

Seq. No. 164714

LIB3177-080-P1-K1-A6 Seq. ID

Method BLASTN NCBI GI g3985952 BLAST score 274 E value 1.0e-153 Match length 290 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 164715

LIB3177-080-P1-K1-A8 Seq. ID

Method BLASTN NCBI GI q4741959 BLAST score 56 E value 2.0e-23 Match length 56 % identity - 100

NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete

cds

164716 Seq. No.

LIB3177-080-P1-K1-A9 Seq. ID

Method BLASTN NCBI GI q4581161 BLAST score 89 E value 7.0e-43

Match length 121 % identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 164717

Seq. ID LIB3177-080-P1-K1-B1

Method BLASTX NCBI GI g1172872 BLAST score 414 E value 4.0e-41 Match length 76 % identity 100

NCBI Description

CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_

(D13042) thiol protease [Arabidopsis thaliana]

>gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 164718

Seq. ID LIB3177-080-P1-K1-B10

Method BLASTN NCBI GI g2244788



```
BLAST score
                    51
                    1.0e-20
. E value
Match length
                    59
                    97
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
 Seq. No.
                   164719
                   LIB3177-080-P1-K1-B11
 Seq. ID
Method
                   BLASTN
```

Method BLASTN
NCBI GI g4510323
BLAST score 135
E value 4.0e-70
Match length 201
% identity 54

NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10

cM, complete sequence

Seq. No. 164720

Seq. ID LIB3177-080-P1-K1-B12

Method BLASTN
NCBI GI g2656028
BLAST score 213
E value 1.0e-116
Match length 243
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 164721

Seq. ID LIB3177-080-P1-K1-B3

Method BLASTX
NCBI GI g4835233
BLAST score 344
E value 1.0e-32
Match length 70
% identity 99

NCBI Description (AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No. 164722

Seq. ID LIB3177-080-P1-K1-B4

Method BLASTN
NCBI GI g3252804
BLAST score 82
E value 6.0e-39
Match length 82
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F26C24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164723

Seq. ID LIB3177-080-P1-K1-B5

Method BLASTX
NCBI GI g1732570
BLAST score 148
E value 5.0e-10



Match length 28 % identity 100

NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No. 164724

Seq. ID LIB3177-080-P1-K1-B6

Method BLASTN
NCBI GI g1769904
BLAST score 87
E value 1.0e-41
Match length 139
% identity 91

NCBI Description A.thaliana psbP gene

Seq. No. 164725

Seq. ID LIB3177-080-P1-K1-B8

Method BLASTN
NCBI GI g3355463
BLAST score 124
E value 1.0e-63
Match length 164
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F12L6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164726

Seq. ID LIB3177-080-P1-K1-B9

Method BLASTX
NCBI GI g4204285
BLAST score 282
E value 9.0e-26
Match length 63

% identity 81

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 164727

Seq. ID LIB3177-080-P1-K1-C12

Method BLASTX
NCBI GI g1169201
BLAST score 286
E value 7.0e-26
Match length 87
% identity 72

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

>gi_421830_pir__S33707 DRT112 protein - Arabidopsis

thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 164728

Seq. ID LIB3177-080-P1-K1-C2

Method BLASTN
NCBI GI g4691223
BLAST score 133
E value 6.0e-69
Match length 197
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15



(ESSA project)

```
Seq. No.
                   164729
Seq. ID
                   LIB3177-080-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q4691223
BLAST score
                   131
E value
                   6.0e-68
Match length
                   135
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
```

Seq. No. 164730

Seq. ID LIB3177-080-P1-K1-C4

Method BLASTX
NCBI GI 9730645
BLAST score 229
E value 1.0e-19
Match length 52
% identity 90

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 164731

Seq. ID LIB3177-080-P1-K1-C5

Method BLASTX
NCBI GI g2738248
BLAST score 491
E value 6.0e-50
Match length 92
% identity 99

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 164732

Seq. ID LIB3177-080-P1-K1-C6

Method BLASTN
NCBI GI g2264316
BLAST score 52
E value 2.0e-20

Match length 304 % identity 40

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRO11, complete sequence [Arabidopsis thaliana]

Seq. No. 164733

Seq. ID LIB3177-080-P1-K1-C7

Method BLASTN NCBI GI g2618601 BLAST score 148



```
5.0e-78
E value
Match length
                  160
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHJ24, complete sequence [Arabidopsis thaliana]
                  164734
Seq. No.
                  LIB3177-080-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g3023857
NCBI GI
BLAST score
                  238
                  1.0e-20
E value
Match length
                  49
                  53
% identity
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN >gi_629591_pir__S48839 guanine nucleotide
                  regulatory protein - rape >gi_563335_emb_CAA83924_ (Z33643)
                  guanine nucleotide regulatory protein [Brassica napus]
                  164735
Seq. No.
                  LIB3177-080-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570338
BLAST score
                  432
E value
                   7.0e-43
                  87
Match length
% identity
                  100
NCBI Description (U90927) glyoxalase II isozyme [Arabidopsis thaliana]
Seq. No.
                  164736
Seq. ID
                  LIB3177-080-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4454036
BLAST score
                   427
E value
                   2.0e-42
Match length
                  79
% identity
                   99
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                   thaliana]
Seq. No.
                   164737
Seq. ID
                  LIB3177-080-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g99759
BLAST score
                  415
E value
                   4.0e-41
Match length
                  82
% identity
                  superoxide dismutase (EC 1.15.1.1) (Fe) - Arabidopsis
NCBI Description
                  thaliana (fragment)
Seq. No.
                   164738
```

Seq. ID LIB3177-080-P1-K1-D11

Method BLASTX
NCBI GI g3157924
BLAST score 190
E value 2.0e-14



Match length 58 % identity 71

NCBI Description (AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883,

gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951

come from this gene. There is a similar ORF on the opposite strand. [... >gi 4063707 (AF104327) extensin-like

protein [Arabidopsis thaliana]

Seq. No. 164739

Seq. ID LIB3177-080-P1-K1-D12

Method BLASTX
NCBI GI g4406814
BLAST score 429
E value 2.0e-42
Match length 88
% identity 98

% identity 98
NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis

thaliana]

Seq. No. 164740

Seq. ID LIB3177-080-P1-K1-D2

Method BLASTX
NCBI GI g1363489
BLAST score 289
E value 1.0e-26
Match length 54

Match length 54 % identity 100

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis

thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No. 164741

Seq. ID LIB3177-080-P1-K1-D3

Method BLASTX
NCBI GI g4741952
BLAST score 270
E value 2.0e-24
Match length 56
% identity 93

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 164742

Seq. ID LIB3177-080-P1-K1-D4

Method BLASTX
NCBI GI g2129630
BLAST score 654
E value 9.0e-69
Match length 118
% identity 99

NCBI Description lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_

(X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)

unknown [Arabidopsis thaliana]

Seq. No. 164743

Seq. ID LIB3177-080-P1-K1-D7

Method BLASTX



NCBI GI g2262164
BLAST score 201
E value 3.0e-16
Match length 64
% identity 66

NCBI Description (AC002329) putative obtusifoliol 14-alpha demethylase

[Arabidopsis thaliana]

Seq. No. 164744

Seq. ID LIB3177-080-P1-K1-D8

Method BLASTX
NCBI GI g4725950
BLAST score 237
E value 5.0e-20
Match length 92
% identity 58

NCBI Description (AL049730) putative Phospholipase D [Arabidopsis thaliana]

>gi_4725951_emb_CAB41722.1_ (AL049730) putative
proline-rich protein [Arabidopsis thaliana]

Seq. No. 164745

Seq. ID LIB3177-080-P1-K1-D9

Method BLASTN
NCBI GI g4335711
BLAST score 178
E value 1.0e-95
Match length 202
% identity 98

% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC F9013 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164746

Seq. ID LIB3177-080-P1-K1-E1

Method BLASTX
NCBI GI g115767
BLAST score 630
E value 6.0e-66
Match length 123
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164747

Seq. ID LIB3177-080-P1-K1-E10

Method BLASTX
NCBI GI g3193323
BLAST score 584
E value 1.0e-60
Match length 116
% identity 99

NCBI Description (AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm,

score: 78.35); identical to Arabidopsis 40S ribosomal



protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

 Seq. No.
 164748

 Seq. ID
 LIB3177-080-P1-K1-E11

 Method
 BLASTX

 NCBI GI
 g1169201

 BLAST score
 328

 E value
 1.0e-30

E value 1.06
Match length 95
% identity 76

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

>gi_421830_pir__S33707 DRT112 protein - Arabidopsis

thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 164749

Seq. ID LIB3177-080-P1-K1-E12

Method BLASTX
NCBI GI g133872
BLAST score 235
E value 1.0e-19
Match length 71
% identity 62

NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)

>gi_282838_pir__S26494 ribosomal protein S1, chloroplast spinach >gi_322404_pir__A44121 small subunit ribosomal
protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi_170143 (M82923) chloroplast ribosomal protein S1

[Spinacia oleracea]

Seq. No. 164750

Seq. ID LIB3177-080-P1-K1-E2

Method BLASTX
NCBI GI g1732570
BLAST score 47
E value 3.0e-27
Match length 80
% identity 81

NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No. 164751

Seq. ID LIB3177-080-P1-K1-E3

Method BLASTN
NCBI GI g3985931
BLAST score 132
E value 3.0e-68
Match length 234
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21H1, complete sequence [Arabidopsis thaliana]

Seq. No. 164752

Seq. ID LIB3177-080-P1-K1-E4

Method BLASTN NCBI GI g3193311 BLAST score 38

201 00010 00



E value 2.0e-12 Match length 58 % identity 91

NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 164753

Seq. ID LIB3177-080-P1-K1-E5

Method BLASTN
NCBI GI g4589410
BLAST score 25
E value 4.0e-05
Match length 59
% identity 49

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 164754

Seq. ID LIB3177-080-P1-K1-E6

Method BLASTN
NCBI GI g58298
BLAST score 138
E value 5.0e-72
Match length 166
% identity 96

NCBI Description Synthetic DNA for A.thaliana ats1A leader spliced to

B.thuringiensis CryIA(c)

Seq. No. 164755

Seq. ID LIB3177-080-P1-K1-E7

Method BLASTN
NCBI GI g4585918
BLAST score 48
E value 2.0e-18

E value 2.0e
Match length 120
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F1013 genomic

sequence, complete sequence

Seq. No. 164756

Seq. ID LIB3177-080-P1-K1-E9

Method BLASTN
NCBI GI 94309683
BLAST score 84
E value 7.0e-40
Match length 92
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 164757

Seq. ID LIB3177-080-P1-K1-F1

Method BLASTX
NCBI GI g4704613
BLAST score 305
E value 4.0e-28
Match length 72
% identity 86

Match length

71



NCBI Description



(AF109695) monodehydroascorbate reductase [Brassica juncea]

```
164758
   Seq. No.
                      LIB3177-080-P1-K1-F10
   Seq. ID
   Method
                      BLASTX
                      g4220485
   NCBI GI
   BLAST score
                      255
E value
                      5.0e-22
                      49
   Match length
                      98
   % identity
                     (AC006069) putative beta-1,3-glucanase [Arabidopsis
   NCBI Description
                      thaliana]
                      164759
   Seq. No.
                      LIB3177-080-P1-K1-F11
   Seq. ID
   Method
                      BLASTN
   NCBI GI
                      q4678291
   BLAST score
                      212
                      1.0e-116
   E value
                      358
   Match length
   % identity
                      98
   NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
                      (ESSA project)
   Seq. No.
                      164760
                      LIB3177-080-P1-K1-F3
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g132110
   BLAST score
                      394
                      2.0e-38
   E value
   Match length
                      78
                      99
   % identity
   NCBI Description
                      RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                      (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                      B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                       (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                      thaliana]
                      164761
   Seq. No.
   Seq. ID
                      LIB3177-080-P1-K1-F5
   Method
                      BLASTN
   NCBI GI
                      g3449329
   BLAST score
                      190
   E value
                      1.0e-102
   Match length
                      397
   % identity
                      98
                      Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
   NCBI Description
                      MDH9, complete sequence [Arabidopsis thaliana]
   Seq. No.
                      164762
   Seq. ID
                      LIB3177-080-P1-K1-F6
                      BLASTN
   Method
   NCBI GI
                      g2970638
   BLAST score
                      35
   E value
                      2.0e-10
```



% identity NCBI Description Brassica napus unknown gene, complete cds 164763 Seq. No. Seq. ID LIB3177-080-P1-K1-G1 Method BLASTX g1871577 NCBI GI BLAST score 188 2.0e-14 E value 52 Match length 65 % identity (Y11553) putative 21kD protein precursor [Medicago sativa] NCBI Description 164764 Seq. No. LIB3177-080-P1-K1-G10 Seq. ID BLASTX Method NCBI GI q421826 BLAST score 240 8.0e-21 E value 71 Match length 65 % identity chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis thaliana] 164765 Seq. No. Seq. ID LIB3177-080-P1-K1-G11 Method BLASTX NCBI GI q282865 812 BLAST score 3.0e-87 E value Match length 150 78 % identity chlorophyll a/b-binding protein - Arabidopsis thaliana NCBI Description >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana] Seq. No. 164766 LIB3177-080-P1-K1-G12 Seq. ID Method BLASTX NCBI GI g4539009 BLAST score 643 E value 2.0e-67 Match length 140 % identity NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 164767

Seq. ID LIB3177-080-P1-K1-G2

Method BLASTX
NCBI GI g3600055
BLAST score 330
E value 6.0e-31
Match length 103



% identity 63

NCBI Description (AF080120) contains similarity to Pisum sativum disease

resistance response protein 206-d (GB:U11716) [Arabidopsis

thaliana]

Seq. No. 164768

Seq. ID LIB3177-080-P1-K1-G3

Method BLASTX
NCBI GI g132110
BLAST score 423
E value 5.0e-46
Match length 98
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164769

Seq. ID LIB3177-080-P1-K1-G4

Method BLASTN
NCBI GI g2264317
BLAST score 110
E value 2.0e-55
Match length 118
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 164770

Seq. ID LIB3177-080-P1-K1-G6

Method BLASTN
NCBI GI g21142
BLAST score 39
E value 5.0e-13
Match length 55
% identity 93

NCBI Description Mustard mRNA for cytosolic glyceraldehyde-3-phosphate

dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)

Seq. No. 164771

Seq. ID LIB3177-080-P1-K1-G7

Method BLASTN
NCBI GI g2264317
BLAST score 246
E value 1.0e-136
Match length 246
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 164772

Seq. ID LIB3177-080-P1-K1-G8

Method BLASTN NCBI GI g3402671



```
BLAST score 50
E value 1.0e-19
Match length 54
% identity 60
NCBI Description Arabidop
```

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 164773

 Seq. ID
 LIB3177-080-P1-K1-H1

 Method
 BLASTX

 NCBI GI
 g2118220

 BLAST score
 164

 E value
 1.0e-11

 Match length
 47

Match length 47 % identity 72

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi 3096941 emb CAA18851.1 (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
>gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No. 164774

Seq. ID LIB3177-080-P1-K1-H10

Method BLASTN
NCBI GI g4220635
BLAST score 437
E value 0.0e+00
Match length 461

Match length 461 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 164775

Seq. ID LIB3177-080-P1-K1-H11

Method BLASTX
NCBI GI g3882273
BLAST score 155
E value 2.0e-10
Match length 97
% identity 30

NCBI Description (AB018319) KIAA0776 protein [Homo sapiens]

Seq. No. 164776

Seq. ID LIB3177-080-P1-K1-H12

Method BLASTX
NCBI GI g2914700
BLAST score 556
E value 3.0e-57
Match length 151
% identity 77

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis



thaliana]

```
Seq. No.
                  164777
Seq. ID
                  LIB3177-080-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2398679
BLAST score
                  408
E value
                  6.0e-40
Match length
                  84
                  90
% identity
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                  synthase [Morinda citrifolia]
                  164778
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-H3
Method
                  BLASTX
                  g1171770
NCBI GI
BLAST score
                  106
E value
                  6.0e-23
Match length
                  61
% identity
                  97
NCBI Description NITRILASE 3 >gi 508735 (U09959) nitrilase [Arabidopsis
                  thaliana]
Seq. No.
                  164779
Seq. ID
                  LIB3177-080-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3953458
BLAST score
                  532
                  2.0e-54
E value
Match length
                  132
                  83
% identity
NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]
Seq. No.
                  164780
Seq. ID
                  LIB3177-080-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q4490734
BLAST score
                  416
E value
                  0.0e + 00
Match length
                  416
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                  project)
Seq. No.
                  164781
Seq. ID
                  LIB3177-080-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1170191
BLAST score
                  516
E value
                  1.0e-52
Match length
                  116
                  91
% identity
NCBI Description
                  HOMEOBOX PROTEIN HD1 >gi 1076449 pir S47535
                  homeodomain-containing protein - rape
                  >gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing
                  protein [Brassica napus] >gi 1090522 prf 2019252A homeobox
```



protein [Brassica napus]

```
164782
Seq. No.
                  LIB3177-080-P1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q115767
BLAST score
                  656
                  5.0e-69
E value
Match length
                  127
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
```

>gi 16368 emb CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

164783 Seq. No. LIB3177-080-P1-K1-H8 Seq. ID Method BLASTN NCBI GI g1877523 54 BLAST score 1.0e-21 E value

Match length 234 % identity 92

NCBI Description Arabidopsis thaliana BAC T7I23, complete sequence

[Arabidopsis thaliana]

164784 Seq. No.

LIB3177-080-P1-K1-H9 Seq. ID

Method BLASTX NCBI GI q541858 BLAST score 441 5.0e-44 E value Match length 86 % identity 97

endoxyloglucan transferase - Arabidopsis thaliana NCBI Description

>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)

endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No. 164785

LIB3177-081-P1-K1-A1 Seq. ID

Method BLASTX NCBI GI q4741960 BLAST score 365 E value 4.0e - 35Match length 90 % identity

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 164786

LIB3177-081-P1-K1-A10 Seq. ID

BLASTX Method NCBI GI g131187 BLAST score 304



E value 3.0e-28 60 Match length 87 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi 72681 pir F1SP3 photosystem I chain III precursor spinach >gi 21303 emb CAA31523 (X13133) PSI subunit IV

preprotein (AA -77 to 154) [Spinacia oleracea]

>gi 226166 prf 1413236A photosystem I reaction center IV

[Spinacia oleracea]

164787 Seq. No.

LIB3177-081-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI g4531434 BLAST score 503 E value 4.0e-51 Match length 132 77 % identity

(AC006224) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 164788

LIB3177-081-P1-K1-A12 Seq. ID

Method BLASTN NCBI GI g4309683 BLAST score 163 E value 9.0e-87 234 Match length 97

% identity NCBI Description Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 164789

LIB3177-081-P1-K1-A2 Seq. ID

Method BLASTX NCBI GI g4741962 BLAST score 198 E value 7.0e-16 Match length 53

74 % identity

NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]

164790 Seq. No.

Seq. ID LIB3177-081-P1-K1-A3

Method BLASTN NCBI GI g4741953 BLAST score 42 E value 4.0e-15 Match length 58 % identity

NCBI Description Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA,

complete cds

Seq. No. 164791

Seq. ID LIB3177-081-P1-K1-A5

Method BLASTX NCBI GI g2911078



BLAST score 590 E value 2.0e-61 Match length 117 % identity 99

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 164792

Seq. ID LIB3177-081-P1-K1-A6

Method BLASTX
NCBI GI g2501812
BLAST score 500
E value 8.0e-51
Match length 117
% identity 84

NCBI Description (U91509) glycolate oxidase [Arabidopsis thaliana]

Seq. No. 164793

Seq. ID LIB3177-081-P1-K1-A9

Method BLASTX
NCBI GI g2213595
BLAST score 493
E value 5.0e-50
Match length 107
% identity 90

NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No. 164794

Seq. ID LIB3177-081-P1-K1-B1

Method BLASTN
NCBI GI g3985958
BLAST score 209
E value 1.0e-114
Match length 456
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 164795

Seq. ID LIB3177-081-P1-K1-B10

Method BLASTX
NCBI GI g282865
BLAST score 342
E value 2.0e-32
Match length 73
% identity 88

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164796

Seq. ID LIB3177-081-P1-K1-B12

Method BLASTX NCBI GI g4827050 BLAST score 181



E value 6.0e-14
Match length 58
% identity 60

NCBI Description ubiquitin specific protease 14 (tRNA-quanine

transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi 940182 (U30888) tRNA-Guanine

Transglycosylase [Homo sapiens]

Seq. No. 164797

Seq. ID LIB3177-081-P1-K1-B2

Method BLASTX
NCBI GI g3548810
BLAST score 169
E value 3.0e-12
Match length 78
% identity 42

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 164798

Seq. ID LIB3177-081-P1-K1-B3

Method BLASTX
NCBI GI g2246621
BLAST score 218
E value 8.0e-18
Match length 57
% identity 82

NCBI Description (AF004393) salt-stress induced tonoplast intrinsic protein

[Arabidopsis thaliana]

Seq. No. 164799

Seq. ID LIB3177-081-P1-K1-B4

98

Method BLASTX
NCBI GI g2119846
BLAST score 700
E value 4.0e-74
Match length 136

% identity

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164800

Seq. ID LIB3177-081-P1-K1-B5

Method BLASTN
NCBI GI g3386593
BLAST score 40
E value 2.0e-13

Match length 120 % identity 83

NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 164801

Seq. ID LIB3177-081-P1-K1-B6

Method BLASTX
NCBI GI g2559012
BLAST score 126
E value 5.0e-18
Match length 75
% identity 65

NCBI Description (AF026293) chaperonin containing t-complex polypeptide 1,

beta subunit; CCT-beta [Homo sapiens] >gi_4090929

(AF026166) chaperonin-containing TCP-1 beta subunit homolog

[Homo sapiens]

Seq. No. 164802

Seq. ID LIB3177-081-P1-K1-B7

Method BLASTN
NCBI GI 94220640
BLAST score 53
E value 1.0e-21
Match length 73
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 164803

Seq. ID LIB3177-081-P1-K1-B9

Method BLASTN
NCBI GI g4585952
BLAST score 163
E value 1.0e-86
Match length 336
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,

complete sequence

Seq. No. 164804

Seq. ID LIB3177-081-P1-K1-C1

Method BLASTX
NCBI GI g1706772
BLAST score 449
E value 5.0e-47
Match length 99
% identity 95

NCBI Description FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE

SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE)

>gi_1076324_pir__S54251 farnesyl-diphosphate

farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana
>gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate

farnesyltransferase [Arabidopsis thaliana]

>gi_806325_dbj_BAA06103_ (D29017) squalene synthase
[Arabidopsis thaliana] >gi_2232212 (AF004560) squalene

synthase 1 [Arabidopsis thaliana]

>gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate

farnesyltransferase [Arabidopsis thaliana] >gi_4098519

(U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.

Seq. ID

164810

LIB3177-081-P1-K1-C6



```
164805
Seq. No.
Seq. ID
                  LIB3177-081-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1169278
BLAST score
                  340
E value
                  3.0e-32
Match length
                  81
                  95
% identity
NCBI Description
                 DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14
                  protein [Arabidopsis thaliana]
                  164806
Seq. No.
                  LIB3177-081-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2911085
BLAST score
                  345
E value
                  7.0e-33
Match length
                  90
% identity
                  83
NCBI Description
                  (AL021960) photosystem II oxygen-evolving complex protein
                  3-like [Arabidopsis thaliana] >qi 3402748 emb CAA20194.1
                  (AL031187) photosystem II oxygen-evolving complex protein 3
                  - like [Arabidopsis thaliana]
Seq. No.
                  164807
                  LIB3177-081-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539329
BLAST score
                  322
E value
                  2.0e-30
Match length
                  63
% identity
                  100
NCBI Description (AL035679) ES43 like protein [Arabidopsis thaliana]
Seq. No.
                  164808
Seq. ID
                  LIB3177-081-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3983125
BLAST score
                  235
E value
                  3.0e-20
Match length
                  58
% identity
                  83
NCBI Description (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  164809
Seq. ID
                  LIB3177-081-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3413700
BLAST score
                  350
E value
                  2.0e-33
Match length
                  89
% identity
NCBI Description
                 (AC004747) putative YME1 protein [Arabidopsis thaliana]
```



```
Method
                  BLASTN
NCBI GI
                  g4567259
                  40
BLAST score
                  1.0e-13
E value
Match length
                  56
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC F3K23 genomic
NCBI Description
                  sequence, complete sequence
                  164811
Seq. No.
                  LIB3177-081-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g115470
NCBI GI
                  363
BLAST score
                  1.0e-34
E value
Match length
                  150
                  53
% identity
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                  DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana
                  >gi 14343 emb CAA46508 (X65541) carbonic anhydrase
                   [Arabidopsis thaliana]
                  164812
Seq. No.
                  LIB3177-081-P1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2245031
BLAST score
                  442
                  0.0e + 00
E value
Match length
                   446
                   100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                   164813
Seq. No.
Seq. ID
                   LIB3177-081-P1-K1-D1
Method
                  BLASTX
NCBI GI
                   q4469003
BLAST score
                   590
E value
                   3.0e-61
Match length
                   133
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   164814
Seq. ID
                   LIB3177-081-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2282584
BLAST score
                   428
                   2.0e-42
E value
                   115
Match length
% identity
                   75
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]
```

Seq. No. 164815

Seq. ID LIB3177-081-P1-K1-D12

Method BLASTX



NCBI GI g282865 BLAST score 607 E value 3.0e-63 Match length 123 % identity 69

NCBI Description -chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164816

Seq. ID LIB3177-081-P1-K1-D2

Method BLASTX
NCBI GI g3184100
BLAST score 179
E value 4.0e-13
Match length 52
% identity 60

NCBI Description (AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 164817

Seq. ID LIB3177-081-P1-K1-D3

Method BLASTX
NCBI GI g4406807
BLAST score 477
E value 4.0e-48
Match length 107
% identity 89

NCBI Description (AC006201) putative elongation factor beta-1 [Arabidopsis

thaliana]

Seq. No. 164818

Seq. ID LIB3177-081-P1-K1-D5

Method BLASTN
NCBI GI g4454447
BLAST score 76
E value 2.0e-35

Match length 88 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164819

Seq. ID LIB3177-081-P1-K1-D6

Method BLASTX
NCBI GI g115767
BLAST score 734
E value 4.0e-78
Match length 141
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]



>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164820

Seq. ID LIB3177-081-P1-K1-D7

Method BLASTX
NCBI GI g4544456
BLAST score 117
E value 1.0e-25
Match length 69
% identity 84

NCBI Description (AC006592) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 164821

Seq. ID LIB3177-081-P1-K1-D8

Method BLASTX
NCBI GI 94406775
BLAST score 297
E value 6.0e-27
Match length 121
% identity 45

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 164822

Seq. ID LIB3177-081-P1-K1-E1

Method BLASTX
NCBI GI 94538963
BLAST score 476
E value 5.0e-48
Match length 110
% identity 83

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 164823

Seq. ID LIB3177-081-P1-K1-E10

Method BLASTX
NCBI GI g282865
BLAST score 719
E value 3.0e-76
Match length 141
% identity 73

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304 emb_CAB41095.1 (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 164824

Seq. ID LIB3177-081-P1-K1-E12

Method BLASTX
NCBI GI g2497733
BLAST score 230
E value 2.0e-19
Match length 60



% identity NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description >gi 1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi 3786018 (AC005499) unknown protein [Arabidopsis thaliana] 164825 Seq. No. LIB3177-081-P1-K1-E2 Seq. ID Method BLASTN g2618601 NCBI GI BLAST score 111 E value 5.0e-56 Match length 115 99 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MHJ24, complete sequence [Arabidopsis thaliana] 164826 Seq. No. LIB3177-081-P1-K1-E6 Seq. ID Method BLASTN g3299824 NCBI GI BLAST score 115 E value 2.0e-58 Match length 143 % identity 95 NCBI Description Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana] 164827 Seq. No. Seq. ID LIB3177-081-P1-K1-E9 Method BLASTN NCBI GI q4544435 BLAST score 103 E value 2.0e-51 Match length 103 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence 164828 Seq. No. Seq. ID LIB3177-081-P1-K1-F1 Method BLASTX NCBI GI g4538897 BLAST score 164 E value 6.0e-12 59 Match length % identity 49 NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana] 164829 Seq. No. Seq. ID LIB3177-081-P1-K1-F10 BLASTX Method NCBI GI g115783 BLAST score 439

2.0e-43 Match length 95 % identity 96

E value



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi 16376 emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 164830

Seq. ID LIB3177-081-P1-K1-F11

Method BLASTN
NCBI GI g3688798
BLAST score 222
E value 1.0e-122
Match length 222
% identity 100

NCBI Description Arabidopsis thaliana gamma tonoplast intrinsic protein 2

(TIP2) mRNA, complete cds

Seq. No. 164831

Seq. ID LIB3177-081-P1-K1-F2

Method BLASTX
NCBI GI g2199574
BLAST score 288
E value 3.0e-26
Match length 53
% identity 100

NCBI Description (AF004293) aquaporin [Brassica rapa]

Seq. No. 164832

Seq. ID LIB3177-081-P1-K1-F6

Method BLASTN
NCBI GI g4558521
BLAST score 92
E value 2.0e-44
Match length 238
% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,

complete sequence

Seq. No. 164833

Seq. ID LIB3177-081-P1-K1-F7

Method BLASTN
NCBI GI g16367
BLAST score 37
E value 3.0e-12
Match length 57
% identity 91

NCBI Description A.thaliana gene (LHCP AB 165) for chlorophyll a/b binding

protein

Seq. No. 164834

Seq. ID LIB3177-081-P1-K1-F9

Method BLASTN
NCBI GI g2764940
BLAST score 45
E value 4.0e-17
Match length 53
% identity 96

NCBI Description A.thaliana GASA4 gene



```
Seq. No.
                  164835
                  LIB3177-081-P1-K1-G1
Seq. ID
                  BLASTX
Method
                  g1769905
NCBI GI
                  512
BLAST score
                  5.0e-52
E value
                  143
Match length
                  70
% identity
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
                  164836
Seq. No.
                  LIB3177-081-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1916349
                  97
BLAST score
E value
                  2.0e-47
Match length
                  169
% identity
                  89
                  Brassica rapa PSI-H subunit (psaH) mRNA, complete cds
NCBI Description
Seq. No.
                  164837
                  LIB3177-081-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q21142
                  51
BLAST score
E value
                  3.0e-20
                  67
Match length
                  94
% identity
                  Mustard mRNA for cytosolic glyceraldehyde-3-phosphate
NCBI Description
                  dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)
Seq. No.
                  164838
                  LIB3177-081-P1-K1-G12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2764940
BLAST score
                  66
E value
                  5.0e-29
Match length
                  127
                  94
% identity
NCBI Description A.thaliana GASA4 gene
                  164839
Seq. No.
                  LIB3177-081-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4741953
BLAST score
                  135
E value
                  3.0e-70
Match length
                  163
                   96
```

% identity

NCBI Description Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA,

complete cds

164840 Seq. No.

Seq. ID LIB3177-081-P1-K1-G3

Method BLASTN

E value

Match length

% identity

1.0e-27

61

95



```
g4580454
NCBI GI
BLAST score
                  92
                  1.0e-44
E value
Match length
                  120
% identity
                  95
NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic
                  sequence, complete sequence
                  164841
Seq. No.
                  LIB3177-081-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g3775987
NCBI GI
                  504
BLAST score
                  2.0e-51
E value
Match length
                  98
% identity
                  100
NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  164842
Seq. ID
                  LIB3177-081-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4584351
BLAST score
                  154
E value
                  2.0e-81
                  198
Match length
% identity
                  95
NCBI Description Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
                  164843
Seq. No.
Seq. ID
                  LIB3177-081-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2809242
BLAST score
                  518
E value
                   6.0e - 53
Match length
                  108
                  99
% identity
NCBI Description (AC002560) F21B7.11 [Arabidopsis thaliana]
Seq. No.
                  164844
Seq. ID
                  LIB3177-081-P1-K1-G7
                  BLASTX
Method
NCBI GI
                  g3149952
BLAST score
                  222
E value
                  1.0e-18
                  52
Match length
% identity
                  83
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
Seq. No.
                  164845
Seq. ID
                  LIB3177-081-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g4558661
BLAST score
                  298
```



(AC007063) putative malate oxidoreductase (NAD) NCBI Description [Arabidopsis thaliana] 164846 Seq. No. LIB3177-081-P1-K1-G9 Seq. ID Method BLASTN NCBI GI q769742 BLAST score 40 5.0e-14 E value Match length 68 90 % identity A.thaliana mRNA for phosphoinositide-specific phospholipase NCBI Description Seq. No. 164847 Seq. ID LIB3177-081-P1-K1-H10 Method BLASTN NCBI GI g2828182 BLAST score 37 1.0e-11 E value Match length 73 92 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MOJ9, complete sequence [Arabidopsis thaliana] 164848 Seq. No. LIB3177-081-P1-K1-H12 Seq. ID Method BLASTX NCBI GI g1345594 BLAST score 384 2.0e-37 E value Match length 84 93 % identity NCBI Description 14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana] Seq. No. 164849 LIB3177-081-P1-K1-H2 Seq. ID Method BLASTN NCBI GI q4733961 105 BLAST score 2.0e-52 E value 113 Match length % identity Arabidopsis thaliana chromosome II BAC F16G22 genomic NCBI Description

sequence, complete sequence

Seq. No. 164850

Seq. ID LIB3177-081-P1-K1-H5

Method BLASTX NCBI GI q4741960 BLAST score 294 E value 1.0e-26 75 Match length 79 % identity

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]



```
Seq. No.
                   164851
                  LIB3177-081-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1402904
BLAST score
                   434
E value
                   4.0e-43
                   86
Match length
% identity
                   97
                  (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164852
                  LIB3177-081-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894574
BLAST score
                   352
                  1.0e-33
E value
Match length
                  73
                   92
% identity
                   (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
                   164853
Seq. No.
                  LIB3177-081-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1053047
BLAST score
                   357
                   4.0e-34
E value
Match length
                   90
                   84
% identity
NCBI Description
                  (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
                  histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
Seq. No.
                  164854
Seq. ID
                  LIB3177-082-P1-K1-A1
Method
                  BLASTN
NCBI GI
                   q2062153
BLAST score
                   74
E value
                   6.0e - 34
Match length
                   126
% identity
NCBI Description
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164855
Seq. ID
                  LIB3177-082-P1-K1-A10
Method
                  BLASTX
                  g119975
                  308
```

NCBI GI BLAST score E value 8.0e-29 Match length 68 % identity 96

FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin NCBI Description

[2Fe-2S] precursor - Arabidopsis thaliana

>gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A

Match length

% identity

65

94



[Arabidopsis thaliana]

```
Seq. No.
                  164856
                  LIB3177-082-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115385
BLAST score
                  203
                  2.0e-16
E value
Match length
                  41
                  98
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  164857
Seq. No.
                  LIB3177-082-P1-K1-A12
Seq. ID
Method
                  BLASTN
                  g3510347
NCBI GI
BLAST score
                  166
                  2.0e-88
E value
Match length
                  194
                  96
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  164858
Seq. No.
                  LIB3177-082-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  214
E value
                  9.0e-18
Match length
                  48
% identity
                  92
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  164859
Seq. ID
                  LIB3177-082-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  q2062153
BLAST score
                  36
E value
                  2.0e-11
Match length
                  75
% identity
NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164860
                  LIB3177-082-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q240069
BLAST score
                  49
E value
                  2.0e-19
```



NCBI Description light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, mRNA, 1548 nt]

Seq. No. 164861

Seq. ID LIB3177-082-P1-K1-A9

Method BLASTN
NCBI GI g3510347
BLAST score 162
E value 3.0e-86
Match length 182
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 164862

Seq. ID LIB3177-082-P1-K1-B1

Method BLASTN
NCBI GI g4490324
BLAST score 95
E value 1.0e-46
Match length 99
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 164863

Seq. ID LIB3177-082-P1-K1-B11

Method BLASTN
NCBI GI g4559344
BLAST score 79
E value 2.0e-36

Match length 163 % identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F27C12 genomic

sequence, complete sequence

Seq. No. 164864

Seq. ID LIB3177-082-P1-K1-B12

Method BLASTX
NCBI GI g416681
BLAST score 242
E value 2.0e-20
Match length 112
% identity 41

NCBI Description ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR

>gi_280404_pir__S26198 H+-transporting ATP synthase (EC
3.6.1.34) delta chain precursor, chloroplast - common
tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP

synthase (delta subunit) [Nicotiana tabacum]

Seq. No. 164865

Seq. ID LIB3177-082-P1-K1-B2

Method BLASTN
NCBI GI g2641637
BLAST score 101
E value 9.0e-50
Match length 183



% identity

NCBI Description Arabidopsis thaliana DnaJ homolog AtJ3 (ATJ3) gene,

complete cds

Seq. No.

164866

Seq. ID

LIB3177-082-P1-K1-B3

Method NCBI GI BLASTX g115767

BLAST score E value

545

Match length

6.0e-56 140

80

% identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.

164867

Seq. ID LIB3177-082-P1-K1-B4

Method NCBI GI

BLASTN

BLAST score E value

g4115370 36

Match length % identity

1.0e-11 65

98

NCBI Description Arabidopsis thaliana chromosome II BAC F27D4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

164868

Seq. ID

LIB3177-082-P1-K1-B5 BLASTX

Method NCBI GI

q464849

BLAST score

175

E value Match length 3.0e-13 31

% identity

100

NCBI Description

TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha

chain - almond $>gi_2041\overline{3}_{emb}C\overline{A}A47\overline{63}5_{(X67162)}$

alpha-tubulin [Prunus dulcis]

Seq. No.

164869

Seq. ID

LIB3177-082-P1-K1-B6

Method

BLASTN

NCBI GI

g16436

BLAST score

58

E value

3.0e-24

Match length

% identity

170 84

NCBI Description A.thaliana gene for pre-ferredoxin

Seq. No.

164870

Seq. ID

LIB3177-082-P1-K1-B8

Method

BLASTX

NCBI GI

g3676296



BLAST score 244 E value 3.0e-21 Match length 60 % identity 77

NCBI Description (U96497) mitochondrial ATPase beta subunit [Nicotiana

sylvestris]

Seq. No. 164871

Seq. ID LIB3177-082-P1-K1-B9

Method BLASTX
NCBI GI g416681
BLAST score 203
E value 5.0e-16
Match length 99
% identity 37

NCBI Description ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR

>gi_280404_pir__S26198 H+-transporting ATP synthase (EC
3.6.1.34) delta chain precursor, chloroplast - common
tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP

synthase (delta subunit) [Nicotiana tabacum]

Seq. No. 164872

Seq. ID LIB3177-082-P1-K1-C1

Method BLASTN
NCBI GI g1732569
BLAST score 113
E value 7.0e-57
Match length 125
% identity 98

NCBI Description Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA,

complete cds

Seq. No. 164873

Seq. ID LIB3177-082-P1-K1-C10

Method BLASTN
NCBI GI g3176701
BLAST score 210
E value 1.0e-115
Match length 242
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T20K24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164874

Seq. ID LIB3177-082-P1-K1-C11

Method BLASTN
NCBI GI g3449323
BLAST score 185
E value 1.0e-100
Match length 197
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZA15, complete sequence [Arabidopsis thaliana]

Seq. No. 164875

Seq. ID LIB3177-082-P1-K1-C12

Method BLASTN



```
g3738088
NCBI GI
BLAST score
                   76
E value
                   6.0e - 35
Match length
                   159
% identity
                   88
NCBI Description Arabidopsis thaliana chromosome II BAC T30L20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   164876
Seq. No.
                   LIB3177-082-P1-K1-C2
Seq. ID
Method
                   BLASTX
                   q541858
NCBI GI
BLAST score
                   805
E value
                   2.0e-86
Match length
                   161
% identity
                   94
NCBI Description
                   endoxyloglucan transferase - Arabidopsis thaliana
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
                   164877
Seq. No.
Seq. ID
                   LIB3177-082-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g4678259
BLAST score
                   267
E value
                   5.0e-24
Match length
                   63
% identity
                   87
                  (AL049657) putative protein [Arabidopsis thaliana]
NCBI Description
                   164878
Seq. No.
Seq. ID
                   LIB3177-082-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q4587542
BLAST score
                   264
E value
                   1.0e-23
Match length
                   51
% identity
NCBI Description
                   (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase
                   with GDSL-motif family. ESTs gb_T45815, gb_T45130 and
                   gb Z38046 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   164879
Seq. ID
                   LIB3177-082-P1-K1-C7
Method
                   BLASTX
                   g1172977
                   166
                   4.0e-12
                   37
                   92
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
```

NCBI GI BLAST score E value Match length

ribosomal protein L18 [Arabidopsis thaliana]

164880 Seq. No.

Seq. ID LIB3177-082-P1-K1-C9

Method BLASTX



NCBI GI g3738091 BLAST score 430 E value 1.0e-42Match length 117 74 % identity (AC005617) similar to symbiotic ammonium transporter, SAT1 NCBI Description [Arabidopsis thaliana] 164881 Seq. No. LIB3177-082-P1-K1-D1 Seq. ID

Method BLASTX NCBI GI g99735 BLAST score 575 E value 1.0e-59 110 Match length 99 % identity

L-ascorbate peroxidase (EC 1.11.1.11) precursor -NCBI Description

Arabidopsis thaliana (fragment)

164882 Seq. No.

LIB3177-082-P1-K1-D10 Seq. ID

Method BLASTN NCBI GI g2341023 56 BLAST score E value 2.0e-23 88 Match length 92

Sequence of BAC F19P19 from Arabidopsis thaliana chromosome NCBI Description

1, complete sequence [Arabidopsis thaliana]

164883 Seq. No.

% identity

LIB3177-082-P1-K1-D12 Seq. ID

Method BLASTN NCBI GI g2815519 232 BLAST score E value 1.0e-128 Match length 236 % identity 100

Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 164884

Seq. ID LIB3177-082-P1-K1-D2

Method BLASTX NCBI GI q3885511 BLAST score 229 E value 3.0e-19Match length 66 % identity 71

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 164885

LIB3177-082-P1-K1-D4 Seq. ID

Method BLASTN NCBI GI g166631 BLAST score 232

BLAST score

Match length

% identity

E value

44

44 100

3.0e-16



```
E value
                  1.0e-128
Match length
                  248
                  98
% identity
NCBI Description A.thaliana chloroplast ATP synthase gamma subunit (atpC1)
                  gene, complete cds
Seq. No.
                  164886
                  LIB3177-082-P1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g12219
BLAST score
                  48
                  2.0e-18
E value
Match length
                  125
% identity
                  84
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
                  164887
Seq. No.
                  LIB3177-082-P1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2815519
BLAST score
                  360
E value
                  0.0e+00
Match length
                  428
                  96
% identity
NCBI Description Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,
                  complete sequence [Arabidopsis thaliana]
                  164888
Seq. No.
                  LIB3177-082-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4008005
                  82
BLAST score
E value
                  1.0e-38
Match length
                  150
% identity
                  89
NCBI Description Arabidopsis thaliana receptor-like protein kinase (RKL1)
                  gene, complete cds
                  164889
Seq. No.
Seq. ID
                  LIB3177-082-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g1871173
BLAST score
                  109
E value
                  1.0e-54
Match length
                  154
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic
                  sequence, complete sequence
Seq. No.
                  164890
Seq. ID
                  LIB3177-082-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4093154
```



```
Arabidopsis thaliana phytochrome-associated protein 1
NCBI Description
                  (PAP1) mRNA, complete cds
Seq. No.
                  164891
                  LIB3177-082-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913727
BLAST score
                  143
                  2.0e-09
E value
Match length
                  28
                  100
% identity
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                  (G6PD) >gi 1174336 emb CAA59012 (X84230)
                  glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  164892
                  LIB3177-082-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567268
BLAST score
                  253
E value
                  4.0e-22
Match length
                  56
                  95
% identity
                  (AC006841) putative fructose biphosphate aldolase
NCBI Description
                  [Arabidopsis thaliana]
                  164893
Seq. No.
Seq. ID
                  LIB3177-082-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2459926
BLAST score
                  154
                  1.0e-10
E value
Match length
                  51
% identity
                  63
                  (AF006197) annexin [Lavatera thuringiaca]
NCBI Description
                  164894
Seq. No.
Seq. ID
                  LIB3177-082-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g2583106
                  166
BLAST score
                  1.0e-88
E value
Match length
                  215
                  93
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164895
Seq. ID
                  LIB3177-082-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4093154
BLAST score
                  59
E value
                  4.0e-25
```

Match length 71 96 % identity

NCBI Description Arabidopsis thaliana phytochrome-associated protein 1

(PAP1) mRNA, complete cds



164896

```
Seq. No.
                  LIB3177-082-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4689466
BLAST score
                  219
                                                               ×3.
                  1.0e-120
E value
                  231
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T23015 genomic
                  sequence, complete sequence
Seq. No.
                  164897
                  LIB3177-082-P1-K1-F10
Seq. ID
Method
                  BLASTN
                  g297877
NCBI GI
                  54
BLAST score
                  3.0e-22
E value
                  66
Match length
                  95
% identity
                  A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
NCBI Description
                  homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana
                  ubiquitin conjugating enzyme mRNA, complete cds
                  164898
Seq. No.
                  LIB3177-082-P1-K1-F11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q887938
BLAST score
                  152
                  3.0e-80
E value
Match length
                  160
% identity
                  99
                  Arabidopsis thaliana clone YAP317 GAST1 protein homolog
NCBI Description
                  mRNA, complete cds
Seq. No.
                  164899
Seq. ID
                  LIB3177-082-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q1755156
BLAST score
                  296
E value
                  2.0e-28
Match length
                  92
% identity
NCBI Description
                  (U75189) germin-like protein [Arabidopsis thaliana]
                  >gi 1755158 (U75190) germin-like protein [Arabidopsis
                  thaliana] >gi 1755170 (U75196) germin-like protein
                   [Arabidopsis thaliana] >gi 1755172 (U75197) germin-like
                  protein [Arabidopsis thaliana] >gi 1755180 (U75201)
                  germin-like protein [Arabidopsis thaliana] >gi 1755190
                   (U75206) germin-like protein [Arabidopsis thaliana]
                  >gi 1934728 (U95035) germin-like protein [Arabidopsis
                  thaliana] >qi 4154285 (AF090733) germin-like protein 1
                   [Arabidopsis thaliana] >qi 4666248 dbj BAA77207.1 (D89055)
                  germin-like protein precursor [Arabidopsis thaliana]
```

Seq. No. 164900

Seq. ID LIB3177-082-P1-K1-F2



Method BLASTN NCBI GI g2213606 294 BLAST score 1.0e-165 E value Match length 298 100 % identity

Genomic sequence for Arabidopsis thaliana BAC F21J9, NCBI Description

complete sequence [Arabidopsis thaliana]

164901 Seq. No.

LIB3177-082-P1-K1-F4 Seq. ID

Method BLASTN g2564050 NCBI GI BLAST score 90 1.0e-43 E value 98 Match length

98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MUA22, complete sequence [Arabidopsis thaliana]

164902 Seq. No.

LIB3177-082-P1-K1-F5 Seq. ID

Method BLASTX NCBI GI g231700 202 BLAST score E value 2.0e-16 Match length 44 % identity 93

22 KD CALMODULIN-LIKE CALCIUM-BINDING PROTEIN (CABP-22) NCBI Description

>gi 479694 pir S35188 calmodulin-related protein (clone CaBP-22) - Arabidopsis thaliana >gi 16209 emb CAA78124 (Z12136) calcium binding protein [Arabidopsis thaliana] >gi_3402708 (AC004261) calcium binding protein [Arabidopsis

thaliana]

Seq. No. 164903

Seq. ID LIB3177-082-P1-K1-F9

Method BLASTX NCBI GI g1592672 BLAST score 363 8.0e-35 E value Match length 102 71 % identity

NCBI Description (X91921) germin1 [Arabidopsis thaliana]

164904 Seq. No.

Seq. ID LIB3177-082-P1-K1-G1

Method BLASTX NCBI GI g132110 BLAST score 623 E value 4.0e-65 Match length 115 % identity 99

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195 emb CAA32702



(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 164905

Seq. ID LIB3177-082-P1-K1-G10

Method BLASTX
NCBI GI g4689386
BLAST score 380
E value 1.0e-36
Match length 144
% identity 56

NCBI Description (AF139468) photosystem I reaction center subunit III [Vigna

radiata]

Seq. No. 164906

Seq. ID LIB3177-082-P1-K1-G12

Method BLASTN
NCBI GI g3046849
BLAST score 209
E value 1.0e-114
Match length 249
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18L3, complete sequence [Arabidopsis thaliana]

Seq. No. 164907

Seq. ID LIB3177-082-P1-K1-G2

Method BLASTX
NCBI GI g3123712
BLAST score 275
E value 3.0e-24
Match length 79
% identity 54

NCBI Description (D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No. 164908

Seq. ID LIB3177-082-P1-K1-G3

Method BLASTN
NCBI GI 94519195
BLAST score 218
E value 1.0e-119
Match length 360
% identity 61

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MQC12, complete sequence

Seq. No. 164909

Seq. ID LIB3177-082-P1-K1-G4

Method BLASTX
NCBI GI g1592679
BLAST score 261
E value 9.0e-23
Match length 71
% identity 77

NCBI Description (X91915) LEA D113 homologue type1 [Arabidopsis thaliana]

Seq. No. 164910

% identity

NCBI Description



```
LIB3177-082-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757394
BLAST score
                  192
                  1.0e-104
E value
                  192
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1904, complete sequence
Seq. No.
                  164911
                  LIB3177-082-P1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  44
E value
                  4.0e-16
                  95
Match length
                  96
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                  (ESSA project)
                  164912
Seq. No.
Seq. ID
                  LIB3177-082-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q3046849
BLAST score
                  334
E value
                  0.0e + 00
Match length
                  409
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164913
Seq. ID
                  LIB3177-082-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  575
E value
                  2.0e-59
Match length
                  108
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543
                                                            (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  164914
Seq. ID
                  LIB3177-082-P1-K1-H10
                  BLASTN
Method
NCBI GI
                  g16192
BLAST score
                  61
E value
                  6.0e-26
Match length
                  200
```

ribulose-1,5-biphosphate carboxylase small subunit (rbcS)

(EC 4.1.1.39)

60

A.thaliana ats1B, ats2B and ats3B gene for



Seq. No. 164915

Seq. ID LIB3177-082-P1-K1-H11

Method BLASTX
NCBI GI g132110
BLAST score 280
E value 2.0e-25
Match length 60
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 164916

Seq. ID LIB3177-082-P1-K1-H12

Method BLASTX
NCBI GI g464621
BLAST score 332
E value 3.0e-31
Match length 110
% identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586

ribosomal protein ML16 - common ice plant

>gi 19539 emb CAA49175 (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 164917

Seq. ID LIB3177-082-P1-K1-H2

Method BLASTX
NCBI GI g118619
BLAST score 160
E value 3.0e-11
Match length 51
% identity 59

NCBI Description SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN

PRECURSOR (IP) >gi_66072_pir__RDBYIS succinate

dehydrogenase (ubiquinone) (EC 1.3.5.1) iron-sulfur protein precursor - yeast (Saccharomyces cerevisiae) >gi_172549 (J05487) succinate dehydrogenase iron-protein subunit (SDH)

(EC 1.3.99.1) [Saccharomyces cerevisiae]

>gi_1360235_emb_CAA97492_ (Z73146) ORF YLL041c

[Saccharomyces cerevisiae]

Seq. No. 164918

Seq. ID LIB3177-082-P1-K1-H4

Method BLASTX
NCBI GI 94455342
BLAST score 820
E value 4.0e-88
Match length 160
% identity 100

NCBI Description (AL035522) O-methyltransferase-like protein [Arabidopsis

thaliana]

Seq. No. 164919



LIB3177-082-P1-K1-H5 Seq. ID Method BLASTX g2494276 NCBI GI BLAST score 176 E value 2.0e-13 Match length 63 52 % identity ELONGATION FACTOR P (EF-P) >gi 1001112 dbj BAA10251 NCBI Description (D64001) elongation factor P [Synechocystis sp.] Seq. No. 164920 LIB3177-082-P1-K1-H7 Seq. ID Method BLASTN NCBI GI g4734003

BLAST score 109 E value 2.0e-54220 Match length 97 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F3L12 genomic

sequence, complete sequence

Seq. No. 164921

LIB3177-082-P1-K1-H9 Seq. ID

Method BLASTX NCBI GI g464621 BLAST score 385 E value 3.0e-37 Match length 119 % identity 67

NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586

ribosomal protein ML16 - common ice plant

>gi_19539_emb_CAA49175 (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 164922

Seq. ID LIB3177-083-P1-K1-A1

Method BLASTX NCBI GI q475719 BLAST score 334 E value 2.0e-31 Match length 119 % identity

NCBI Description (U08467) RNA-binding protein 2 [Arabidopsis thaliana]

Seq. No. 164923

Seq. ID LIB3177-083-P1-K1-A10

Method BLASTX NCBI GI g166835 BLAST score 183 E value 4.0e-14 Match length 41 % identity

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase

activase [Arabidopsis thaliana] >gi 2642170 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 164924

Seq. ID

Method



```
Seq. ID
                   LIB3177-083-P1-K1-A12
Method
                  BLASTN
NCBI GI
                   q4741939
BLAST score
                   123
E value
                   4.0e-63
Match length
                  139
                   97
% identity
NCBI Description Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete
Seq. No.
                  164925
Seq. ID
                  LIB3177-083-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g3434970
BLAST score
                  137
E value
                   3.0e-71
Match length
                  153
                  97
% identity
NCBI Description Arabidopsis thaliana AtERF-3 mRNA for ethylene responsive
                  element binding factor 3, complete cds
Seq. No.
                  164926
Seq. ID
                  LIB3177-083-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g99735
BLAST score
                  252
E value
                  3.0e-22
Match length
                  59
% identity
                  86
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                  Arabidopsis thaliana (fragment)
Seq. No.
                  164927
Seq. ID
                  LIB3177-083-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3859658
BLAST score
                  268
E value
                  1.0e-149
Match length
                  296
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                  (ESSAII project)
Seq. No.
                  164928
Seq. ID
                  LIB3177-083-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4741929
BLAST score
                  321
E value
                  9.0e-30
Match length
                  95
% identity
NCBI Description
                  (AF130253) membrane related protein CP5 [Arabidopsis
                  thaliana]
Seq. No.
                  164929
```

22110

LIB3177-083-P1-K1-B12

BLASTX

Seq. No.

Seq. ID

164934

LIB3177-083-P1-K1-C10



```
NCBI GI
                   g2062158
BLAST score
                   672
E value
                   8.0e-71
Match length
                   139
% identity
                   47
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164930
Seq. ID
                   LIB3177-083-P1-K1-B2
Method
                   BLASTN
NCBI GI
                   g4741959
BLAST score
                   166
E value
                   2.0e-88
Match length
                   228
% identity
                   93
NCBI Description
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
                   cds
Seq. No.
                  164931
Seq. ID
                  LIB3177-083-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  147
E value
                   6.0e-10
                   42
Match length
% identity
                   79
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   164932
Seq. ID
                  LIB3177-083-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  246
E value
                   1.0e-136
Match length
                  254
                   99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
Seq. No.
                   164933
Seq. ID
                  LIB3177-083-P1-K1-C1
Method
                  BLASTX
NCBI GI
                   g417381
BLAST score
                  362
E value
                   3.0e - 80
Match length
                  155
% identity
                  99
NCBI Description
                  NITRILASE 1 > gi 99738 pir S22398 nitrilase (EC 3.5.5.1) -
                  Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445)
                  nitrilase I [Arabidopsis thaliana]
```



```
Method
                   BLASTN
                   q4741939
NCBI GI
BLAST score
                   112
                   1.0e-56
E value
Match length
                   124
% identity
                   98
NCBI Description
                  Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete
                   164935
Seq. No.
                  LIB3177-083-P1-K1-C11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1532162
BLAST score
                   407
E value
                   0.0e + 00
Match length
                   441
                   100
% identity
NCBI Description
                  Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
                  AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                   genes, partial cds, AT.I.24-7, ascorbate peroxidase
                   (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
Seq. No.
                   164936
                  LIB3177-083-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1490552
BLAST score
                  85
E value
                  1.0e-40
Match length
                   97
                   97
% identity
                 Arabidopsis thaliana S-adenosylmethionine decarboxylase
NCBI Description
                   (SAMdc) mRNA, complete cds
Seq. No.
                  164937
                  LIB3177-083-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629518
                   551
BLAST score
E value
                   9.0e-57
Match length
                   116
% identity
                   91
NCBI Description glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small
                  chain - Arabidopsis thaliana (fragment)
Seq. No.
                   164938
                  LIB3177-083-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2264305
BLAST score
                   94
                   7.0e-46
E value
Match length
                   121
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK23, complete sequence [Arabidopsis thaliana]
```

Seq. No. 164939

Seq. ID LIB3177-083-P1-K1-C5



Method BLASTX NCBI GI g125576 BLAST score 528 7.0e-54E value Match length 123 % identity 86

NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) $>gi_99744_pir_S16583$ phosphoribulokinase (EC

2.7.1.19) precursor - Arabidopsis thaliana

>gi_16441_emb CAA41155 (X58149) Ribulose-5-phosphate

kinase [Arabidopsis thaliana]

Seq. No.

164940

LIB3177-083-P1-K1-D1 Seq. ID

Method BLASTX NCBI GI g1172441 BLAST score 180 E value 3.0e-13 Match length 49 78 % identity

POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi 99685 pir S21883 NCBI Description

> DNA-binding protein POSF21 - Arabidopsis thaliana >gi 16429 emb CAA43366 (X61031) posF21 [Arabidopsis

thaliana] >gi 4589968 gb AAD26486.1 AC007169 18 (AC007169)

DNA-binding protein POSF21 [Arabidopsis thaliana]

Seq. No. 164941

Seq. ID LIB3177-083-P1-K1-D12

Method BLASTX NCBI GI g1170939 BLAST score 668 E value 2.0e-70Match length 133 94

% identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi_1084408_pir__S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867 (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 164942

Seq. ID LIB3177-083-P1-K1-D5

Method BLASTN NCBI GI q3688798 BLAST score 107 E value 1.0e-53 Match length 127 % identity 96

NCBI Description Arabidopsis thaliana gamma tonoplast intrinsic protein 2

(TIP2) mRNA, complete cds

Seq. No. 164943

Seq. ID LIB3177-083-P1-K1-D6

Method BLASTX NCBI GI g2832625 BLAST score 214



```
E value
                   3.0e-17
Match length
                   73
% identity
                   55
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  164944
Seq. ID
                  LIB3177-083-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  q4741959
BLAST score
                  189
E value
                   1.0e-102
Match length
                   263
                   93
% identity
NCBI Description
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
                  164945
Seq. No.
Seq. ID
                  LIB3177-083-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g129817
BLAST score
                  530
E value
                  2.0e-54
Match length
                  106
% identity
                  97
NCBI Description BASIC PEROXIDASE E PRECURSOR >gi_81653_pir__JU0458
                  peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana
                  >gi_166807 (M58381) peroxidase [Arabidopsis thaliana]
Seq. No.
                  164946
Seq. ID
                  LIB3177-083-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3929651
BLAST score
                  458
E value
                  6.0e-46
Match length
                  90
% identity
                  100
NCBI Description
                  (AJ131206) microbody NAD-dependent malate dehydrogenase
                   [Arabidopsis thaliana]
Seq. No.
                  164947
Seq. ID
                  LIB3177-083-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4757410
BLAST score
                  200
E value
                  1.0e-109
                  271
Match length
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVE11, complete sequence
```

Seq. No. 164948

Seq. ID LIB3177-083-P1-K1-E2

Method BLASTX
NCBI GI g322577
BLAST score 665
E value 4.0e-70
Match length 128

Match length

NCBI Description

% identity

69 100



```
% identity
                  98
NCBI Description Raf protein kinase homolog CTR1 - Arabidopsis thaliana
Seq. No.
                  164949
                  LIB3177-083-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4741945
BLAST score
                  82
                  1.0e-38
E value
Match length
                  122
                  92
% identity
NCBI Description
                  Arabidopsis thaliana Lhcb2 protein (Lhcb2.2) mRNA, complete
Seq. No.
                  164950
                  LIB3177-083-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4583542
BLAST score
                  614
                  5.0e-64
E value
Match length
                  152
                  86
% identity
                  (Y16847) 16 kDa polypeptide of oxygen-evolving complex
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  164951
Seq. ID
                  LIB3177-083-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g166705
BLAST score
                  70
E value
                  1.0e-31
Match length
                  70
                  100
% identity
NCBI Description Arabidopsis thaliana glyceraldehyde-3-phosphate
                  dehydrogenase C subunit (GapC) gene, complete cds
Seq. No.
                  164952
                  LIB3177-083-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  502
E value
                  5.0e-51
Match length
                  103
                  10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  164953
Seq. ID
                  LIB3177-083-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q2506443
BLAST score
                  337
E value
                  4.0e-32
```

22115

CHLOROPLAST >gi_2117520_pir JQ1285

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

glyceraldehyde-3-phosphate dehydrogenase (NADP+)



(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi_1402885_emb_CAA66816_ (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No. 164954

LIB3177-083-P1-K1-F2 Seq. ID

Method BLASTN NCBI GI g2956689 46 BLAST score 4.0e-17 E value Match length 124 88 % identity

NCBI Description Arabidopsis thaliana mRNA for PSBY (Ycf32-related

chloroplast thylakoid membrane proteins)

164955 Seq. No.

LIB3177-083-P1-K1-G1 Seq. ID

Method BLASTX NCBI GI g1617270 BLAST score 69 E value 2.0e-48 Match length 133 % identity 80

NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

164956 Seq. No.

LIB3177-083-P1-K1-G11 Seq. ID

Method BLASTN NCBI GI g4585890 89 BLAST score 7.0e-43E value Match length 93

% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T3G21 genomic

sequence, complete sequence

Seq. No. 164957

Seq. ID LIB3177-083-P1-K1-G12

Method BLASTX NCBI GI g4454037 BLAST score 370 E value 6.0e-36 Match length 65 % identity 100

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 164958

Seq. ID LIB3177-083-P1-K1-G2

Method BLASTX NCBI GI g2245118 BLAST score 323 E value 6.0e-30 Match length 110

% identity (Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description 164959 Seq. No. Seq. ID LIB3177-083-P1-K1-G3 Method BLASTX NCBI GI g1399380 BLAST score 176 E value 3.0e-13 Match length 45 71 % identity (U43683) S-adenosyl-L-methionine:delta24-sterol-C-NCBI Description methyltransferase [Glycine max] 164960 Seq. No. Seq. ID LIB3177-083-P1-K1-G5 Method BLASTN NCBI GI g4741959 BLAST score 84 E value 9.0e-40 Match length 141 % identity 94 NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds Seq. No. 164961 Seq. ID LIB3177-083-P1-K1-G8 Method BLASTN

NCBI GI q3212846 BLAST score 253 E value 1.0e-140

Match length 317 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 164962

Seq. ID LIB3177-083-P1-K1-H1

Method BLASTX NCBI GI g3450889 BLAST score 447 E value 2.0e-44 Match length 96 % identity 100

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 164963

Seq. ID LIB3177-083-P1-K1-H11

Method BLASTN NCBI GI g3869072 BLAST score 138 E value 7.0e-72 Match length 162 96 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB24, complete sequence [Arabidopsis thaliana]



Seq. No. Seq. ID

164964

LIB3177-083-P1-K1-H12

```
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  380
                   7.0e-37
E value
Match length
                  73
                   97
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  164965
Seq. No.
Seq. ID
                  LIB3177-083-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4741948
BLAST score
                  475
E value
                  6.0e-48
Match length
                  94
% identity
                  96
NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164966
                  LIB3177-083-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3046856
BLAST score
                  40
E value
                  5.0e-14
Match length
                  60
% identity
                  92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXI22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164967
Seq. ID
                  LIB3177-083-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2499327
BLAST score
                  359
E value
                  3.0e-34
Match length
                  119
% identity
                  62
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
                  (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH
                  dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                  >gi 643090 emb CAA58887.1_{-} (X84078) NADH dehydrogenase
                  [Arabidopsis thaliana]
Seq. No.
                  164968
Seq. ID
                  LIB3177-083-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4056497
BLAST score
                  199
E value
                  1.0e-15
Match length
                  52
% identity
NCBI Description (AC005896) putative histone H2B [Arabidopsis thaliana]
```



```
Seq. No.
                   164969
Seq. ID
                   LIB3177-083-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   477
E value
                   3.0e-48
                   95
Match length
                   96
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164970
                   LIB3177-083-P1-K1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16446
BLAST score
                   50
E value
                   9.0e-20
Match length
                   86
% identity
                   90
NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide
Seq. No.
                   164971
                   LIB3177-083-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1769905
BLAST score
                   519
E value
                   7.0e-53
Match length
                   142
                   71
% identity
NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   164972
Seq. ID
                   LIB3177-083-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   378
E value
                   9.0e-37
Match length
                   74
% identity
                   99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   164973
```

Seq. ID LIB3177-084-P1-K1-A10

Method BLASTX
NCBI GI g3075398
BLAST score 315
E value 3.0e-29



Match length 88 % identity 76

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 164974

Seq. ID LIB3177-084-P1-K1-A11

Method BLASTX
NCBI GI g4512683
BLAST score 766
E value 7.0e-82
Match length 145
% identity 100

NCBI Description (AC006931) putative lipase [Arabidopsis thaliana]

>gi_4559323_gb_AAD22985.1_AC007087_4 (AC007087) putative

lipase [Arabidopsis thaliana]

Seq. No. 164975

Seq. ID LIB3177-084-P1-K1-A12

Method BLASTX
NCBI GI g3128195
BLAST score 577
E value 7.0e-60
Match length 119
% identity 98

NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana] (

Seq. No. 164976

Seq. ID LIB3177-084-P1-K1-A2

Method BLASTX
NCBI GI g2829133
BLAST score 489
E value 1.0e-49
Match length 95
% identity 98

NCBI Description (AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis

thaliana] >gi_4490745_emb_CAB38907.1_ (AL035708)

adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]

Seq. No. 164977

Seq. ID LIB3177-084-P1-K1-A3

Method BLASTX
NCBI GI g2119848
BLAST score 395
E value 1.0e-38
Match length 84
% identity 89

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]



```
Seq. No.
                  164978
Seq. ID
                  LIB3177-084-P1-K1-A5
Method
                  BLASTX
                  g4539292
NCBI GI
BLAST score
                  470
E value
                  4.0e-47
Match length
                  87
% identity
                  100
NCBI Description
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
Seq. No.
                  164979
Seq. ID
                  LIB3177-084-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q115470
BLAST score
                  492
E value
                  7.0e-50
Match length
                  116
                  84
% identity
NCBI Description
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                  DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                  (EC 4.2.1.1) precursor - Arabidopsis thaliana
                  >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                   [Arabidopsis thaliana]
Seq. No.
                  164980
Seq. ID
                  LIB3177-084-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  559
E value
                  1.0e-57
Match length
                  111
% identity
                  48
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  164981
Seq. ID
                  LIB3177-084-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g99772
BLAST score
                  521
E value
                  3.0e-53
Match length
                  130
% identity
                  82
NCBI Description
                  ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana
                  >gi 166936 (J05540) ubiquitin extension protein (UBQ6)
                  [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin
                  extension protein (UBQ6) [Arabidopsis thaliana]
```

Seq. No. 164982

Seq. ID LIB3177-084-P1-K1-B11

Method BLASTX
NCBI GI 94455271
BLAST score 386
E value 2.0e-37
Match length 129



% identity NCBI Description (AL035527) serine protease-like protein [Arabidopsis thaliana] Seq. No. 164983 Seq. ID LIB3177-084-P1-K1-B12 Method BLASTX NCBI GI g417381 BLAST score 414 E value 5.0e-41Match length 83 % identity 99 NCBI Description NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) -Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana] Seq. No. 164984 Seq. ID LIB3177-084-P1-K1-B2 Method BLASTX NCBI GI g3914740 BLAST score 272 E value 1.0e-24 Match length 64 % identity 86 NCBI Description 60S RIBOSOMAL PROTEIN L26 >qi 2160300 dbj BAA18941 (D78495) ribosomal protein [Brassica rapa] Seq. No. 164985 Seq. ID LIB3177-084-P1-K1-B3 Method BLASTN NCBI GI g2264316 BLAST score 92 E value 3.0e-44Match length 349 % identity 38 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana] Seq. No. 164986 Seq. ID LIB3177-084-P1-K1-B4 Method BLASTX NCBI GI g4371282 BLAST score 569 E value 8.0e-59 Match length 122 96 % identity NCBI Description (AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana] Seq. No. 164987 Seq. ID LIB3177-084-P1-K1-B5 Method BLASTX NCBI GI g2435604

. BLAST score 82 E value 9.0e-11

Match length 69 % identity 45



```
NCBI Description
                  (AF026213) strong similarity to Saccharomyces cerevisiae
                  endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]
                  164988
Seq. No.
                  LIB3177-084-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589440
BLAST score
                  171
E value
                  2.0e-91
Match length
                  210
% identity
                  94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
                  164989
Seq. No.
Seq. ID
                  LIB3177-084-P1-K1-B7
Method
                  BLASTX
                  g3850573
NCBI GI
BLAST score
                  723
                  8.0e-77
E value
Match length
                  146
                  97
% identity
NCBI Description
                  (AC005278) Similar to gi_1652733 glycogen operon protein
                  GlgX from Synechocystis sp. genome gb_D90908. ESTs
                  gb_H36690, gb_AA712462, gb_AA651230 and gb N95932 come from
                  this gene. [Arabidopsis thaliana]
                  164990
Seq. No.
                  LIB3177-084-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  745
E value
                  2.0e-79
Match length
                  144
                  98
% identity
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164991
Seq. ID
                  LIB3177-084-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1170247
BLAST score
                  445
E value
                  2.0e-44
Match length
                  104
% identity
                  78
NCBI Description HEVEIN-LIKE PROTEIN PRECURSOR >gi 407248 (U01880)
                  pre-hevein-like protein [Arabidopsis thaliana]
```

Seq. No. 164992

Seq. ID LIB3177-084-P1-K1-C10

Method BLASTX NCBI GI g4587564 BLAST score 581 E value 3.0e-60 Match length 119



% identity NCBI Description (AC006550) Strong similarity to gb X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb T42998, gb Z18178, gb T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024 Seq. No. 164993 LIB3177-084-P1-K1-C12 Seq. ID Method BLASTX NCBI GI g3882356 BLAST score 255 E value 6.0e-22 97 Match length 54 % identity (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis NCBI Description

thaliana]

164994 Seq. No.

LIB3177-084-P1-K1-C2 Seq. ID

Method BLASTX NCBI GI g3478700 BLAST score 517

E value 1.0e-52 Match length 118 % identity 86

NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]

Seq. No. 164995

LIB3177-084-P1-K1-C4 Seq. ID

Method BLASTX g3136336 NCBI GI BLAST score 152 E value 4.0e-10 Match length 99 28 % identity

NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]

Seq. No. 164996

LIB3177-084-P1-K1-C6 Seq. ID

Method BLASTX NCBI GI q4585935 BLAST score 537 E value 3.0e-55Match length 104 97 % identity

NCBI Description (AC007211) putative chlorophyll A/B binding protein

[Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1

(AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 164997

LIB3177-084-P1-K1-C7 Seq. ID

Method BLASTN NCBI GI g166645 BLAST score 69 E value 5.0e-31Match length 113 % identity 91



```
NCBI Description Arabidopsis thaliana light-harvesting chlorophyll
                   a/b-binding protein (Cab4) mRNA, complete cds
Seq. No.
                   164998
                   LIB3177-084-P1-K1-C8 -
Seq. ID
Method
                   BLASTX
NCBI GI
                   q520478
BLAST score
                   541
E value
                   2.0e-55
Match length
                   111
% identity
                   98
NCBI Description
                  (U09137) pyruvate dehydrogenase El beta subunit
                   [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                   dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   164999
Seq. ID
                   LIB3177-084-P1-K1-C9
Method
                   BLASTX
                   g1082054
NCBI GI
BLAST score
                   301
E value
                   2.0e-27
Match length
                   56
                   100
% identity
NCBI Description (Z49859) copper transporter protein [Arabidopsis thaliana]
Seq. No.
                  165000
Seq. ID
                  LIB3177-084-P1-K1-D1
Method
                  BLASTN
NCBI GI
                   q4531433
BLAST score
                   187
E value
                   1.0e-101
Match length
                   251
% identity
                   94
NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic
                   sequence, complete sequence
Seq. No.
                   165001
Seq. ID
                  LIB3177-084-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q115778
BLAST score
                  114
E value
                   4.0e-48
Match length
                  103
% identity
                   90
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-1) (LHCP) >gi_282896_pir__S22511 chlorophyll
                  a/b-binding protein (cab-\overline{1}) - white mustard
                  >gi_21138_emb_CAA34459_ (X16436) chlorophyll a/b-binding
                  protein (AA 1-266) [Sinapis alba] >gi_21140_emb_CAA33903
                   (X15894) chlorophyll a/b-binding polypeptide [Sīnapis alba]
```

Seq. No. 165002

Seq. ID LIB3177-084-P1-K1-D11

Method BLASTX
NCBI GI g3914442
BLAST score 419
E value 3.0e-41



Match length 105 % identity 78

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No. 165003

Seq. ID LIB3177-084-P1-K1-D2

Method BLASTX
NCBI GI g461550
BLAST score 352
E value 1.0e-33
Match length 89
% identity 84

NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR

>gi_81635_pir__B39732 H+-transporting ATP synthase (EC

3.6.1.34) gamma-1 chain precursor, chloroplast Arabidopsis thaliana >gi_166632 (M61741) ATP synthase

gamma-subunit [Arabidopsis thaliana]

Seq. No. 165004

Seq. ID LIB3177-084-P1-K1-D3

Method BLASTX
NCBI GI g416758
BLAST score 340
E value 4.0e-32
Match length 110
% identity 61

NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)

carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120 prf 1908426A carboxypeptidase Y [Arabidopsis

thaliana]

Seq. No. 165005

Seq. ID LIB3177-084-P1-K1-D5

Method BLASTN
NCBI GI g2656028
BLAST score 349
E value 0.0e+00
Match length 357
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 165006

Seq. ID LIB3177-084-P1-K1-D7

Method BLASTN
NCBI GI g166645
BLAST score 178
E value 8.0e-96
Match length 178
% identity 100

NCBI Description Arabidopsis thaliana light-harvesting chlorophyll

a/b-binding protein (Cab4) mRNA, complete cds

Seq. No. 165007

Seq. ID LIB3177-084-P1-K1-D8



Method BLASTN
NCBI GI g1657620
BLAST score 287
E value 1.0e-160
Match length 291
% identity 100
NCBI Description Arabidom

NCBI Description Arabidopsis thaliana putative acyl-coA dehydrogenase G6p

(AtG6) mRNA, complete cds

Seq. No. 165008

Seq. ID LIB3177-084-P1-K1-D9

Method BLASTX
NCBI GI g1408473
BLAST score 431
E value 5.0e-47
Match length 100
% identity 96

NCBI Description (U48939) actin depolymerizing factor 2 [Arabidopsis

thaliana]

Seq. No. 165009

Seq. ID LIB3177-084-P1-K1-E10

Method BLASTX
NCBI GI 94585882
BLAST score 239
E value 3.0e-20
Match length 46
% identity 100

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 165010

Seq. ID LIB3177-084-P1-K1-E11

Method BLASTX
NCBI GI g132102
BLAST score 718
E value 3.0e-76
Match length 136
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165011

Seq. ID LIB3177-084-P1-K1-E2

Method BLASTN
NCBI GI g3869075
BLAST score 49
E value 2.0e-19
Match length 57

% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]



165012 Seq. No. LIB3177-084-P1-K1-E3 Seq. ID Method BLASTX NCBI GI q3915865 BLAST score 292 E value 1.0e-26 59 Match length 93 % identity NCBI Description 40S RIBOSOMAL PROTEIN S4 Seq. No. 165013 LIB3177-084-P1-K1-E5 Seq. ID Method BLASTX NCBI GI g2832355 497 BLAST score 3.0e-50E value Match length 113 % identity 87

NCBI Description (Y14074) HMG protein [Arabidopsis thaliana]

165014 Seq. No.

Seq. ID LIB3177-084-P1-K1-E6

Method BLASTX NCBI GI g430947 275 BLAST score E value 1.0e-24 Match length 85 67 % identity

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 165015

LIB3177-084-P1-K1-E7 Seq. ID

Method BLASTN NCBI GI g457403 BLAST score 161 E value 3.0e-85 Match length 161 100 % identity

NCBI Description Arabidopsis thaliana mRNA for MAP kinase, complete cds

Seq. No. 165016

Seq. ID LIB3177-084-P1-K1-E8

Method BLASTN NCBI GI q4678705 BLAST score 448 E value 0.0e + 00Match length 456 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7

(ESSA project)

Seq. No. 165017

Seq. ID LIB3177-084-P1-K1-E9

Method BLASTN NCBI GI g4454447 BLAST score 312



E value 1.0e-175 Match length 316 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165018

Seq. ID LIB3177-084-P1-K1-F10

Method BLASTX
NCBI GI g1172969
BLAST score 534
E value 1.0e-54
Match length 112
% identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033

ribosomal protein L11.e - Arabidopsis thaliana

>gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16

[Arabidopsis thaliana]

Seq. No. 165019

Seq. ID LIB3177-084-P1-K1-F11

Method BLASTN
NCBI GI g3047074
BLAST score 455
E value 0.0e+00
Match length 455
% identity 100

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 165020

Seq. ID LIB3177-084-P1-K1-F12

Method BLASTN
NCBI GI g2477521
BLAST score 29
E value 2.0e-06

Match length 412 % identity 18

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165021

Seq. ID LIB3177-084-P1-K1-F3

Method BLASTN
NCBI GI g3063690
BLAST score 301
E value 1.0e-169
Match length 364
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11

(ESSAII project)

Seq. No. 165022

Seq. ID LIB3177-084-P1-K1-F4

Method BLASTX
NCBI GI g1350956
BLAST score 587
E value 7.0e-61



Match length 117 % identity 98 NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22) 165023 Seq. No. LIB3177-084-P1-K1-F5 Seq. ID Method BLASTN NCBI GI g3043414 BLAST score 77 2.0e-35 E value 179 Match length % identity 93 NCBI Description Arabidopsis thaliana mRNA for At-hsc70-3 protein Seq. No. 165024 LIB3177-084-P1-K1-F6 Seq. ID Method BLASTX NCBI GI q4741962 BLAST score 532 2.0e-54 E value 144 Match length % identity 57 NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana] 165025 Seq. No. LIB3177-084-P1-K1-F8 Seq. ID Method BLASTX NCBI GI g2498731 BLAST score 197 E value 4.0e-15 Match length 45 % identity 80 NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog -Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana] Seq. No. 165026 Seq. ID LIB3177-084-P1-K1-F9 Method BLASTX NCBI GI g4406774 BLAST score 754 E value 2.0e-80 Match length 149 % identity 98 NCBI Description (AC006836) putative nonsense-mediated mRNA decay protein, 5' partial [Arabidopsis thaliana] Seq. No. 165027 Seq. ID LIB3177-084-P1-K1-G10

Method BLASTX NCBI GI g132074 BLAST score 665 E value 4.0e-70 Match length 122 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR



(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana

Seq. No. 165028

Seq. ID LIB3177-084-P1-K1-G11

Method BLASTX
NCBI GI g3885511
BLAST score 420
E value 3.0e-41
Match length 103
% identity 82

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 165029

Seq. ID LIB3177-084-P1-K1-G12

Method BLASTX
NCBI GI g2811028
BLAST score 660
E value 2.0e-69
Match length 149
% identity 89

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188

(AF007271) similar to S. cerevisiae SIK1P (PID:g984964)

[Arabidopsis thaliana]

Seq. No. 165030

Seq. ID LIB3177-084-P1-K1-G2

Method BLASTX
NCBI GI g132074
BLAST score 589
E value 3.0e-61
Match length 110
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165031

Seq. ID LIB3177-084-P1-K1-G4

Method BLASTX
NCBI GI g4678941
BLAST score 443
E value 6.0e-44
Match length 89
% identity 99

NCBI Description (AL049711) gamma response I protein [Arabidopsis thaliana]

Seq. No. 165032

Seq. ID LIB3177-084-P1-K1-G5

Method BLASTN
NCBI GI 94314374
BLAST score 297
E value 1.0e-166
Match length 462



% identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165033 LIB3177-084-P1-K1-G6 Seq. ID Method BLASTX NCBI GI g1173218 BLAST score 616 E value 3.0e-64 Match length 122 99 % identity 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal NCBI Description protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] Seq. No. 165034 LIB3177-084-P1-K1-G7 Seq. ID Method BLASTN NCBI GI g2264316 91 BLAST score 2.0e-43 E value 404 Match length 36 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRO11, complete sequence [Arabidopsis thaliana] 165035 Seq. No. LIB3177-084-P1-K1-G8 Seq. ID BLASTX Method NCBI GI g2330797 BLAST score 226 1.0e-18 E value Match length 114 % identity 43 NCBI Description (Z98601) zinc finger protein [Schizosaccharomyces pombe] Seq. No. 165036 Seq. ID LIB3177-084-P1-K1-G9 Method BLASTX NCBI GI g4741960 BLAST score 358 E value 3.0e - 34Match length 76 % identity NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 165037

Seq. ID LIB3177-084-P1-K1-H10

Method BLASTX NCBI GI q115385 BLAST score 555 E value 4.0e-57 Match length 111 % identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting



chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                  165038
                  LIB3177-084-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3983125
BLAST score
                  645
E value
                  9.0e-68
Match length
                  126
                  100
% identity
NCBI Description
                  (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  165039
                  LIB3177-084-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  75
E value
                  2.0e-56
                  107
Match length
                  87
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  165040
                  LIB3177-084-P1-K1-H4
Seq. ID
Method
                  BLASTN
                  g2576362
NCBI GI
BLAST score
                  115
E value
                  2.0e-58
Match length
                  123
% identity
NCBI Description
                  Arabidopsis thaliana amino acid transport protein mRNA,
                  complete cds
Seq. No.
                  165041
                  LIB3177-084-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  475
E value
                  9.0e-48
Match length
                  91
% identity
                  100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165042
Seq. ID
                  LIB3177-084-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1145697
BLAST score
                  316
E value
```

22133

2.0e-29

68 94

Match length

% identity

NCBI Description



```
NCBI Description
                   (U39485) delta tonoplast integral protein [Arabidopsis
                   thaliana]
                   165043
Seq. No.
Seq. ID
                   LIB3177-084-P1-K1-H8
Method
                  BLASTX
                   g282833
NCBI GI
BLAST score
                   344
E value
                   7.0e-33
Match length
                   78
                   91
% identity
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
Seq. No.
                  165044
                  LIB3177-085-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3337347
BLAST score
                   185
E value
                   1.0e-99
Match length
                   445
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F13P17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165045
Seq. ID
                  LIB3177-085-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  q4662640
BLAST score
                   446
E value
                   0.0e + 00
Match length
                   458
% identity
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   165046
Seq. ID
                  LIB3177-085-P1-K1-A11
Method
                  BLASTX
NCBI GI
                   q3928758
BLAST score
                  555
E value
                   3.0e-57
Match length
                  116
% identity
                   91
NCBI Description
                  (AB007987) Lipoic acid synthase [Arabidopsis thaliana]
                  >gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid
                  synthase [Arabidopsis thaliana]
Seq. No.
                  165047
Seq. ID
                  LIB3177-085-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4512615
BLAST score
                  164
E value
                  3.0e-55
Match length
                  116
% identity
                  100
```

(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb F14478



comes from this gene. [Arabidopsis thaliana]

```
Seq. No.
                  165048
                  LIB3177-085-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  q2832625
NCBI GI
BLAST score
                  693
                  3.0e-73
E value
Match length
                  128
% identity
                  100
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  165049
Seq. No.
                  LIB3177-085-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263771
BLAST score
                  515
E value
                  2.0e-52
                  152
Match length
                  70
% identity
                  (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                  precursor [Arabidopsis thaliana]
                  >gi 4726121 gb AAD28321.1 AC006436 12 (AC006436) putative
                  nonspecific lipid-transfer protein precursor [Arabidopsis
                  thaliana]
                  165050
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4204285
                  505
BLAST score
E value
                  2.0e-51
Match length
                  125
                  75
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  165051
                  LIB3177-085-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2358139
BLAST score
                  306
                  1.0e-172
E value
                  306
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  165052
Seq. ID
                  LIB3177-085-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2501188
BLAST score
                  608
E value
                  3.0e-63
Match length
                  146
% identity
                  84
```

22135

NCBI Description THIAZOLE BIOSYNTHETIC ENZYME >gi 2129750 pir S71191 TH14



protein homolog - Arabidopsis thaliana >gi_1113783 (U17589)
Thi1 protein [Arabidopsis thaliana]

 Seq. No.
 165053

 Seq. ID
 LIB3177-085-P1-K1-A7

 Method
 BLASTN

 NCBI GI
 g3420042

BLAST score 136
E value 2.0e-70
Match length 429
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165054

Seq. ID LIB3177-085-P1-K1-A8

Method BLASTN
NCBI GI g4589419
BLAST score 373
E value 0.0e+00
Match length 429
% identity 48

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2I5, complete sequence

Seq. No. 165055

Seq. ID LIB3177-085-P1-K1-A9

Method BLASTN
NCBI GI g2760316
BLAST score 303
E value 1.0e-170
Match length 373
% identity 97

NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 165056

Seq. ID LIB3177-085-P1-K1-B1

Method BLASTX
NCBI GI g3885511
BLAST score 420
E value 3.0e-41
Match length 103
% identity 82

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 165057

Seq. ID LIB3177-085-P1-K1-B10

Method BLASTX
NCBI GI g132102
BLAST score 729
E value 2.0e-77
Match length 138
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 165058

Seq. ID LIB3177-085-P1-K1-B11

Method BLASTX
NCBI GI g3914826
BLAST score 498
E value 1.0e-50
Match length 98
% identity 100

NCBI Description DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR >gi_2330560_emb_CAA69972_ (Y08722) chloroplast

single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_2330564_emb_CAA69717_ (Y08463) chloroplast

single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_4115372 (AC005967) chloroplast single subunit

DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No. 165059

Seq. ID LIB3177-085-P1-K1-B2

Method BLASTX
NCBI GI g4455248
BLAST score 363
E value 1.0e-34
Match length 77
% identity 100

NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No. 165060

Seq. ID LIB3177-085-P1-K1-B3

Method BLASTX
NCBI GI 94337175
BLAST score 668
E value 2.0e-70
Match length 148
% identity 90

NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906,

gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 165061

Seq. ID LIB3177-085-P1-K1-B4

Method BLASTN
NCBI GI 94454447
BLAST score 24
E value 5.0e-04
Match length 159
% identity 76

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165062

Seq. ID LIB3177-085-P1-K1-B5



Method BLASTN NCBI GI g16407 BLAST score 207 E value 1.0e-112 Match length 207 100 % identity NCBI Description Arabidopsis thaliana PIP1b gene Seq. No. 165063 LIB3177-085-P1-K1-B6 Seq. ID Method BLASTX NCBI GI g3142289

BLAST score 48 2.0e-53 E value Match length 118 % identity 92

(AC002411) Strong similarity to beta-keto-Coa synthase NCBI Description gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No. 165064

LIB3177-085-P1-K1-B7 Seq. ID

Method BLASTX NCBI GI g2497733 BLAST score 591 2.0e-61 E value Match length 117

97 % identity

NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description

>gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown

protein [Arabidopsis thaliana]

Seq. No. 165065

Seq. ID LIB3177-085-P1-K1-B8

Method BLASTX NCBI GI g4263655 BLAST score 205 6.0e-26 E value Match length 74

76 % identity

NCBI Description (AC006136) putative reverse transcriptase [Arabidopsis

thaliana]

165066 Seq. No.

Seq. ID LIB3177-085-P1-K1-B9

Method BLASTX NCBI GI q4336756 BLAST score 688 E value 1.0e-72 Match length 134 % identity 97

NCBI Description (AF104453) catalase [Brassica juncea]

165067 Seq. No.

Seq. ID LIB3177-085-P1-K1-C10

Method BLASTX NCBI GI g3688799



```
BLAST score 168
E value 1.0e-11
Match length 53
% identity 68
NCBI Description (AF0571 thalian
```

NCBI Description (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

LIB3177-085-P1-K1-C11

Method BLASTX
NCBI GI g1769905
BLAST score 49
E value 1.0e-21

E value 1.0 Match length 86 % identity 69

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3177-085-P1-K1-C12

165069

Method BLASTN
NCBI GI 94835223
BLAST score 437
E value 0.0e+00
Match length 462
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3

(ESSA project)

Seq. No. 165070

Seq. ID LIB3177-085-P1-K1-C2

Method BLASTX
NCBI GI 94454036
BLAST score 642
E value 2.0e-75
Match length 139
% identity 99

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 165071

Seq. ID LIB3177-085-P1-K1-C3

Method BLASTX
NCBI GI g4538963
BLAST score 523
E value 2.0e-53
Match length 136
% identity 60

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 165072

Seq. ID LIB3177-085-P1-K1-C5

Method BLASTN NCBI GI g3236234 BLAST score 244



```
1.0e-135
E value
Match length
                  324
                  93
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165073
                  LIB3177-085-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g4415907
NCBI GI
BLAST score
                  538
E value
                  4.0e-55
Match length
                  108
                  97
% identity
                  (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
NCBI Description
                  >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative
                  60S ribosomal protein L24 [Arabidopsis thaliana]
                  165074
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4220627
BLAST score
                  128
E value
                  1.0e-65
Match length
                  468
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K20J1, complete sequence [Arabidopsis thaliana]
                  165075
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q4741960
BLAST score
                  589
E value
                  4.0e-61
Match length
                  126
% identity
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  165076
Seq. ID
                  LIB3177-085-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2160168
BLAST score
                  752
E value
                  3.0e-80
Match length
                  151
% identity
                  (AC000132) Strong similarity to R. communis
NCBI Description
                  phosphoglycerate mutase (gb X70652). ESTs
```

gb T41853, gb T76648 come from this gene. [Arabidopsis

thaliana]

Seq. No. 165077

Seq. ID LIB3177-085-P1-K1-D11

Method BLASTX
NCBI GI g4102703
BLAST score 268

Seq. ID

Method



```
E value
                  1.0e-23
                  56
Match length
                  98
% identity
                   (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
NCBI Description
                  thaliana]
                  165078
Seq. No.
                  LIB3177-085-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132102
BLAST score
                  767
E value
                  6.0e-82
Match length
                  140
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  165079
Seq. No.
                  LIB3177-085-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828185
BLAST score
                  166
E value
                  2.0e-88
Match length
                  317
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUD21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165080
                  LIB3177-085-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                  517
                  9.0e-53
E value
Match length
                  100
                  97
% identity
                  40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  165081
Seq. ID
                  LIB3177-085-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4455251
BLAST score
                  443
E value
                  6.0e-44
Match length
                  132
% identity
                  67
NCBI Description
                  (AL035523) magnesium-protoporphyrin IX
                  methyltransferase-like protein [Arabidopsis thaliana]
Seq. No.
                  165082
```

22141

LIB3177-085-P1-K1-D5

BLASTX

Match length

% identity

341



```
NCBI GI
                    q1657621
 BLAST score
                    774
 E value
                    9.0e-83
 Match length
                    159
  % identity
                    92
NCBI Description
                   (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
                    putative acyl-coA dehydrogenase [Arabidopsis thaliana]
  Seq. No.
                    165083
  Seq. ID
                    LIB3177-085-P1-K1-D8
 Method
                    BLASTN
 NCBI GI
                    q2564046
 BLAST score
                    178
 E value
                    2.0e-95
 Match length
                    471
  % identity
                    99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MGI19, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    165084
  Seq. ID
                    LIB3177-085-P1-K1-D9
 Method
                    BLASTX
 NCBI GI
                    q2894564
 BLAST score
                    127
 E value
                    9.0e-28
 Match length
                    65
  % identity
                    98
 NCBI Description (AL021890) putative protein [Arabidopsis thaliana]
  Seq. No.
                    165085
                    LIB3177-085-P1-K1-E1
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4741960
 BLAST score
                    472
 E value
                    2.0e-47
 Match length
                    109
  % identity
                    83
 NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
  Seq. No.
                    165086
  Seq. ID
                    LIB3177-085-P1-K1-E11
                    BLASTX
 Method
 NCBI GI
                    g4741940
  BLAST score
                    637
 E value
                    1.0e-66
                    119
 Match length
  % identity
                    68
  NCBI Description (AF134120) Lhca2 protein [Arabidopsis thaliana]
  Seq. No.
                    165087
  Seq. ID
                    LIB3177-085-P1-K1-E12
  Method
                    BLASTN
  NCBI GI
                    g2618601
  BLAST score
                    301
 E value
                    1.0e-169
```



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 165088
Seq. ID LIB3177-085-P1-K1-E2
```

Method BLASTX
NCBI GI g4539459
BLAST score 165
E value 8.0e-12
Match length 58
% identity 57

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 165089

Seq. ID LIB3177-085-P1-K1-E3

Method BLASTX
NCBI GI g1175012
BLAST score 149
E value 3.0e-39
Match length 87
% identity 99

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN

B) (TMP-B) >gi 396218 emb CAA49155 (X69294) transmembrane

protein TMP-B [Arabidopsis thaliana]

Seq. No. 165090

Seq. ID LIB3177-085-P1-K1-E5

Method BLASTX
NCBI GI g133709
BLAST score 149
E value 2.0e-09
Match length 45
% identity 60

NCBI Description CYANELLE 30S RIBOSOMAL PROTEIN S10 >gi_70927_pir__R3KT10

ribosomal protein S10 - Cyanophora paradoxa cyanelle

>gi_11391_emb_CAA36388_ (X52143) ribosomal protein S10 (AA
1-105) [Cyanophora paradoxa] >gi_336632 (M35206) ribosomal
protein S10 (rps10; rpsJ) [Cyanophora paradoxa] >gi_1016150

(U30821) ribosomal protein S10 [Cyanophora paradoxa]

Seq. No. 165091

Seq. ID LIB3177-085-P1-K1-E6

Method BLASTX
NCBI GI g282865
BLAST score 616
E value 3.0e-64
Match length 123
% identity 70

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]

>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 165092

Seq. ID LIB3177-085-P1-K1-E7



Method BLASTN
NCBI GI g2244950
BLAST score 145
E value 9.0e-76
Match length 201
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 165093

Seq. ID LIB3177-085-P1-K1-E8

Method BLASTX
NCBI GI g2970036
BLAST score 145
E value 6.0e-09
Match length 35
% identity 83

NCBI Description (D88537) delta 9 desaturase [Arabidopsis thaliana]

Seq. No. 165094

Seq. ID LIB3177-085-P1-K1-E9

Method BLASTX
NCBI GI g4544443
BLAST score 167
E value 9.0e-12
Match length 33
% identity 100

NCBI Description (AC006592) putative mitochondrial uncoupling protein

[Arabidopsis thaliana]

Seq. No. 165095

Seq. ID LIB3177-085-P1-K1-F10

Method BLASTX
NCBI GI g4741952
BLAST score 366
E value 4.0e-35
Match length 108
% identity 68

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 165096

Seq. ID LIB3177-085-P1-K1-F11

Method BLASTX
NCBI GI g3249100
BLAST score 516
E value 9.0e-53
Match length 103
% identity 94

NCBI Description (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698

and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]

Seq. No. 165097

Seq. ID LIB3177-085-P1-K1-F12

Method BLASTX NCBI GI g417381 BLAST score 668



E value 2.0e-70 Match length 150 % identity 88

NITRILASE 1 >gi 99738 pir S22398 nitrilase (EC 3.5.5.1) -NCBI Description

Arabidopsis thaliana >gi 16400 emb CAA45041 (X63445)

nitrilase I [Arabidopsis thaliana]

165098 Seq. No.

LIB3177-085-P1-K1-F2 Seq. ID

Method BLASTX NCBI GI g115767 706 BLAST score 7.0e-75 E value Match length 132 % identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165099

LIB3177-085-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI q4741952 BLAST score 552 E value 7.0e-57 Match length 108 97 % identity

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

165100 Seq. No.

LIB3177-085-P1-K1-F5 Seq. ID

Method BLASTN NCBI GI q2462264 BLAST score 33 E value 7.0e-09 Match length 53

91 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 165101

Seq. ID LIB3177-085-P1-K1-F6

Method BLASTX NCBI GI q2583125 BLAST score 368 E value 4.0e-35 Match length 108 % identity

NCBI Description (AC002387) putative transketolase precursor [Arabidopsis

thaliana]

165102 Seq. No.

Seq. ID LIB3177-085-P1-K1-F7

Method BLASTX



g417103 NCBI GI BLAST score 453 3.0e-45 E value 92 Match length 100 % identity HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] $>gi_4885\overline{7}7$ (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 165103

Seq. ID LIB3177-085-P1-K1-F8

Method BLASTN
NCBI GI g2262135
BLAST score 340
E value 0.0e+00
Match length 456
% identity 100

NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15

cM, complete sequence

Seq. No. 165104

Seg. ID LIB3177-085-P1-K1-F9

Method BLASTX
NCBI GI g320558
BLAST score 511
E value 4.0e-52
Match length 117
% identity 89

NCBI Description DNA-binding protein - Arabidopsis thaliana >gi_601843

(M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No. 165105

Seq. ID LIB3177-085-P1-K1-G1

Method BLASTX
NCBI GI g1755160
BLAST score 526
E value 1.0e-53
Match length 114
% identity 89

NCBI Description (U75191) germin-like protein [Arabidopsis thaliana]

>gi 1755174 (U75198) germin-like protein [Arabidopsis



thaliana]

Seq. No. 165106 LIB3177-085-P1-K1-G10 Seq. ID Method BLASTX NCBI GI g3915847

BLAST score 650 2.0e-68 E value 131 Match length 96 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative

40S ribosomal protein S2 [Arabidopsis thaliana]

165107 Seq. No.

LIB3177-085-P1-K1-G11 Seq. ID

Method BLASTX NCBI GI q113026 BLAST score 729 2.0e-77 E value Match length 151 91 % identity

ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) NCBI Description

>gi 68211 pir WZRPI isocitrate lyase (EC 4.1.3.1) - rape

>gi 255220 bbs 112862 isocitrate lyase, threo-D

S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf_ 1913424A

isocitrate lyase [Brassica napus]

165108 Seq. No.

LIB3177-085-P1-K1-G12 Seq. ID

Method BLASTX g1922944 NCBI GI BLAST score 244 E value 7.0e-21Match length 69 % identity 74

(AC000106) Strong similarity to Picea histone H2A NCBI Description

(gb X67819). ESTs gb ATTS3874, gb T46627, gb T14194 come from

this gene. [Arabidopsis thaliana]

Seq. No. 165109

Seq. ID LIB3177-085-P1-K1-G2

Method BLASTX NCBI GI g132110 BLAST score 657 E value 4.0e-69 Match length 122 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165110



```
LIB3177-085-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510385
BLAST score
                  571
E value
                  5.0e-59
Match length
                  142
                  75
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                  165111
Seq. No.
                  LIB3177-085-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2191126
BLAST score
                  208
E value
                  1.0e-113
                  208
Match length
% identity
                  100
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  165112
                  LIB3177-085-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3912997
BLAST score
                  509
E value
                  9.0e-52
Match length
                  113
% identity
                  94
NCBI Description FLORAL HOMEOTIC PROTEIN AGL15 >gi 2129535 pir S71200 AGL15
                  protein - Arabidopsis thaliana >gi_790635 (U22528) AGL15
                  [Arabidopsis thaliana]
                  165113
Seq. No.
                  LIB3177-085-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1161926
BLAST score
                  326
                  3.0e-30
E value
                  161
Match length
% identity
                  46
NCBI Description (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
                  max]
Seq. No.
                  165114
Seq. ID
                  LIB3177-085-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4586021
BLAST score
                  719
                  2.0e-76
E value
Match length
                  138
```

% identity 100

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 165115

Seq. ID LIB3177-085-P1-K1-G9

Method BLASTX NCBI GI q282865



```
594
BLAST score
                  1.0e-61
E value
                  120
Match length
                  69
% identity
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  165116
Seq. No.
                  LIB3177-085-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  g4263525
NCBI GI
BLAST score
                  617
                  2.0e-64
E value
                  143
Match length
                  85
% identity
                  (AC004044) putative photosystem I reaction center subunit
NCBI Description
                  II precursor [Arabidopsis thaliana]
Seq. No.
                  165117
                  LIB3177-085-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160151
                  601
BLAST score
E value
                  2.0e-62
Match length
                  129
                  89
% identity
NCBI Description
                  (AC000375) Strong similarity to Brassica aspartic protease
                   (gb_X77260). [Arabidopsis thaliana]
                  165118
Seq. No.
                  LIB3177-085-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  533
E value
                   9.0e-55
Match length
                  101
% identity
                   99
NCBI Description
                 (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                  165119
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1550740
BLAST score
                   436
E value
                  8.0e-49
                  99
Match length
                  99
% identity
NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
```

165120 Seq. No.

Seq. ID LIB3177-085-P1-K1-H2

Method BLASTX NCBI GI g541858



BLAST score 657 E value 4.0e-69 Match length 126 % identity 99

NCBI Description endoxyloglucan transferase - Arabidopsis thaliana >gi 469484 dbj BAA03921 (D16454) endo-xyloglucan

>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)

endo-xyloglucan transferase [Arabidopsīs thaliana]

Seq. No. 165121

Seq. ID LIB3177-085-P1-K1-H3

Method BLASTX
NCBI GI g2654122
BLAST score 321
E value 9.0e-30
Match length 102
% identity 66

NCBI Description (AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No. 165122

Seq. ID LIB3177-085-P1-K1-H4

Method BLASTX
NCBI GI g115783
BLAST score 589
E value 3.0e-61
Match length 112
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 165123

Seq. ID LIB3177-085-P1-K1-H5

Method BLASTX
NCBI GI g336392
BLAST score 336
E value 7.0e-40
Match length 129
% identity 75

NCBI Description (J05215) ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 165124

Seq. ID LIB3177-085-P1-K1-H6

Method BLASTN
NCBI GI g3228389
BLAST score 253
E value 1.0e-140
Match length 473
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 165125

Seq. ID LIB3177-085-P1-K1-H7

Method BLASTX NCBI GI g4586256



```
BLAST score 598
E value 3.0e-62
Match length 144
% identity 82
NCBI Description (AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]
Seq. No. 165126
```

Seq. ID LIB3177-085-P1-K1-H8

Method BLASTX
NCBI GI g2618723
BLAST score 650
E value 3.0e-68
Match length 130
% identity 96

NCBI Description (U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]

>gi_4389514_gb_AAB70451_ (AC000104) Identical to

Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis

thaliana]

 Seq. No.
 165127

 Seq. ID
 LIB3177-085-P1-K1-H9

 Method
 BLASTN

 NCBI GI
 g2191126

 BLAST score
 355

 E value
 0.0e+00

E value 0.0e+00
Match length 371
% identity 99

NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 165128

Seq. ID LIB3177-086-P1-K1-A1

Method BLASTX
NCBI GI g4585966
BLAST score 547
E value 2.0e-56
Match_length 110
% identity 95

NCBI Description (AC005287) Putative dihyrdolipoamide acetyltransferase

[Arabidopsis thaliana]

Seq. No. 165129

Seq. ID LIB3177-086-P1-K1-A11

Method BLASTX
NCBI GI g2581783
BLAST score 410
E value 3.0e-40
Match length 89
% identity 92

NCBI Description (U94998) class 1 non-symbiotic hemoglobin [Arabidopsis

thaliana] >gi_4678203_gb_AAD26949.1_AC007134_7 (AC007134)

class 1 non-symbiotic hemoglobin (AHB1) [Arabidopsis

thaliana]

Seq. No. 165130



```
LIB3177-086-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829891
                  396
BLAST score
E value
                  9.0e-39
                  91
Match length
                  87
% identity
                  (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165131
                  LIB3177-086-P1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220644
                  155
BLAST score
                  9.0e-82
E value
                  395
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
                  165132
Seq. No.
                  LIB3177-086-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g543841
NCBI GI
                  543
BLAST score
E value
                   9.0e-56
Match length
                  108
% identity
                   97
                  ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875
NCBI Description
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >qi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                  165133
Seq. ID
                  LIB3177-086-P1-K1-A5
Method
                  BLASTX
NCBI GI
                   g1175013
                   531
BLAST score
                   2.0e-54
E value
Match length
                  119
% identity
                   87
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084
NCBI Description
                   plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                   >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                   protein 2a [Arabidopsis thaliana]
Seq. No.
                   165134
                   LIB3177-086-P1-K1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q928931
BLAST score
                   203
E value
                   1.0e-110
                   227
Match length
                   97
% identity
```

NCBI Description A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases



```
165135
Seq. No.
Seq. ID
                   LIB3177-086-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q132677
BLAST score
                   71
                   8.0e-36
E value
Match length
                   112
% identity
                   75
                   50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
NCBI Description
                   >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor,
                   chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_
                   (Z11508) Plastid ribosomal protein CL15 [Arabidopsis
                   thalianal
                   165136
Seq. No.
Seq. ID
                   LIB3177-086-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   q99696
BLAST score
                   314
                   4.0e-29
E value
Match length
                   84
% identity
                   76
NCBI Description
                   glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                   chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                   >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                   synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                   aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                   synthetase [Arabidopsis thaliana]
Seq. No.
                   165137
Seq. ID
                   LIB3177-086-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g1402908
BLAST score
                   197
E value
                   5.0e-65
Match length
                   132
% identity
                   93
NCBI Description
                   (X98315) peroxidase [Arabidopsis thaliana]
                   >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                   peroxidase [Arabidopsis thaliana]
Seq. No.
                   165138
Seq. ID
                   LIB3177-086-P1-K1-B11
Method
                   BLASTX
                   q2062161
                   668
                   2.0e-70
                   126
% identity
                   50
```

NCBI GI BLAST score E value Match length

(AC001645) jasmonate inducible protein isolog [Arabidopsis NCBI Description

thaliana]

Seq. No. 165139

Seq. ID LIB3177-086-P1-K1-B12

Method BLASTX



```
q3450842
NCBI GI
BLAST score
                  403
                  1.0e-39
E value
Match length
                  86
% identity
                  87
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  165140
                  LIB3177-086-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4587641
BLAST score
                  212
E value
                  1.0e-115
Match length
                  373
% identity
                  99
NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  165141
                  LIB3177-086-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  557
E value
                  2.0e-57
Match length
                  103
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  165142
Seq. ID
                  LIB3177-086-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4584110
BLAST score
                  299
E value
                  4.0e-27
Match length
                  111
% identity
NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]
Seq. No.
                  165143
                  LIB3177-086-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510336
BLAST score
                  47
E value
                  3.0e-17
Match length
                  146
                  88
% identity
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 165144

Seq. ID LIB3177-086-P1-K1-C1

Method BLASTX NCBI GI g3242722



```
BLAST score
                  778
E value
                  3.0e-83
                  147
Match length
                  100
% identity
                 (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                  thaliana]
                  165145
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-C10
                  BLASTX
Method
NCBI GI
                  g4582787
BLAST score
                  473
E value
                  1.0e-47
Match length
                  109
                  82
% identity
NCBI Description (AJ012281) adenosine kinase [Zea mays]
                  165146
Seq. No.
                  LIB3177-086-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3273743
BLAST score
                  281
E value
                  2.0e-49
Match length
                  118
% identity
                  80
                 (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi_3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
                  165147
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  294
                  2.0e-26
E value
Match length
                  105
% identity
                  61
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi 99658 pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi_445607_prf__1909354A adenylate translocator
                  [Arabidopsis thaliana]
Seq. No.
                  165148
                  LIB3177-086-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  q2058282
NCBI GI
BLAST score
                  371
                  1.0e-35
E value
Match length
                  101
% identity
```

NCBI Description (X97377) atranbpla [Arabidopsis thaliana]

Seq. No. 165149

Seq. ID LIB3177-086-P1-K1-C4



Method BLASTN
NCBI GI g4757409
BLAST score 414
E value 0.0e+00
Match length 443
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVC8, complete sequence

Seq. No. 165150

Seq. ID LIB3177-086-P1-K1-C5

Method BLASTX
NCBI GI g2832363
BLAST score 656
E value 6.0e-69
Match length 125
% identity 100

NCBI Description (Y14075) HMG protein [Arabidopsis thaliana]

>gi 3367575 emb CAA20027 (AL031135) HMG delta protein

[Arabidopsis thaliana]

Seq. No. 165151

Seq. ID LIB3177-086-P1-K1-C6

Method BLASTN
NCBI GI g4490324
BLAST score 320
E value 1.0e-180
Match length 340

% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 165152

Seq. ID LIB3177-086-P1-K1-C7

Method BLASTX
NCBI GI g2246621
BLAST score 342
E value 1.0e-32
Match length 71
% identity 96

NCBI Description (AF004393) salt-stress induced tonoplast intrinsic protein

[Arabidopsis thaliana]

Seq. No. 165153

Seq. ID LIB3177-086-P1-K1-C8

Method BLASTX
NCBI GI g3914740
BLAST score 491
E value 9.0e-50
Match longth 106

Match length 106 % identity 91

NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941

(D78495) ribosomal protein [Brassica rapa]

Seq. No. 165154

Seq. ID LIB3177-086-P1-K1-C9

Method BLASTX



NCBI GI g421826 BLAST score 284 E value 1.0e-25 Match length 73 % identity 74

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 165155

Seq. ID LIB3177-086-P1-K1-D1

Method BLASTN
NCBI GI g4309683
BLAST score 132
E value 2.0e-68
Match length 152
% identity 97

NCBI Description Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 165156

Seq. ID LIB3177-086-P1-K1-D10

Method BLASTX
NCBI GI g115767
BLAST score 626
E value 2.0e-65
Match length 119
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165157

Seq. ID LIB3177-086-P1-K1-D11

Method BLASTX
NCBI GI g4585935
BLAST score 499
E value 4.0e-58
Match length 114
% identity 100

NCBI Description (AC007211) putative chlorophyll A/B binding protein

[Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1

(AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 165158

Seq. ID LIB3177-086-P1-K1-D12

Method BLASTN
NCBI GI g2584827
BLAST score 173
E value 2.0e-92
Match length 339
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,



complete sequence [Arabidopsis thaliana]

Seq. No. 165159 LIB3177-086-P1-K1-D2 Seq. ID BLASTX Method NCBI GI q4587541 BLAST score 653 1.0e-68 E value 132 Match length 97 % identity (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase NCBI Description with GDSL-motif family. ESTs gb_T44453, gb_T04815, gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from this gene. [Arabidopsis thaliana] 165160 Seq. No. LIB3177-086-P1-K1-D3 Seq. ID Method BLASTN NCBI GI g3510347 BLAST score 229 1.0e-126 E value Match length 373 100 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana] Seq. No. 165161 LIB3177-086-P1-K1-D4 Seq. ID Method BLASTX NCBI GI g3157944 BLAST score 308 E value 4.0e-59 Match length 122 % identity 94 NCBI Description (AC002131) Very strong similarity to aminomethyltransferase precursor gb U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T137 $\overline{4}$ 2, gb_Z265 $\overline{4}$ 5, gb_T2075 $\overline{3}$ and gb_W43123 come from this ge Seq. No. 165162 Seq. ID LIB3177-086-P1-K1-D6 Method BLASTX NCBI GI g4741962 BLAST score 280 E value 2.0e-50 Match length 145 % identity NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana] Seq. No. 165163 Seq. ID LIB3177-086-P1-K1-D7 Method BLASTX

Method BLASTX
NCBI GI g2119846
BLAST score 323
E value 6.0e-58
Match length 120



% identity NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 165164 Seq. ID LIB3177-086-P1-K1-D8 Method BLASTX NCBI GI q2695965 BLAST score 171 E value 3.0e-12 Match length 126 % identity

NCBI Description (AL010186) pks4 [Mycobacterium tuberculosis]

Seq. No. 165165

Seq. ID LIB3177-086-P1-K1-D9

Method BLASTX
NCBI GI g3157944
BLAST score 356
E value 2.0e-34
Match length 75
% identity 95

NCBI Description (AC002131) Very strong similarity to aminomethyltransferase

precursor gb U79769 from Mesembryanthemum crystallinum.

ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773,

 $gb_N380\overline{3}8$, $gb_T137\overline{4}2$, $gb_Z265\overline{4}5$, $gb_T2075\overline{3}$ and gb_W43123

come from this ge

Seq. No. 165166

Seq. ID LIB3177-086-P1-K1-E10

Method BLASTN
NCBI GI g3702732
BLAST score 199
E value 1.0e-108
Match length 290
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGF10, complete sequence [Arabidopsis thaliana]

Seq. No. 165167

Seq. ID LIB3177-086-P1-K1-E2

Method BLASTN
NCBI GI g4581084
BLAST score 256
E value 1.0e-142
Match length 298
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence

Seq. No. 165168

Seq. ID LIB3177-086-P1-K1-E3



Seq. No. 165169
Seq. ID LIB3177-086-P1-K1-E4

Method BLASTX
NCBI GI g2497733
BLAST score 143
E value 1.0e-35
Match length 79

% identity 99

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown

protein [Arabidopsis thaliana]

Seq. No. 165170

Seq. ID LIB3177-086-P1-K1-E5

Method BLASTN
NCBI GI g598068
BLAST score 207
E value 1.0e-113
Match length 222
% identity 98

NCBI Description Arabidopsis thaliana cinnamyl alcohol dehydrogenase (CAD1)

mRNA, cds 3' end

Seq. No. 165171

Seq. ID LIB3177-086-P1-K1-E6

Method BLASTN
NCBI GI g1465367
BLAST score 64
E value 1.0e-27
Match length 128
% identity 88

NCBI Description A.thaliana mRNA for RAP-1 protein

Seq. No. 165172

Seq. ID LIB3177-086-P1-K1-E8

Method BLASTX
NCBI GI g4455244
BLAST score 514
E value 2.0e-52
Match length 102
% identity 100

NCBI Description (AL035523) MtN3-like protein [Arabidopsis thaliana]

Seq. No. 165173

Seq. ID LIB3177-086-P1-K1-E9

Method BLASTX NCBI GI g4506635



```
BLAST score
                   267
E value
                   8.0e-37
                   109
Match length
                   65
% identity
                   ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S
NCBI Description
                   RIBOSOMAL PROTEIN L32 >gi 71335 pir R5HU32 ribosomal
                   protein L32 - human >gi 71336 pir R5MS32 ribosomal protein
                   L32 - mouse >gi_71337_pir_ R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048 (X03342) rpL32 (aa 1-135) [Homo
                   sapiens] >gi_57117_emb_CAA29777_ (X06483) ribosomal protein
                   L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal
                   protein L32-3A [Mus musculus] >gi_226004_prf__1405339A
                   ribosomal protein L32 [Rattus norvegicus]
Seq. No.
                   165174
                   LIB3177-086-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3298443
BLAST score
                   280
E value
                   7.0e-25
Match length
                   70
                   73
% identity
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacum]
```

Seq. No. 165175

Seq. ID LIB3177-086-P1-K1-F11 Method BLASTX NCBI GI g3650028 BLAST score 582 E value 3.0e-60 Match length 134 % identity 89

NCBI Description (AC005396) putative 22 kDa peroxisomal membrane protein

[Arabidopsis thaliana]

Seq. No. 165176

LIB3177-086-P1-K1-F12 Seq. ID

Method -BLASTX NCBI GI q1168728 BLAST score 711 E value 2.0e-75 Match length 132 % identity

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi 598071 (L37883)

cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 165177

Seq. ID LIB3177-086-P1-K1-F2

Method BLASTN NCBI GI g3980374 BLAST score 46 E value 4.0e-17

Match length 146 % identity 83

NCBI Description Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

% identity

67



```
Seq. No.
                   165178
Seq. ID
                  LIB3177-086-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3096931
BLAST score
                   557
                   2.0e-57
E value
Match length
                  113
% identity
                   96
NCBI Description
                  (AL023094) putative ribosomal protein S16 [Arabidopsis
                  thaliana]
Seq. No.
                  165179
                  LIB3177-086-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                   400
                   6.0e-39
E value
                  123
Match length
% identity
                   70
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                   >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
                   165180
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-F5
Method
                  BLASTN
NCBI GI
                   q3738275
BLAST score
                   228
E value
                   1.0e-125
Match length
                   421
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165181
Seq. ID
                   LIB3177-086-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g2160716
BLAST score
                   430
E value
                   0.0e + 00
Match length
                   442
% identity
                   99
NCBI Description Arabidopsis thaliana GUT15 mRNA, complete cds
Seq. No.
                   165182
Seq. ID
                   LIB3177-086-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   g3287695
BLAST score
                   396
                   2.0e-38
E value
Match length
                  107
```

22162

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2



gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No. 165183

Seq. ID LIB3177-086-P1-K1-F9

Method BLASTN
NCBI GI g16428
BLAST score 124
E value 3.0e-63
Match length 245
% identity 98

NCBI Description A.thaliana posF21 gene

Seq. No. 165184

Seq. ID LIB3177-086-P1-K1-G10

Method BLASTX
NCBI GI g2632059
BLAST score 655
E value 7.0e-69
Match length 145
% identity 88

NCBI Description (AJ002596) patatin-like protein [Arabidopsis thaliana]

Seq. No. 165185

Seq. ID LIB3177-086-P1-K1-G11

Method BLASTX
NCBI GI g2341034
BLAST score 303
E value 7.0e-28
Match length 63
% identity 95

NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 165186

Seq. ID LIB3177-086-P1-K1-G12

Method BLASTX
NCBI GI g4585935
BLAST score 714
E value 9.0e-76
Match length 134
% identity 100

NCBI Description (AC007211) putative chlorophyll A/B binding protein

[Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1

(AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 165187

Seq. ID LIB3177-086-P1-K1-G2

Method BLASTX
NCBI GI g2738248
BLAST score 745
E value 2.0e-79
Match length 144
% identity 97

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 165188



```
LIB3177-086-P1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3348076
BLAST score
                   189
E value
                   1.0e-102
Match length
                   241
                   95
% identity
                   Arabidopsis thaliana isochorismate synthase mRNA, complete
NCBI Description
                   165189
Seq. No.
Seq. ID
                   LIB3177-086-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1363488
BLAST score
                   315
E value
                   3.0e-29
                   66
Match length
                   95
% identity
                   IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
NCBI Description
                   IAA8 [Arabidopsis thaliana] >gi 4314364 gb_AAD15575
                   (AC006340) auxin-induced IAA8 protein [Arabidopsis
                   thaliana]
                   165190
Seq. No.
                   LIB3177-086-P1-K1-G5
Seq. ID
Method
                   BLASTX
                   g119975
NCBI GI
BLAST score
                   408
E value
                   5.0e-40
Match length
                   92
                   90
% identity
                   FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
NCBI Description
                   [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
Seq. No.
                   165191
Seq. ID
                   LIB3177-086-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1363489
BLAST score
                   375
E value
                   3.0e-36
Match length
                   102
% identity
                   75
NCBI Description
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   165192
Seq. ID
                   LIB3177-086-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g3892709
BLAST score
                   448
E value
                   1.0e-44
```

22164

90

98

Match length % identity



```
NCBI Description
                 (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                  165193
Seq. ID
                  LIB3177-086-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1076440
BLAST score
                  374
                  6.0e-36
E value
Match length
                  84
                  86
% identity
NCBI Description
                  acyl-CoA binding protein - rape >gi 1076441 pir S49102
                  acyl-CoA binding protein - rape >gi 509265 emb CAA54390
                  (X77134) acyl-CoA binding protein [Brassica napus]
Seq. No.
                  165194
Seq. ID
                  LIB3177-086-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2281089
BLAST score
                  55
E value
                  9.0e-32
Match length
                  74
% identity
                  82
NCBI Description
                  (AC002333) Sm protein F isolog [Arabidopsis thaliana]
Seq. No.
                  165195
                  LIB3177-086-P1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  139
                  4.0e-72
E value
                  390
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  165196
Seq. No.
                  LIB3177-086-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  91
E value
                  6.0e-44
Match length
                  176
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165197
Seq. ID
                  LIB3177-086-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  165
E value
                  7.0e-58
Match length
                  112
% identity
                  90
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
```

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis



thaliana]

```
165198
Seq. No.
                  LIB3177-086-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3510247
                  174
BLAST score
                  5.0e-93
E value
                  427
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F19D11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  165199
Seq. No.
                  LIB3177-086-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493052
BLAST score
                  373
                  8.0e-36
E value
                  70
Match length
                  100
% identity
                  ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
NCBI Description
                  >gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of
                  mitochondrial Fl-ATPase [Arabidopsis thaliana]
Seq. No.
                  165200
Seq. ID
                  LIB3177-086-P1-K1-H8
                  BLASTX
Method
NCBI GI
                  q3201618
BLAST score
                  464
E value
                  2.0e-46
Match length
                  87
                  99
% identity
NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]
Seq. No.
                  165201
Seq. ID
                  LIB3177-086-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q4455248
BLAST score
                  408
E value
                   7.0e-40
                  87
Match length
% identity
                  100
NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]
Seq. No.
                  165202
                  LIB3177-087-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2760327
BLAST score
                  339
E value
                  2.0e-32
Match length
                  65
                  71
% identity
NCBI Description
                  (AC002130) F1N21.12 [Arabidopsis thaliana]
Seq. No.
                  165203
Seq. ID
                  LIB3177-087-P1-K1-A10
```



Method BLASTN
NCBI GI 94733953
BLAST score 270
E value 1.0e-150
Match length 274
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F13011 genomic

sequence, complete sequence

Seq. No. 165204

Seq. ID LIB3177-087-P1-K1-A12

Method BLASTX
NCBI GI g99736
BLAST score 424
E value 5.0e-42
Match length 88
% identity 99

NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -

Arabidopsis thaliana >gi_16187_emb_CAA46814_ (X66016) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No. 165205

Seq. ID LIB3177-087-P1-K1-A2

Method BLASTX
NCBI GI g132074
BLAST score 576
E value 1.0e-59
Match length 107
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (\overline{EC} 4. $\overline{1.1.39}$) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165206

Seq. ID LIB3177-087-P1-K1-A3

Method BLASTN
NCBI GI g2760168
BLAST score 135
E value 3.0e-70
Match length 151
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 165207

Seq. ID LIB3177-087-P1-K1-A4

Method BLASTX
NCBI GI g2495365
BLAST score 461
E value 2.0e-46
Match length 105
% identity 87

NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127 prf 1908431B

heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No. 165208

% identity

NCBI Description

82



```
LIB3177-087-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  q4559369
NCBI GI
                  509
BLAST score
E value
                  1.0e-54
Match length
                  114
                  94
% identity
                  (AC006585) putative Rieske iron-sulfur protein [Arabidopsis
NCBI Description
                  thaliana]
                  165209
Seq. No.
                  LIB3177-087-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2464899
BLAST score
                  551
                  1.0e-56
E value
Match length
                  136
% identity
                  81
                  (Z99708) geranylgeranyl pyrophosphate synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165210
                  LIB3177-087-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273196
BLAST score
                  263
E value
                  3.0e-23
                  60
Match length
                  92
% identity
NCBI Description
                  (AB010915) responce regulator1 [Arabidopsis thaliana]
                  >gi 3323583 (AF057282) two-component response regulator
                  homolog [Arabidopsis thaliana] >gi 3953597 dbj BAA34726
                   (AB008487) response regulator 4 [Arabidopsis thaliana]
Seq. No.
                  165211
Seq. ID
                  LIB3177-087-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q466160
BLAST score
                  370
                  2.0e-35
E value
Match length
                  83
% identity
NCBI Description
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
                  >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                  elegans >gi 289769 (L14429) putative [Caenorhabditis
                  elegans]
Seq. No.
                  165212
Seq. ID
                  LIB3177-087-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g464985
BLAST score
                  163
E value
                  8.0e-12
Match length
                  38
```

LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN

BLAST score

E value

412

9.0e-41



>gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

```
165213
Seq. No.
                  LIB3177-087-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g4337175
NCBI GI
BLAST score
                  647
                  6.0e-68
E value
                  132
Match length
% identity
                  96
                  (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  165214
                  LIB3177-087-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  631
E value
                  4.0e-66
Match length
                  118
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  165215
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1651828
BLAST score
                  443
E value
                  5.0e-44
Match length
                  136
% identity
NCBI Description (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
Seq. No.
                  165216
                  LIB3177-087-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2677614
BLAST score
                  521
E value
                  3.0e-53
Match length
                  102
% identity
                  100
NCBI Description (Y07625) NLM1 protein (NodLikeMip1) [Arabidopsis thaliana]
Seq. No.
                  165217
                  LIB3177-087-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2506443
```



Match length 81 100 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description CHLOROPLAST >gi 2117520 pir JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi 1402885 emb CAA66816 (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana] Seq. No. 165218 LIB3177-087-P1-K1-B6 Seq. ID Method BLASTX NCBI GI q1709203 BLAST score 121 E value 3.0e-19 Match length 73 70 % identity NCBI Description MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMP 1) (INOSITOL MONOPHOSPHATASE 1) >gi_1098977 (U39444) myo-inositol monophosphatase 1 [Lycopersicon esculentum] Seq. No. 165219 LIB3177-087-P1-K1-B7 Seq. ID Method BLASTX g4585882 NCBI GI BLAST score 517 E value 9.0e-53 Match length 104 % identity 98 (AC005850) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana] Seq. No. 165220 Seq. ID LIB3177-087-P1-K1-B8 Method BLASTN NCBI GI q2477521 BLAST score 43 E value 8.0e-15 Match length 417 % identity 14 NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165221 Seq. ID LIB3177-087-P1-K1-C1 Method BLASTX NCBI GI g3914740

Method BLASTX
NCBI GI g3914740
BLAST score 555
E value 4.0e-57
Match length 138
% identity 80

NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi_2160300 dbj BAA18941

(D78495) ribosomal protein [Brassica rapa]

NCBI Description

thaliana]



```
Seq. No.
                  165222
                  LIB3177-087-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1914685
BLAST score
                  300
E value
                  2.0e-27
Match length
                  76
% identity
                  78
                 (Y12014) RAD23 protein, isoform II [Daucus carota]
NCBI Description
Seq. No.
                  165223
                  LIB3177-087-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3269293
BLAST score
                  269
E value
                  1.0e-23
                  101
Match length
                  56
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                  165224
Seq. No.
                  LIB3177-087-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1769904
BLAST score
                  31
E value
                  1.0e-08
Match length
                  51
                  90
% identity
NCBI Description A.thaliana psbP gene
Seq. No.
                  165225
                  LIB3177-087-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121075
BLAST score
                  459
E value
                  7.0e-46
Match length
                  140
% identity
                  69
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >qi 166725
                   (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi_861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi_445119_prf__1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No.
                  165226
Seq. ID
                  LIB3177-087-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2160694
BLAST score
                  509
E value
                  5.0e-52
Match length
                  101
% identity
                  100
```

22171

(U73528) B' regulatory subunit of PP2A [Arabidopsis

E value

Match length

% identity

2.0e-29

104

62



```
Seq. No.
                  165227
                  LIB3177-087-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g555977
                  239
BLAST score
                  1.0e-132
E value
                  251
Match length
                  99
% identity
                  Arabidopsis thaliana metallothionein-like protein (AtMT-q)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  165228
                  LIB3177-087-P1-K1-C5
Seq. ID
                  BLASTX
Method
                  g1809305
NCBI GI
BLAST score
                  348
E value
                  8.0e - 34
Match length
                  86
                  95
% identity
                  (U72241) histone H1-3 [Arabidopsis thaliana] >gi_1809315
NCBI Description
                   (U73781) histone H1-3 [Arabidopsis thaliana]
                  >gi_4406813_gb_AAD20121_ (AC006201) Histone H1 [Arabidopsis
                  thaliana]
                  165229
Seq. No.
                  LIB3177-087-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023848
BLAST score
                  332
                  4.0e-31
E value
                  64
Match length
                  100
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                  >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                  thaliana]
Seq. No.
                  165230
                  LIB3177-087-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1769907
BLAST score
                  580
E value
                   5.0e-60
Match length
                  125
% identity
                  88
NCBI Description
                  (X92975) xyloglucan endo-transglycosylase [Arabidopsis
                  thaliana]
Seq. No.
                   165231
                  LIB3177-087-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129672
BLAST score
                  318
```

NCBI Description photosystem II reaction center protein, 6.1K - Arabidopsis



thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No. 165232

Seq. ID LIB3177-087-P1-K1-D1

Method BLASTX
NCBI GI g629562
BLAST score 454
E value 2.0e-45
Match length 107
% identity 87

NCBI Description sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis

thaliana >gi_2129743_pir__S68024 sulfate

adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210)

sulfate adenylyltransferase [Arabidopsis thaliana]

>gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana]
>gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis

thaliana]

Seq. No. 165233

Seq. ID LIB3177-087-P1-K1-D10

Method BLASTX
NCBI GI g2119848
BLAST score 587
E value 6.0e-61
Match length 109
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 165234

Seq. ID LIB3177-087-P1-K1-D11

Method BLASTN
NCBI GI 94490324
BLAST score 209
E value 1.0e-114
Match length 260
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 165235

Seq. ID LIB3177-087-P1-K1-D12

Method BLASTX
NCBI GI g1175010
BLAST score 89
E value 1.0e-36

Match length 98



% identity 84
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082
plasma membrane intrinsic protein 1a - Arabidopsis thaliana
>gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
protein 1a [Arabidopsis thaliana]

Seq. No. 165236 Seq. ID LIB3177-087-P1-K1-D2

Method BLASTX
NCBI GI g121907
BLAST score 346
E value 1.0e-32
Match length 129
% identity 59

NCBI Description HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 - Arabidopsis thaliana >gi_16320_emb_CAA44316_ (X62459) Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215)

histone H1-2C [Arabidopsis thaliana]

Seq. No. 165237

Seq. ID LIB3177-087-P1-K1-D3

Method BLASTX
NCBI GI g4240122
BLAST score 409
E value 4.0e-40
Match length 86
% identity 97

NCBI Description (AB007802) cytochrome b5 [Arabidopsis thaliana]

Seq. No. 165238

Seq. ID LIB3177-087-P1-K1-D4

Method BLASTN
NCBI GI g1769904
BLAST score 191
E value 1.0e-103

E value 1.0e-10 Match length 199 % identity 99

NCBI Description A.thaliana psbP gene

Seq. No. 165239

Seq. ID LIB3177-087-P1-K1-D6

Method BLASTX
NCBI GI g1363492
BLAST score 575
E value 2.0e-59
Match length 147
% identity 73

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 165240

Seq. ID LIB3177-087-P1-K1-D7

Method BLASTN NCBI GI g3212846 BLAST score 460



```
0.0e + 00
E value
                    460
Match length
                    100
% identity
                    Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    165241
                    LIB3177-087-P1-K1-D8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2119846
                    680
BLAST score
                    9.0e-72
E value
                    133
Match length
                    97
% identity
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                    Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                    photosystem II type I chlorophyll a /b binding protein
                    [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                    II type I chlorophyll a/b binding protein [Arabidopsis
                    thaliana] >gi 3337371 (AC004481) photosystem II type I
                    chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                    165242
                    LIB3177-087-P1-K1-D9
Seq. ID
                    BLASTX
Method
                    g1742963
NCBI GI
                    538
BLAST score
E value
                    4.0e-55
                    104
Match length
                    100
% identity
                   (Y09944) gamma-glutamylcysteine synthetase [Arabidopsis
NCBI Description
                    thaliana]
                    165243
Seq. No.
                    LIB3177-087-P1-K1-E1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1703108
                    670
BLAST score
                    1.0e-70
E value
                    129
Match length
% identity
                    100
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                    thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
Seq. No.
                    165244
                    LIB3177-087-P1-K1-E10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q481812
```

NCBI GI g481812 BLAST score 269 E value 8.0e-24 Match length 51 % identity 53

NCBI Description DNA-binding protein GT-2 - Arabidopsis thaliana

>gi_416490_emb_CAA51289 (X72780) GT-2 factor [Arabidopsis



thaliana]

```
165245
Seq. No.
Seq. ID
                   LIB3177-087-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   622
E value
                   5.0e-65
Match length
                   118
% identity
                   100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
                   165246
Seq. No.
Seq. ID
                   LIB3177-087-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g4220645
BLAST score
                   250
E value
                   1.0e-138
Match length
                   250
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYA6, complete sequence [Arabidopsis thaliana]
                   165247
Seq. No.
                   LIB3177-087-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132110
                   457
BLAST score
                   9.0e - 46
E value
Match length
                   93
% identity
                   95
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   165248
Seq. ID
                   LIB3177-087-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g4454587
BLAST score
                   128
E value
                   4.0e-66
Match length
                   140
% identity
                   98
                   Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
```

22176

165249

LIB3177-087-P1-K1-E7

Seq. No.

Seq. ID

BLASTN Method a4558586 NCBI GI 267 BLAST score 1.0e-148 E value Match length 279 99 % identity Arabidopsis thaliana chromosome 1 BAC T518 sequence, NCBI Description complete sequence 165250 Seq. No. LIB3177-087-P1-K1-E8 Seq. ID Method BLASTN q1769904 NCBI GI 36 BLAST score E value 1.0e-11 40 Match length 97 % identity NCBI Description A.thaliana psbP gene 165251 Seq. No. LIB3177-087-P1-K1-E9 Seq. ID Method BLASTX g2959736 NCBI GI BLAST score 455 E value 2.0e-45 143 Match length % identity 62 (Y13651) homologous to GATA-binding transcription factors NCBI Description [Arabidopsis thaliana] Seq. No. 165252 LIB3177-087-P1-K1-F1 Seq. ID Method BLASTX NCBI GI g1169278 BLAST score 305 9.0e-28 E value Match length 83 % identity 86

NCBI Description DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 165253

Seq. ID LIB3177-087-P1-K1-F11

Method BLASTX
NCBI GI g2129637
BLAST score 98
E value 5.0e-04
Match length 72

Match length 72 % identity 19

NCBI Description low temperature-induced protein cor47 - Arabidopsis

thaliana >gi_975646_emb_CAA62449_ (X90959) dehydrin

[Arabidopsis thaliana]

Seq. No. 165254

Seq. ID LIB3177-087-P1-K1-F12

Method BLASTX NCBI GI g2118220



```
BLAST score
                   403
E value
                   3.0e-39
                 . 115
Match length
                   51
% identity
```

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16

٠.

kDa proteolipid [Arabidopsis thaliana]

>gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >qi 4589976 gb AAD26493.1 AC007195 7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

```
Seq. No.
                   165255
                   LIB3177-087-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464621
BLAST score
                   666
E value
                   4.0e-70
                   157
Match length
```

82

% identity 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 NCBI Description

ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

```
165256
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-F3
```

Method BLASTX NCBI GI g1145697 BLAST score 557 2.0e-57 E value Match length 115 % identity 97

(U39485) delta tonoplast integral protein [Arabidopsis NCBI Description

thaliana]

```
Seq. No.
                   165257
```

LIB3177-087-P1-K1-F4 Seq. ID

Method BLASTN NCBI GI g2656024 BLAST score 61 E value 1.0e-25 243 Match length

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K15E6

165258 Seq. No.

% identity

Seq. ID LIB3177-087-P1-K1-F5

87

BLASTN Method NCBI GI q3805839 BLAST score 143 E value 8.0e-75

Seq. ID Method

NCBI GI



```
Match length
                  232
                  97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
NCBI Description
                  (ESSAII project)
                  165259
Seq. No.
                  LIB3177-087-P1-K1-F6
Seq. ID
                  BLASTN
Method
                  g3399678
NCBI GI
BLAST score
                  208
                  1.0e-113
E value
                  432
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  165260
Seq. No.
                  LIB3177-087-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  g115783
NCBI GI
BLAST score
                  534
                  9.0e-55
E value
                  105
Match length
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  165261
                  LIB3177-087-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399900
BLAST score
                   471
                   2.0e-47
E value
                  106
Match length
% identity
                   87
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5)
NCBI Description
                   (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic
                   protein Athb-1 - Arabidopsis thaliana
                   >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein
                   [Arabidopsis thaliana]
                   165262
Seq. No.
                   LIB3177-087-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244759
BLAST score
                   504
E value
                   3.0e-51
Match length
                   112
                   85
% identity
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
                   165263
Seq. No.
```

GI g2062164

BLASTX

LIB3177-087-P1-K1-G11

E value

Match length

1.0e-147



```
535
BLAST score
                  5.0e-55
E value
Match length
                  101
                  99
% identity
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  165264
Seq. No.
                  LIB3177-087-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421826
BLAST score
                  535
                  7.0e-55
E value
Match length
                  114
                  89
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
                  165265
Seq. No.
                  LIB3177-087-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341479
BLAST score
                  157
                  2.0e-10
E value
Match length
                  88
% identity
                   36
                  (AJ000513) hypothetical protein [Pseudanabaena sp.]
NCBI Description
Seq. No.
                  165266
Seq. ID
                  LIB3177-087-P1-K1-G3
Method
                  BLASTX
NCBI GI
                   q4678923
BLAST score
                   173
E value
                   2.0e-12
Match length
                   53
% identity
                   62
NCBI Description
                  (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                   165267
Seq. ID
                  LIB3177-087-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g4757414
BLAST score
                   77
E value
                   2.0e-35
Match length
                  179
% identity
                   89
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
Seq. No.
                   165268
Seq. ID
                   LIB3177-087-P1-K1-G5
                   BLASTN
Method
NCBI GI
                   g4757407
BLAST score
                   265
```

E value



```
100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQD19, complete sequence
                  165269
Seq. No.
                  LIB3177-087-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3386615
                  514
BLAST score
E value
                  4.0e-60
                  123
Match length
                  100
% identity
                  (AC004665) putative phosphomannomutase [Arabidopsis
NCBI Description
                  thaliana]
                  165270
Seq. No.
                  LIB3177-087-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g132110
NCBI GI
BLAST score
                  570
                  6.0e-59
E value
                  107
Match length
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165271
                  LIB3177-087-P1-K1-G9
Seq. ID
Method
                  BLASTN
                  q4587641
NCBI GI
                  212
BLAST score
E value
                  1.0e-116
Match length
                  266
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  165272
Seq. ID
                  LIB3177-087-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1435022
BLAST score
                  226
E value
                  2.0e-18
Match length
                  98
% identity
                   46
NCBI Description (D26576) DNA-binding protein [Daucus carota]
Seq. No.
                  165273
                  LIB3177-087-P1-K1-H10
Seq. ID
                  BLASTN
Method
                  g3335356
NCBI GI
BLAST score
                  365
```

22181

0.0e+00



```
386
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  165274
Seq. No.
                  LIB3177-087-P1-K1-H11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3128138
BLAST score
                  408
                  0.0e+00
E value
Match length
                  453
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFO20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165275
                  LIB3177-087-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558661
BLAST score
                  622
                  4.0e-65
E value
                  121
Match length
                  99
% identity
                   (AC007063) putative malate oxidoreductase (NAD)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  165276
                  LIB3177-087-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4200249
BLAST score
                  232
E value
                  3.0e-19
Match length
                  115
                   42
% identity
                  (AL035297) hypothetical protein [Homo sapiens]
NCBI Description
                  165277
Seq. No.
                  LIB3177-087-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4589965
BLAST score
                  110
E value
                   6.0e-44
Match length
                   97
% identity
                   95
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
Seq. No.
                  165278
                  LIB3177-087-P1-K1-H4
Seq. ID
Method
                  BLASTN
```

Method BLASIN
NCBI GI g4159709
BLAST score 254
E value 1.0e-141
Match length 275
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLN21, complete sequence



165279 Seq. No. LIB3177-087-P1-K1-H5 Seq. ID BLASTX Method q113026 NCBI GI 676 BLAST score 2.0e-71 E value 131 Match length 93 % identity ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) NCBI Description >gi 68211 pir WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi 255220 bbs 112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142 prf_1913424A isocitrate lyase [Brassica napus] Seq. No. 165280 LIB3177-087-P1-K1-H6 Seq. ID BLASTX Method NCBI GI g4006934 473 BLAST score 1.0e-47 E value Match length 112 79 % identity (AJ012571) glutathione transferase [Arabidopsis thaliana] NCBI Description Seq. No. 165281 LIB3177-087-P1-K1-H7 Seq. ID BLASTX Method q4538963 NCBI GI BLAST score 546 4.0e-56 E value 136 Match length 79 % identity (AL049488) chlorophyll a/b-binding protein-like NCBI Description [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] Seq. No. 165282 LIB3177-087-P1-K1-H8 Seq. ID Method BLASTX NCBI GI q4582468 BLAST score 389 5.0e-38 E value Match length 86 % identity 92 NCBI Description (AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana] Seq. No. 165283

LIB3177-087-P1-K1-H9 Seq. ID

Method BLASTX NCBI GI g2129672 BLAST score 275 2.0e-24 E value Match length 98

Match length

% identity

113

88



```
% identity
                   59
                   photosystem II reaction center protein, 6.1K - Arabidopsis
NCBI Description
                   thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center
                   [Arabidopsis thaliana]
Seq. No.
                   165284
                   LIB3177-088-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                   523
                   2.0e-53
E value
Match length
                   141
                   72
% identity
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165285
                   LIB3177-088-P1-K1-A10
Seq. ID
Method
                   BLASTX
                   g4454049
NCBI GI
BLAST score
                   336
E value
                   2.0e-31
Match length
                   122
% identity
                   61
                   (AL035394) 98b like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   165286
                   LIB3177-088-P1-K1-A11
Seq. ID
                   BLASTX
Method
                   q3868857
NCBI GI
                   448
BLAST score
                   1.0e-44
E value
                   86
Match length
                   99
% identity
                   (AB013886) RAV1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   165287
                   LIB3177-088-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q421826
BLAST score
                   281
E value
                    2.0e-25
                   75
Match length
                   71
% identity
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                    >gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                    thaliana]
Seq. No.
                    165288
                   LIB3177-088-P1-K1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                    g1755156
BLAST score
                    513
E value
                    3.0e-52
```

Match length

% identity

60



```
(U75189) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi_1755158 (U75190) germin-like protein [Arabidopsis
                   thaliana] >gi 1755170 (U75196) germin-like protein
                   [Arabidopsis thaliana] >gi 1755172 (U75197) germin-like
                   protein [Arabidopsis thaliana] >gi_1755180 (U75201)
                   germin-like protein [Arabidopsis thaliana] >gi_1755190
                   (U75206) germin-like protein [Arabidopsis thaliana]
                   >gi_1934728 (U95035) germin-like protein [Arabidopsis
                   thaliana] >gi_4154285 (AF090733) germin-like protein 1
                   [Arabidopsis thaliana] >gi_4666248_dbj_BAA77207.1_ (D89055)
                   germin-like protein precursor [Arabidopsis thaliana]
                   165289
Seq. No.
                   LIB3177-088-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244894
                   461
BLAST score
                   3.0e-46
E value
                   110
Match length
                   79
% identity
                   (Z97338) similarity to cycloartenol synthase [Arabidopsis
NCBI Description
                   thaliana]
                   165290
Seq. No.
                   LIB3177-088-P1-K1-A5
Seq. ID
                   BLASTN
Method
                   g4388714
NCBI GI
                   192
BLAST score
                   1.0e-104
E value
                   377
Match length
                   76
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F5K7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   165291
Seq. No.
                   LIB3177-088-P1-K1-A6
Seq. ID
Method
                   BLASTX
                   g541858
NCBI GI
                   662
BLAST score
E value
                   1.0e-69
                   130
Match length
% identity
                   endoxyloglucan transferase - Arabidopsis thaliana
NCBI Description
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                   165292
                   LIB3177-088-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   q4049348
NCBI GI
BLAST score
                   266
E value
                   3.0e-23
```

22185

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Match length

% identity

113

100



165293 Seq. No. LIB3177-088-P1-K1-A8 Seq. ID Method BLASTN NCBI GI q2262135 BLAST score 340 E value 0.0e + 00Match length 432 100 % identity Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 NCBI Description cM, complete sequence Seq. No. 165294 LIB3177-088-P1-K1-A9 Seq. ID Method BLASTN NCBI GI g3080352 BLAST score 87 3.0e-41 E value Match length 101 97 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project) 165295 Seq. No. Seq. ID LIB3177-088-P1-K1-B1 Method BLASTX NCBI GI q4586256 BLAST score 491 1.0e-49 E value 95 Match length 100 % identity (AL049640) probable photosystem I chain XI precursor NCBI Description [Arabidopsis thaliana] 165296 Seq. No. Seq. ID LIB3177-088-P1-K1-B11 Method BLASTX NCBI GI g2119846 BLAST score 618 E value 1.0e-64 Match length 127 % identity 94 chlorophyll a/b-binding protein type I precursor Lhb1B2 -NCBI Description Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] 165297 Seq. No. LIB3177-088-P1-K1-B12 Seq. ID BLASTX Method NCBI GI g115783 BLAST score 596 5.0e-62 E value



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana] 165298 Seq. No. LIB3177-088-P1-K1-B3 Seq. ID BLASTX Method g4538963 NCBI GI 642 BLAST score 2.0e-67 E value 118 Match length 77 % identity (AL049488) chlorophyll a/b-binding protein-like NCBI Description [Arabidopsis thaliana] >gi 4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] 165299 Seq. No. LIB3177-088-P1-K1-B4 Seq. ID BLASTX Method NCBI GI g4262229 BLAST score 403 1.0e-51 E value Match length 115 95 % identity (AC006200) unknown protein [Arabidopsis thaliana] NCBI Description 165300 Seq. No. LIB3177-088-P1-K1-B5 Seq. ID BLASTN Method g2584827 NCBI GI BLAST score 253 E value 1.0e-140 Match length 273 98 % identity NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165301 LIB3177-088-P1-K1-B6 Seq. ID Method BLASTN NCBI GI q4512690 BLAST score 304 1.0e-170 E value Match length 336 99 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence 165302 Seq. No.

Seq. ID LIB3177-088-P1-K1-B7

Method BLASTX
NCBI GI g2149640
BLAST score 675
E value 3.0e-71
Match length 137
% identity 97



```
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
                  165303
Seq. No.
                  LIB3177-088-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169476
                  654
BLAST score
                  9.0e-69
E value
                  125
Match length
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  165304
Seq. No.
                  LIB3177-088-P1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g135449
                  185
BLAST score
                  4.0e-14
E value
                  50
Match length
                  72
% identity
                  TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1
NCBI Description
                  chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1
                  tubulin [Zea mays]
                  165305
Seq. No.
                  LIB3177-088-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g2129634
NCBI GI
BLAST score
                  311
                  1.0e-28
E value
                  121
Match length
                  54
% identity
                  lectin-like protein - Arabidopsis thaliana
NCBI Description
                  >gi_995619_emb_CAA62665_ (X91259) lectin like protein
                  [Arabidopsis thaliana]
                  165306
Seq. No.
                  LIB3177-088-P1-K1-C12
Seq. ID
Method
                  BLASTN
                  g4757409
NCBI GI
                  32
BLAST score
                  2.0e-08
E value
                  384
Match length
                  71
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
                  165307
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3548803
BLAST score
                  285
                  2.0e-25
E value
                  129
Match length
% identity
                   44
```



```
(AC005313) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative
                  SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
                  165308
Seq. No.
                  LIB3177-088-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  g166765
NCBI GI
                  561
BLAST score
                  6.0e-58
E value
                  107
Match length
% identity
                  100
                  (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165309
                  LIB3177-088-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2062160
                  422
BLAST score
                  1.0e-41
E value
                  104
Match length
                  37
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  165310
Seq. No.
                  LIB3177-088-P1-K1-C5
Seq. ID
Method
                  BLASTX
                  g4455242
NCBI GI
                  347
BLAST score
                  7.0e-33
E value
Match length
                  69
                  97
% identity
                  (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165311
                  LIB3177-088-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454036
BLAST score
                   543
E value
                   7.0e-56
Match length
                  100
                   100
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165312
Seq. ID
                   LIB3177-088-P1-K1-C7
                  BLASTX
Method
NCBI GI
                   g136636
BLAST score
                   432
E value
                   1.0e-42
Match length
                   80
% identity
                   99
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
```



>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
>gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
[Arabidopsis thaliana]

```
Seq. No.
                  165313
                  LIB3177-088-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168748
BLAST score
                  652
                  2.0e-68
E value
Match length
                  128
% identity
                  63
                  CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 -
NCBI Description
                  Arabidopsis thaliana >gi 16223 emb_CAA78057 (Z12022)
                  calmodulin [Arabidopsis thaliana]
Seq. No.
                  165314
                  LIB3177-088-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a541799
BLAST score
                  54
E value
                  2.0e-09
                  35
Match length
                  100
% identity
                  light-harvesting chlorophyll a/b-binding protein - ginkgo
NCBI Description
```

Seq. No. 165315

Seq. ID LIB3177-088-P1-K1-D10

Method BLASTN
NCBI GI g3738275
BLAST score 333
E value 0.0e+00
Match length 333
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]

>gi_349443 (L23107) light-harvesting chlorophyll a/b binding protein of photosystem II [Ginkgo biloba]

Seq. No. 165316

Seq. ID LIB3177-088-P1-K1-D11

Method BLASTN
NCBI GI g4662640
BLAST score 344
E value 0.0e+00
Match length 344
% identity 30

NCBI Description Arabidopsis thaliana chromosome II BAC F15K19 genomic

sequence, complete sequence

Seq. No. 165317

Seq. ID LIB3177-088-P1-K1-D12

Method BLASTX



```
g115783
NCBI GI
BLAST score
                  567
                  1.0e-58
E value
                  106
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  165318
Seq. No.
                  LIB3177-088-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  g3913733
NCBI GI
                  498
BLAST score
E value
                  1.0e-50
                  95
Match length
                  99
% identity
                  HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME
NCBI Description
                  (GLYOXALASE II) (GLX II) >gi 1924921 emb_CAA69644_ (Y08357)
                  hydroxyacylglutathione hydrolase [Arabidopsis thaliana]
                  165319
Seq. No.
                  LIB3177-088-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980768
BLAST score
                  545
                  6.0e - 56
E value
                  148
Match length
                  70
% identity
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                  165320
Seq. No.
                  LIB3177-088-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3882081
BLAST score
                  594
                   8.0e-62
E value
Match length
                  123
                   33
% identity
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
                   165321
Seq. No.
                  LIB3177-088-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g131398
BLAST score
                   451
E value
                   4.0e-45
                  107
Match length
                   86
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi 72714 pir F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
```

photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,



gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 165322 LIB3177-088-P1-K1-D6 Seq. ID Method BLASTN g3892698 NCBI GI BLAST score 71 E value 1.0e-31 297 Match length 95 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2

(ESSAII project)

Seq. No. 165323

Seq. ID LIB3177-088-P1-K1-D7

Method BLASTX
NCBI GI g1575699
BLAST score 510
E value 7.0e-52
Match length 102
% identity 98

NCBI Description (U70478) putative leucoanthocyanidin dioxygenase

[Arabidopsis thaliana] >gi_3292813_emb_CAA19803_ (AL031018) putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis

thaliana]

Seq. No. 165324

Seq. ID LIB3177-088-P1-K1-D8

Method BLASTN
NCBI GI g4587641
BLAST score 229
E value 1.0e-126
Match length 422
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Seq. No. 165325

Seq. ID LIB3177-088-P1-K1-D9

Method BLASTN
NCBI GI g12219
BLAST score 69
E value 2.0e-30
Match length 182
% identity 93

NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)

Seq. No. 165326

Seq. ID LIB3177-088-P1-K1-E1

Method BLASTX
NCBI GI g461899
BLAST score 614
E value 5.0e-64
Match length 127
% identity 98

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR



(PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No. 165327

Seq. ID LIB3177-088-P1-K1-E10

Method BLASTX
NCBI GI g2583134
BLAST score 364
E value 1.0e-34
Match length 75
% identity 92

NCBI Description (AC002387) putative proline-rich protein [Arabidopsis

thaliana]

Seq. No. 165328

Seq. ID LIB3177-088-P1-K1-E11

Method BLASTX
NCBI GI g3047077
BLAST score 714
E value 9.0e-76
Match length 145
% identity 99

NCBI Description (AF058914) contains similarity to the conserved C-terminal

domain of helicases (Pfam: helicase_C.hmm, score: 90.11),

similar to DEAD-box helicases [Arabidopsis thaliana]

Seq. No. 165329

Seq. ID LIB3177-088-P1-K1-E12

Method BLASTX
NCBI GI g2129772
BLAST score 502
E value 7.0e-51
Match length 113
% identity 82

NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 -

Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No. 165330

Seq. ID LIB3177-088-P1-K1-E2

Method BLASTX
NCBI GI g1709006
BLAST score 340
E value 2.0e-32
Match length 76
% identity 86

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_726032 (U17241) S-adenosylmethionine synthetase [Actinidia

chinensis]

Seq. No. 165331

Seq. ID LIB3177-088-P1-K1-E4

Method BLASTX



```
q4105696
NCBI GI
BLAST score
                  559
                  1.0e-57
E value
                  102
Match length
                   99
% identity
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
Seq. No.
                  165332
                  LIB3177-088-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4589964
BLAST score
                  178
                  8.0e-13
E value
Match length
                  38
% identity
                   89
NCBI Description (AC007169) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                   165333
                  LIB3177-088-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q461550
BLAST score
                   302
E value
                   1.0e-27
                   97
Match length
% identity
                   66
                  ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_81635_pir__B39732 H+-transporting ATP synthase (EC
3.6.1.34) gamma-1 chain precursor, chloroplast -
                   Arabidopsis thaliana >gi_166632 (M61741) ATP synthase
                   gamma-subunit [Arabidopsis thaliana]
Seq. No.
                   165334
Seq. ID
                   LIB3177-088-P1-K1-E7
                  BLASTX
Method
NCBI GI
                   q3660187
BLAST score
                   217
                   2.0e-17
E value
                   72
Match length
                   54
% identity
                   Chain A, E2-C, An Ubiquitin Conjugating Enzyme Required For
NCBI Description
                   The Destruction Of Mitotic Cyclins >gi_3660188_pdb_1E2C_B
                   Chain B, E2-C, An Ubiquitin Conjugating Enzyme Required For
                   The Destruction Of Mitotic Cyclins >gi_3660189_pdb_1E2C_C
                   Chain C, E2-C, An Ubiquitin Conjugating Enzyme Required For
                   The Destruction Of Mitotic Cyclins >gi 4388942 pdb 2E2C
                   E2-C, An Ubiquitin Conjugating Enzyme Required For The
                   Destruction Of Mitotic Cyclins
Seq. No.
                   165335
                   LIB3177-088-P1-K1-E8
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3914442
BLAST score 226
E value 4.0e-19
Match length 77
% identity 61

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR



(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

165336 Seq. No. LIB3177-088-P1-K1-E9 Seq. ID Method BLASTX g120667 NCBI GI 596 BLAST score 5.0e-62 E value 123 Match length 98 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] 165337 Seq. No. LIB3177-088-P1-K1-F1 Seq. ID Method BLASTX NCBI GI g1402908 BLAST score 537 4.0e-55 E value Match length 119 % identity 88 (X98315) peroxidase [Arabidopsis thaliana] NCBI Description >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana] 165338 Seq. No. LIB3177-088-P1-K1-F11 Seq. ID Method BLASTN NCBI GI q3292807 BLAST score 233 1.0e-128 E value 379 Match length 99 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 NCBI Description (ESSAII project) 165339 Seq. No. LIB3177-088-P1-K1-F12 Seq. ID Method BLASTX NCBI GI q4678948 BLAST score 461 E value 2.0e-46 Match length 93 % identity NCBI Description (AL049711) putative protein [Arabidopsis thaliana] 165340

Seq. No.

Seq. ID LIB3177-088-P1-K1-F2

BLASTX Method NCBI GI g1171577



BLAST score 167
E value 1.0e-11
Match length 100
% identity 39

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 165341

Seq. ID LIB3177-088-P1-K1-F3

Method BLASTX
NCBI GI g115767
BLAST score 626
E value 2.0e-65
Match length 137
% identity 84

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165342

Seq. ID LIB3177-088-P1-K1-F5

Method BLASTX
NCBI GI g3128217
BLAST score 691
E value 4.0e-73
Match length 141
% identity 96

NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

>gi_3337374 (AC004481) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 165343

Seq. ID LIB3177-088-P1-K1-F6

Method BLASTN
NCBI GI g3785992
BLAST score 172
E value 5.0e-92
Match length 322
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165344

Seq. ID LIB3177-088-P1-K1-F8

Method BLASTX
NCBI GI g2832661
BLAST score 343
E value 2.0e-32
Match length 115
% identity 66

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 165345

Seq. No.

165350



```
LIB3177-088-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4566505
BLAST score
                   437
                   3.0e-43
E value
                  131
Match length
                   63
% identity
                   (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
NCBI Description
                   [Hordeum vulgare]
                   165346
Seq. No.
                  LIB3177-088-P1-K1-G11
Seq. ID
                  BLASTX
Method
                   q2494144
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
                   64
Match length
                   69
% identity
                   (AC002329) predicted leucine-rich protein [Arabidopsis
NCBI Description
                   thaliana]
                   165347
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-G12
Method
                   BLASTX
                   q4432860
NCBI GI
BLAST score
                   107
                   1.0e-04
E value
Match length
                   122
                   12
% identity
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165348
                   LIB3177-088-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q114339
                   521
BLAST score
                   3.0e-53
E value
                   125
Match length
                   83
% identity
                  PLASMA MEMBRANE ATPASE 3 (PROTON PUMP)
NCBI Description
                   >gi 67974 pir PXMUP3 H+-transporting ATPase (EC 3.6.1.35)
                   type 3, plasma membrane - Arabidopsis thaliana >gi_166625
                   (J04737) ATPase [Arabidopsis thaliana]
Seq. No.
                   165349
                   LIB3177-088-P1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4102703
BLAST score
                   662
E value
                   1.0e-69
Match length
                   134
                   99
% identity
                  (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
NCBI Description
                   thaliana]
```



LIB3177-088-P1-K1-G4 Seq. ID

BLASTN Method q11244 NCBI GI BLAST score 377 0.0e + 00E value 392 Match length 99 % identity

A.thaliana chloroplast DNA for transfer RNA-Ile and NCBI Description

ribosomal protein

165351 Seq. No.

Seq. ID LIB3177-088-P1-K1-G5

Method BLASTN NCBI GI q3510343 BLAST score 157 7.0e-83 E value Match length 462 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJC20, complete sequence [Arabidopsis thaliana]

165352 Seq. No.

Seq. ID LIB3177-088-P1-K1-G6

Method BLASTN q3201608 NCBI GI BLAST score 307 1.0e-172 E value 385 Match length 99 % identity

Arabidopsis thaliana chromosome II BAC F7F1 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

165353 Seq. No.

Seq. ID LIB3177-088-P1-K1-G7

Method BLASTX NCBI GI g1145697 BLAST score 591 E value 2.0e-61 Match length 120 % identity 51

NCBI Description (U39485) delta tonoplast integral protein [Arabidopsis

thaliana]

165354 Seq. No.

Seq. ID LIB3177-088-P1-K1-G9

Method BLASTX NCBI GI g1175011 BLAST score 566 2.0e-58 E value Match length 106 % identity 100

PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN NCBI Description

A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)

plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No. 165355



```
LIB3177-088-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g2062167
NCBI GI
BLAST score
                  609
                  2.0e-63
E value
                  115
Match length
% identity
                  100
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  165356
Seq. No.
                  LIB3177-088-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g121075
NCBI GI
BLAST score
                  555
                   4.0e-57
E value
                  134
Match length
% identity
                   84
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 166725
NCBI Description
                   (M82921) H-Protein precursor [Arabidopsis thaliana]
                   >gi 861215 (U27144) glycine decarboxylase complex H-protein
                   precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                   glycine decarboxylase complex H-protein [Arabidopsis
                   thaliana] >gi_445119_prf__1908425A Gly
                   decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
                   165357
Seq. No.
                   LIB3177-088-P1-K1-H11
Seq. ID
Method
                   BLASTX
                   g2289011
NCBI GI
                   581
BLAST score
                   3.0e-60
E value
                   131
Match length
                   40
% identity
                   (AC002335) MYB transcription factor isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165358
                   LIB3177-088-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4432856
BLAST score
                   686
                   2.0e-72
E value
Match length
                   135
                   99
% identity
NCBI Description (AC006300) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                   165359
Seq. ID
                   LIB3177-088-P1-K1-H2
Method
                   BLASTX
                   q2618723
NCBI GI
BLAST score
                   463
E value
                   1.0e-46
Match length
                   96
                   92
% identity
                  (U49073) IAA17 [Arabidopsis thaliana] >gi_2921756
NCBI Description
```

(AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]



>gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No. 165360

Seq. ID LIB3177-088-P1-K1-H3

Method BLASTX
NCBI GI g4508075
BLAST score 168
E value 2.0e-12
Match length 47
% identity 66

NCBI Description (AC005882) 50259 [Arabidopsis thaliana]

Seq. No. 165361

Seq. ID LIB3177-088-P1-K1-H4

Method BLASTN
NCBI GI g166633
BLAST score 114
E value 3.0e-57
Match length 246
% identity 99

NCBI Description Arabidopsis thaliana vacuolar H+ - pyrophosphatase (AVP-3)

mRNA, complete cds

Seq. No. 165362

Seq. ID LIB3177-088-P1-K1-H5

Method BLASTN
NCBI GI 94589409
BLAST score 335
E value 0.0e+00
Match length 375
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F17P19, complete sequence

Seq. No. 165363

Seq. ID LIB3177-088-P1-K1-H8

Method BLASTX
NCBI GI 9459009
BLAST score 166
E value 6.0e-12
Match length 46
% identity 65

NCBI Description (U00037) similar to multifunctional aminoacyl-tRNA

synthetase, especially to the prolyl-tRNA synthetase region

[Caenorhabditis elegans]

Seq. No. 165364

Seq. ID LIB3177-088-P1-K1-H9

Method BLASTX
NCBI GI g132110
BLAST score 429
E value 2.0e-42
Match length 84
% identity 98

BLAST score

Match length

E value

492

93

6.0e-50



```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165365
Seq. ID
                  LIB3177-089-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3786017
BLAST score
                  346
E value
                  3.0e - 33
Match length
                  69
% identity
                  99
NCBI Description (AC005499) putative non-green plastid inner envelope
                  membrane protein [Arabidopsis thaliana]
Seq. No.
                  165366
Seq. ID
                  LIB3177-089-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g4468103
BLAST score
                  110
E value
                  3.0e-55
Match length
                  197
                  89
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                  (ESSA project)
Seq. No.
                  165367
Seq. ID
                  LIB3177-089-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4455284
BLAST score
                  367
                  2.0e-35
E value
Match length
                  82
% identity
                  84
NCBI Description (AL035527) beta-glucosidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  165368
Seq. ID
                  LIB3177-089-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g207553
BLAST score
                  34
E value
                  1.0e-09
Match length
                  50
% identity
                  92
NCBI Description Rat transcription factor UBF2 mRNA
                  165369
Seq. No.
Seq. ID
                  LIB3177-089-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q115767
```



```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir_A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >qi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  165370
Seq. No.
                  LIB3177-089-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168258
                  478
BLAST score
                  3.0e-48
E value
                  114
Match length
                  85
% identity
                  ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (TRANSAMINASE A) >gi_693692 (U15034) aspartate
                  aminotransferase [Arabidopsis thaliana]
                  165371
Seq. No.
                  LIB3177-089-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2119846
NCBI GI
BLAST score
                  549
                  1.0e-56
E value
                  107
Match length
                  97
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165372
                  LIB3177-089-P1-K1-A6
Seq. ID
                  BLASTN
Method
                  g2244788
NCBI GI
                  102
BLAST score
                  2.0e-50
E value
                  170
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  165373
Seq. No.
                  LIB3177-089-P1-K1-A7
Seq. ID
Method
                   BLASTN
                   q4467094
NCBI GI
```

Method BLASTN
NCBI GI g4467094
BLAST score 151
E value 1.0e-79
Match length 232
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10

E value

Match length

% identity

1.0e-137

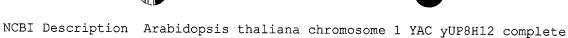
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99



```
(ESSA project)
Seq. No.
                   165374
Seq.-ID
                   LIB3177-089-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g4467094
BLAST score
                   39
E value
                   1.0e-12
Match length
                   135
% identity
                   82
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                   (ESSA project)
Seq. No.
                   165375
Seq. ID
                   LIB3177-089-P1-K1-B1
Method
                   BLASTN
NCBI GI
                   g4741959
BLAST score
                   122
E value
                   3.0e-62
Match length
                   168
% identity
                   93
NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
Seq. No.
                   165376
Seq. ID
                  LIB3177-089-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  313
E value
                   4.0e - 34
Match length
                  114
% identity
                  70
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  165377
Seq. ID
                  LIB3177-089-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3273743
BLAST score
                  597
E value
                  3.0e-62
Match length
                  116
% identity
NCBI Description
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                  thaliana] >gi 3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
Seq. No.
                  165378
Seq. ID
                  LIB3177-089-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g2358139
BLAST score
                  248
```





```
sequence [Arabidopsis thaliana]
Seq. No.
                   165379
Seq. ID
                   LIB3177-089-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1621463
BLAST score
                   49
E value
                   3.0e-51
Match length
                   134
% identity
                   75
NCBI Description (U73104) laccase [Liriodendron tulipifera]
Seq. No.
                   165380
Seq. ID
                   LIB3177-089-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g3985932
BLAST score
                   73
E value
                   8.0e-33
Match length
                   326
% identity
                   83
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K22J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165381
Seq. ID
                   LIB3177-089-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g2252863
BLAST score
                   305
E value
                   5.0e-28
Match length
                   96
% identity
                   31
NCBI Description
                  (AF013294) similar to nucleolin protein [Arabidopsis
                   thaliana]
Seq. No.
                   165382
Seq. ID
                   LIB3177-089-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2252863
BLAST score
                   285
E value
                   2.0e-25
Match length
                   99
% identity
                   53
NCBI Description
                  (AF013294) similar to nucleolin protein [Arabidopsis
                   thaliana]
Seq. No.
                  165383
Seq. ID
                  LIB3177-089-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2760833
BLAST score
                  427
E value
                  5.0e-50
Match length
                  105
% identity
                  97
NCBI Description
                  (AC003105) unknown protein [Arabidopsis thaliana]
Seq. No.
                  165384
```

Seq. No.

Seq. ID

165389

LIB3177-089-P1-K1-C4



```
Seq. ID
                    LIB3177-089-P1-K1-B9
Method
                    BLASTX
NCBI GI
                    q3286693
BLAST score
                    645
E value
                    9.0e-68
Match length
                    130
% identity
                    99
NCBI Description
                    (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                    (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                    165385
Seq. ID
                    LIB3177-089-P1-K1-C10
Method
                   BLASTN
NCBI GI
                    q3608126
BLAST score
                    308
E value
                    1.0e-173
Match length
                    370
% identity
                    98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T32F12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165386
Seq. ID
                   LIB3177-089-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g1710424
BLAST score
                   528
E value
                   5.0e-54
Match length
                   123
% identity
                   88
NCBI Description
                   50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
                   >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887__(Z49787) chloroplast
                   ribosomal large subunit protein L21 [Arabidopsis thaliana]
Seq. No.
                   165387
Seq. ID
                   LIB3177-089-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3894197
BLAST score
                   685
E value
                   2.0e-72
Match length
                   136
% identity
                   97
NCBI Description
                   (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   165388
Seq. ID
                   LIB3177-089-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q4589428
BLAST score
                   446
E value
                   0.0e + 00
Match length
                   488
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFH8, complete sequence
```

NCBI GI

BLAST score

g115767

698



```
Method
                    BLASTX
NCBI GI
                    g3080395
BLAST score
                    254
E value
                    7.0e-22
Match length
                    103
% identity
                    61
NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    165390
Seq. ID
                    LIB3177-089-P1-K1-C6
Method
                    BLASTX
NCBI GI
                    g1208408
BLAST score
                    344
E value
                    6.0e-33
                    74
Match length
% identity
                    91
NCBI Description
                   (D14824) nitrite reductase [Arabidopsis thaliana]
                    >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase
[Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248)
                    nitrate reductase [Arabidopsis thaliana]
Seq. No.
                    165391
Seq. ID
                   LIB3177-089-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q535780
BLAST score
                    703
E value
                    2.0e-74
Match length
                   135
% identity
                    100
NCBI Description (D26609) transmembrane protein [Arabidopsis thaliana]
Seq. No.
                   165392
Seq. ID
                   LIB3177-089-P1-K1-C8
Method
                   BLASTN
NCBI GI
                   g4454004
BLAST score
                   362
E value
                   0.0e + 00
Match length
                   374
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                   (ESSAII project)
Seq. No.
                   165393
Seq. ID
                   LIB3177-089-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   q4105798
BLAST score
                   342
E value
                   3.0e-32
Match length
                   94
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                   165394
Seq. ID
                   LIB3177-089-P1-K1-D1
Method
                   BLASTX
```



E value 7.0e-74
Match length 143
% identity 94

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165395

Seq. ID LIB3177-089-P1-K1-D11

Method BLASTX
NCBI GI g1922937
BLAST score 477
E value 4.0e-48
Match length 93
% identity 100

NCBI Description (AC000106) Similar to Glycine SRC2 (gb_AB000130). ESTs

gb_H76869,gb_T21700,gb_ATTS5089 come from this gene.

[Arabidopsis thaliana]

Seq. No. 165396

Seq. ID LIB3177-089-P1-K1-D12

Method BLASTX
NCBI GI g131398
BLAST score 586
E value 9.0e-61
Match length 135
% identity 88

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 165397

Seq. ID LIB3177-089-P1-K1-D3

Method BLASTN
NCBI GI g3763944
BLAST score 120
E value 7.0e-61
Match length 372
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No. 165398

Seq. ID LIB3177-089-P1-K1-D4

Method BLASTX
NCBI GI 92062161
BLAST score 165



```
E value
                   2.0e-11
Match length
                   140
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165399
Seq. ID
                   LIB3177-089-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g133938
BLAST score
                   563
E value
                   5.0e-58
Match length
                   147
% identity
                   75
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70866_pir_ R3SP3
                   ribosomal protein S3 - spinach chloroplast
                   >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3
                   [Spinacia oleracea]
Seq. No.
                   165400
Seq. ID
                  LIB3177-089-P1-K1-D7
Method
                  BLASTX
NCBI GI
                   g4741952
BLAST score
                   563
E value
                   4.0e-58
Match length
                  108
% identity
                   73
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  165401
                  LIB3177-089-P1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3548797
BLAST score
                  116
E value
                  2.0e-58
Match length
                  348
% identity
                  95
NCBI Description Arabidopsis thaliana chromosome II BAC T18E12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165402
Seq. ID
                  LIB3177-089-P1-K1-D9
Method
                  BLASTX
                  g4490737
                  577
                  9.0e-60
                  126
```

NCBI GI BLAST score E value Match length % identity

(AL035708) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 165403

Seq. ID LIB3177-089-P1-K1-E10

Method BLASTX NCBI GI g3869280 BLAST score 610 E value 2.0e-63 Match length 151



% identity NCBI Description (AF064786) beta-galactosidase precursor [Carica papaya] Seq. No. 165404 Seq. ID LIB3177-089-P1-K1-E12 Method BLASTX NCBI GI q3236240 BLAST score 62 E value 9.0e-46 Match length 117 % identity 77 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana] Seq. No. 165405 Seq. ID LIB3177-089-P1-K1-E2 Method BLASTX NCBI GI q132074 BLAST score 629 E value 7.0e-66 Match length 114 % identity 100 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063 pir RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana Seq. No. 165406 Seq. ID LIB3177-089-P1-K1-E3 Method BLASTN NCBI GI g3152602 BLAST score 256 E value 1.0e-142 Match length 328 % identity 99 NCBI Description Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165407 Seq. ID LIB3177-089-P1-K1-E5 Method BLASTX NCBI GI g1363489 BLAST score 95 E value 1.0e-55 Match length 114 % identity 95 thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis NCBI Description thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana] Seq. No. 165408 Seq. ID LIB3177-089-P1-K1-E6 Method BLASTX NCBI GI g421836

Method BLASTX
NCBI GI g421836
BLAST score 503
E value 3.0e-51
Match length 102
% identity 99



NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

Seq. No. 165409

Seq. ID LIB3177-089-P1-K1-E7

Method BLASTX
NCBI GI g461903
BLAST score 226
E value 4.0e-19
Match length 50
% identity 92

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 405129

(L14844) cyclophilin [Arabidopsis thaliana]

>gi_4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl

isomerase ROC1 [Arabidopsis thaliana]

Seq. No. 165410

Seq. ID LIB3177-089-P1-K1-E8

Method BLASTN
NCBI GI g1707006
BLAST score 304
E value 1.0e-170
Match length 357
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165411

Seq. ID LIB3177-089-P1-K1-E9

Method BLASTN
NCBI GI 94589434
BLAST score 148
E value 1.0e-77
Match length 263
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ7, complete sequence

Seq. No. 165412

Seq. ID LIB3177-089-P1-K1-F1

Method BLASTN
NCBI GI g166695
BLAST score 107
E value 2.0e-53
Match length 138
% identity 93

NCBI Description Arabidopsis thaliana recombination and DNA-damage

resistance protein (DRT112) mRNA, complete cds

Seq. No. 165413

Seq. ID LIB3177-089-P1-K1-F11

Method BLASTX
NCBI GI g4204285
BLAST score 342
E value 3.0e-32
Match length 80



% identity

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No.

165414

Seq. ID

LIB3177-089-P1-K1-F2

Method NCBI GI BLASTN g3193282

BLAST score

E value

77 1.0e-35

Match length

132

% identity

90

NCBI Description Arabidopsis thaliana BAC T14P8

Seq. No.

165415

Seq. ID

LIB3177-089-P1-K1-F3

Method NCBI GI BLASTX g135860

BLAST score E value

629

Match length

3.0e-67

147

% identity

67

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi_99761_pir S22202 tonoplast intrinsic

protein gamma - Arabidopsīs thaliana

>gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic

protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129 prf 1908432B tonoplast intrinsic protein gamma

[Arabidopsis thaliana]

Seq. No.

165416

Seq. ID

LIB3177-089-P1-K1-F4

Method

BLASTN

NCBI GI

q2688838 94

BLAST score E value

2.0e-45

Match length

198

% identity

87

NCBI Description

Thlaspi goesingense ATP phosphoribosyltransferase (THG1)

mRNA, complete cds

Seq. No.

165417

Seq. ID

LIB3177-089-P1-K1-F5

Method NCBI GI

BLASTX

g2119846

BLAST score

745

E value

2.0e-79

Match length

148

% identity

95

NCBI Description

chlorophyll a/b-binding protein type I precursor Lhb1B2 -Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)

photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]



```
Seq. No.
                   165418
Seq. ID
                   LIB3177-089-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g1946354
BLAST score
                   319
E value
                   1.0e-179
Match length
                   379
% identity
                   96
NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic
                   sequence, complete sequence
Seq. No.
                   165419
Seq. ID
                   LIB3177-089-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g2618599
BLAST score
                   66
E value
                   1.0e-28
Match length
                   185
% identity
                   84
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165420
Seq. ID
                  LIB3177-089-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   g1769905
BLAST score
                   272
E value
                   4.0e-24
Match length
                   102
% identity
                   57
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   165421
Seq. ID
                  LIB3177-089-P1-K1-F9
Method
                  BLASTN
NCBI GI
                   g2656030
BLAST score
                  33
E value
                   6.0e-09
Match length
                  168
% identity
                  80
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUL8
Seq. No.
                  165422
Seq. ID
                  LIB3177-089-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  569
E value
                  7.0e-59
Match length
                  105
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
```

22212

Al precursor - Arabidopsis thaliana

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

BLAST score

Match length

E value

142

24

3.0e-09



```
Seq. No.
                   165423
Seq. ID
                   LIB3177-089-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q730645
BLAST score
                   675
E value
                   3.0e-71
Match length
                  144
% identity
                   92
NCBI Description
                  40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal
                  protein S15 - Arabidopsis thaliana >gi 313152_emb_CAA80679
                   (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                   >gi_313188_emb_CAA80681 (Z23162) ribosomal protein S15
                   [Arabidopsis thaliana] >gi_1903366_gb_AAB70449 (AC000104)
                   Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                   gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                  165424
                  LIB3177-089-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3386593
BLAST score
                  230
E value
                  1.0e-126
Match length
                  463
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165425
Seq. ID
                  LIB3177-089-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g295792
BLAST score
                  205
E value
                  1.0e-34
Match length
                  99
% identity
                  83
NCBI Description
                  (X13611) ribulose bisphosphate carboxylase [Arabidopsis
                  thalianal
Seq. No.
                  165426
Seq. ID
                  LIB3177-089-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  384
E value
                  1.0e-37
Match length
                  80
% identity
NCBI Description
                  (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                  165427
Seq. ID
                  LIB3177-089-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3298544
```



% identity 100 NCBI Description (AC004681) unknown protein [Arabidopsis thaliana] Seq. No. 165428

Seq. ID LIB3177-089-P1-K1-G6

Method BLASTN
NCBI GI 94580745
BLAST score 107
E value 1.0e-53
Match length 122
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence,

complete sequence

Seq. No. 165429

Seq. ID LIB3177-089-P1-K1-G7

Method BLASTN
NCBI GI g3702735
BLAST score 291
E value 1.0e-163
Match length 295
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQL5, complete sequence [Arabidopsis thaliana]

Seq. No. 165430

Seq. ID LIB3177-089-P1-K1-G8

Method BLASTN
NCBI GI g3702735
BLAST score 127
E value 3.0e-65
Match length 150
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQL5, complete sequence [Arabidopsis thaliana]

Seq. No. 165431

Seq. ID LIB3177-089-P1-K1-G9

Method BLASTX
NCBI GI g282865
BLAST score 538
E value 3.0e-55
Match length 111
% identity 67

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 165432

Seq. ID LIB3177-089-P1-K1-H1

Method BLASTX
NCBI GI g132863
BLAST score 597
E value 4.0e-62



Match length 113 % identity 97

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2

>gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2

[Sinapis alba]

Seq. No. 165433

Seq. ID LIB3177-089-P1-K1-H10

Method BLASTX
NCBI GI g3122038
BLAST score 268
E value 2.0e-23
Match length 113
% identity 50

NCBI Description DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (COLLAPSIN

RESPONSE MEDIATOR PROTEIN 4) (CRMP-4) >gi_1399542 (U52104)

rCRMP-4 [Rattus norvegicus]

Seq. No. 165434

Seq. ID LIB3177-089-P1-K1-H11

Method BLASTX
NCBI GI g1769905
BLAST score 532
E value 2.0e-54
Match length 142
% identity 73

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No. 165435

Seq. ID LIB3177-089-P1-K1-H12

Method BLASTX
NCBI GI g4220457
BLAST score 646
E value 9.0e-68
Match length 156
% identity 31

NCBI Description (AC006216) Similar to gi_3413714 T19L18.21 putative

myrosinase-binding prote \overline{i} n from Arabidopsis thaliana BAC

gb_AC004747. EST gb_N96478 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 165436

Seq. ID LIB3177-089-P1-K1-H2

Method BLASTX
NCBI GI 94249379
BLAST score 517
E value 7.0e-53
Match length 105
% identity 96

NCBI Description (AC005966) Strong similarity to gb_X82030 chloroplast RNA

binding protein (RNP1) from Phaseolus vulgaris.

[Arabidopsis thaliana]

Seq. No. 165437

Seq. ID LIB3177-089-P1-K1-H3

Method BLASTX



NCBI GI g115385 BLAST score 66 E value 3.0e-67 Match length 137 % identity 95 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 165438 Seq. ID LIB3177-089-P1-K1-H4 Method BLASTX NCBI GI q4583542 BLAST score 428 E value 4.0e-42

Match length 154 % identity 62

NCBI Description (Y16847) 16 kDa polypeptide of oxygen-evolving complex

[Arabidopsis thaliana]

Seq. No. 165439

Seq. ID LIB3177-089-P1-K1-H6

Method BLASTN NCBI GI g4185120 BLAST score 82 E value 2.0e-38 Match length 130 % identity 72

NCBI Description Arabidopsis thaliana chromosome 1 BAC F5F19 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 165440

Seq. ID LIB3177-089-P1-K1-H8

Method BLASTX NCBI GI g421826 BLAST score 421 E value 2.0e-41 Match length 121 % identity 71

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 165441

Seq. ID LIB3177-089-P1-K1-H9

Method BLASTN NCBI GI g3046851 BLAST score 48 E value 6.0e-18

Match length 128 % identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 165442

Seq. ID LIB3177-090-P1-K1-A10

Method BLASTX



NCBI GI q3068713 BLAST score 366 E value 5.0e-35 Match length 72 % identity 100 NCBI Description (AF049236) unknown [Arabidopsis thaliana] Seq. No. 165443 Seq. ID LIB3177-090-P1-K1-A11 Method BLASTX NCBI GI g115767 BLAST score 731 E value 9.0e-78Match length 143 % identity 96 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein $ab16\overline{5}$ - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 165444 Seq. ID LIB3177-090-P1-K1-A12 Method BLASTX NCBI GI q4193388 BLAST score 396 E value 2.0e-38 Match length 122 % identity 67 NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis] Seq. No. 165445 Seq. ID LIB3177-090-P1-K1-A2 Method BLASTX NCBI GI g1934726 BLAST score 519 E value 5.0e-53 Match length 124 % identity 85 NCBI Description (U95034) germin-like protein [Arabidopsis thaliana] Seq. No. 165446 Seq. ID LIB3177-090-P1-K1-A3 Method BLASTX

NCBI GI q1617268 BLAST score 300 E value 1.0e-27 Match length 72 % identity 85

NCBI Description (Z72153) acyl CoA synthetase [Brassica napus]

Seq. No. 165447

Seq. ID LIB3177-090-P1-K1-A4

Method BLASTX



```
NCBI GI
                   g1546706
BLAST score
                   537
E value
                   9.0e-68
Match length
                   148
% identity
                   93
NCBI Description (X98855) peroxidase ATP8a [Arabidopsis thaliana]
Seq. No.
                   165448
Seq. ID
                   LIB3177-090-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   q2618599
BLAST score
                   42
E value
                   3.0e-14
Match length
                   231
% identity
                   82
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165449
Seq. ID
                   LIB3177-090-P1-K1-A6
Method
                  BLASTN
NCBI GI
                   g3047074
BLAST score
                  160
E value
                  1.0e-84
Match length
                   421
% identity
                   95
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                   165450
Seq. ID
                  LIB3177-090-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g4376087
BLAST score
                  257
E value
                  1.0e-142
Match length
                  289
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  165451
Seq. ID
                  LIB3177-090-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g4581084
BLAST score
                  260
E value
                  1.0e-144
Match length
                  377
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic
                  sequence, complete sequence
```

Seq. No. 165452

Seq. ID LIB3177-090-P1-K1-B1

Method BLASTN
NCBI GI g3510339
BLAST score 457
E value 0.0e+00
Match length 484



```
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165453
                   LIB3177-090-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204266
BLAST score
                   449
E value
                   7.0e-45
Match length
                   114
% identity
                   83
NCBI Description (AC005223) 52263 [Arabidopsis thaliana]
Seq. No.
                   165454
Seq. ID
                  LIB3177-090-P1-K1-B11
Method
                  BLASTX
NCBI GI
                   g2213882
BLAST score
                   584
E value
                   1.0e-60
Match length
                  133
% identity
                   83
NCBI Description
                  (AF004165) 2-isopropylmalate synthase [Lycopersicon
                  pennellii]
Seq. No.
                  165455
                  LIB3177-090-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3688799
BLAST score
                  415
E value
                  9.0e-41
Match length
                  108
% identity
                  78
NCBI Description
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  165456
Seq. ID
                  LIB3177-090-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q3510339
BLAST score
                  150
E value
                  1.0e-78
Match length
                  154
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165457
Seq. ID
                  LIB3177-090-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  q402614
BLAST score
                  130
E value
                  7.0e-67
Match length
                  248
% identity
                  86
```

NCBI Description B.rapa chloroplast mRNA for ribosomal protein L32



```
Seq. No.
                   165458
Seq. ID
                   LIB3177-090-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g113026
BLAST score
                   542
E value
                   1.0e-55
Match length
                   123
% identity
                   86
NCBI Description ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                   >gi_68211_pir _WZRPI isocitrate lyase (EC 4.1.3.1) - rape
                   >gi 255220 bbs 112862 isocitrate lyase, threo-D
                   S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                   napus, seedlings, Peptide, 576 aa] >gi 167144 (L08482)
                   isocitrate lyase [Brassica napus] >gi_447142 prf 1913424A
                   isocitrate lyase [Brassica napus]
Seq. No.
                   165459
Seq. ID
                  LIB3177-090-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2143227
BLAST score
                  222
E value
                  2.0e-18
Match length
                  68
% identity
                  74
NCBI Description (Y13356) glyoxysomal isocitrate lyase [Brassica napus]
Seq. No.
                  165460
Seq. ID
                  LIB3177-090-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q2246621
BLAST score
                  403
E value
                  3.0e-39
Match length
                  90
% identity
                  83
NCBI Description (AF004393) salt-stress induced tonoplast intrinsic protein
                  [Arabidopsis thaliana]
Seq. No.
                  165461
                  LIB3177-090-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119848
BLAST score
                  661
E value
                  1.0e-69
Match length
                  129
% identity
                  96
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                  Arabidopsis thaliana >gi_16366_emb_CAA45789 (X64459)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128229 (AC004077) putative
```

photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 165462

Seq. ID LIB3177-090-P1-K1-B9

Method BLASTX



```
NCBI GI
                   g4741948
BLAST score
                   720
E value
                   2.0e-76
Match length
                  138
% identity
                   99
NCBI Description
                  (AF134124) Lhcb2 protein [Arabidopsis thaliana]
                  165463
Seq. No.
                  LIB3177-090-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835233
BLAST score
                  546
E value
                   3.0e-56
Match length
                  113
% identity
                   96
NCBI Description
                  (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  165464
                  LIB3177-090-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3763944
BLAST score
                  92
E value
                  2.0e-44
Match length
                  212
% identity
                  86
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                  165465
Seq. ID
                  LIB3177-090-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4262225
BLAST score
                  337
E value
                  2.0e-31
Match length
                  80
% identity
                  70
NCBI Description
                  (AC006200) putative phosphatidic acid phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                  165466
Seq. ID
                  LIB3177-090-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1709205
BLAST score
                  567
E value
                  2.0e-58
Match length
                  140
% identity
                  75
                  MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL
NCBI Description
                  MONOPHOSPHATASE 3) >gi 1098971 (U39059) myo-inositol
                  monophosphatase 3 [Lycopersicon esculentum]
```

Seq. No. 165467

Seq. ID LIB3177-090-P1-K1-C2

Method BLASTX NCBI GI g3080371 BLAST score 743



E value 4.0e-79 136 Match length 100 % identity NCBI Description (AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana] Seq. No. 165468 LIB3177-090-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g543841 BLAST score 560 E value 1.0e-57 129 Match length 87 % identity ADP-RIBOSYLATION FACTOR 1 >gi 322518_pir__\$28875 NCBI Description ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana] Seq. No. 165469 LIB3177-090-P1-K1-C4 Seq. ID Method BLASTX NCBI GI g115385 BLAST score 554 E value 4.0e-57 Match length 107 99 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 165470 LIB3177-090-P1-K1-C5 Seq. ID Method BLASTX NCBI GI g1363489 BLAST score 348 4.0e-35 E value Match length 100 78 % identity thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis NCBI Description thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana] 165471 Seq. No. Seq. ID LIB3177-090-P1-K1-C6

Method BLASTX
NCBI GI g2191138
BLAST score 716
E value 6.0e-76
Match length 142
% identity 100

NCBI Description (AF007269) A IG002N01.18 gene product [Arabidopsis

thaliana]

Seq. No. 165472



```
Seq. ID
                  LIB3177-090-P1-K1-C7
Method
                  BLASTX
                  g2160158
NCBI GI
BLAST score
                  474
E value
                  1.0e-47
Match length
                  90
                  99
% identity
NCBI Description
                  (AC000132) Similar to elongation factor 1-gamma
                  (gb EF1G XENLA). ESTs gb T20564,qb T45940,qb T04527 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  165473
Seq. ID
                  LIB3177-090-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3445196
                  43
```

BLAST score E value 4.0e-15 Match length 107 85 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. ID LIB3177-090-P1-K1-C9 Method BLASTX NCBI GI g132074 BLAST score 793 E value 6.0e-85 Match length 145 100 % identity

Seq. No.

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165475

Seq. ID LIB3177-090-P1-K1-D1

165474

Method BLASTX NCBI GI g1755156 BLAST score 546 E value 5.0e-56 Match length 152 % identity 75

NCBI Description

(U75189) germin-like protein [Arabidopsis thaliana] >gi_1755158 (U75190) germin-like protein [Arabidopsis thaliana] >gi_1755170 (U75196) germin-like protein [Arabidopsis thaliana] >gi_1755172 (U75197) germin-like protein [Arabidopsis thaliana] >gi_1755180 (U75201) germin-like protein [Arabidopsis thaliana] >gi 1755190 (U75206) germin-like protein [Arabidopsis thaliana] >gi_1934728 (U95035) germin-like protein [Arabidopsis
thaliana] >gi_4154285 (AF090733) germin-like protein 1 [Arabidopsis thaliana] >gi 4666248 dbj BAA77207.1 (D89055)

germin-like protein precursor [Arabidopsis thaliana]

Seq. No. 165476

Seq. ID LIB3177-090-P1-K1-D10



BLASTX Method NCBI GI g115767 BLAST score 53 E value 9.0e-72 Match length 137 94 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368 emb CAA27540 (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] 165477 Seq. No. Seq. ID LIB3177-090-P1-K1-D11 Method BLASTN NCBI GI g2351066 BLAST score 228 E value 1.0e-125 Match length 446 96 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana] 165478 Seq. No. Seq. ID LIB3177-090-P1-K1-D12 Method BLASTN NCBI GI q3449326 BLAST score 415 E value 0.0e + 00Match length 446 % identity 99 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana] Seq. No. 165479 Seq. ID LIB3177-090-P1-K1-D2 Method BLASTN NCBI GI q4757405 BLAST score 376 E value 0.0e+00Match length 488 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No. 165480

Seq. ID LIB3177-090-P1-K1-D3

Method BLASTX
NCBI GI g120675
BLAST score 547
E value 4.0e-56
Match length 141
% identity 66

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66011 pir DEIS3C glyceraldehyde-3-phosphate



dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
>gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
alba]

Seq. No. 165481

Seq. ID LIB3177-090-P1-K1-D6

Method BLASTX
NCBI GI g3643594
BLAST score 344
E value 2.0e-32
Match length 70
% identity 97

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 165482

Seq. ID LIB3177-090-P1-K1-D7

Method BLASTX
NCBI GI 94741960
BLAST score 587
E value 7.0e-61
Match length 130
% identity 86

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 165483

Seq. ID LIB3177-090-P1-K1-D9

Method BLASTX
NCBI GI g1408473
BLAST score 588
E value 6.0e-61

Match length 113 % identity 99

NCBI Description (U48939) actin depolymerizing factor 2 [Arabidopsis

thaliana]

Seq. No. 165484

Seq. ID LIB3177-090-P1-K1-E1

Method BLASTX
NCBI GI g2129636
BLAST score 639
E value 6.0e-67
Match length 134
% identity 92

NCBI Description lipase - Arabidopsis thaliana >qi 1145627 (U38916) lipase

[Arabidopsis thaliana]

Seq. No. 165485

Seq. ID LIB3177-090-P1-K1-E10

Method BLASTX
NCBI GI g4741948
BLAST score 301
E value 2.0e-27
Match length 132
% identity 52

NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 165486

Match length

% identity

85

91

NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana]



Seq. ID LIB3177-090-P1-K1-E11 Method BLASTX NCBI GI q115767 BLAST score 760 E value 4.0e-81 Match length 146 % identity 99 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 165487 Seq. ID LIB3177-090-P1-K1-E12 Method BLASTN NCBI GI q2584827 BLAST score 173 E value 2.0e-92 Match length 391 % identity 96 NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165488 Seq. ID LIB3177-090-P1-K1-E2 Method BLASTX NCBI GI q2129636 BLAST score 399 E value 7.0e-39 Match length 85 89 % identity NCBI Description lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase [Arabidopsis thaliana] Seq. No. 165489 Seq. ID LIB3177-090-P1-K1-E3 Method BLASTX NCBI GI q2781354 BLAST score 493 E value 2.0e-64 131 Match length 92 % identity NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana] Seq. No. 165490 Seq. ID LIB3177-090-P1-K1-E4 Method BLASTX NCBI GI q2781354 BLAST score 402 E value 3.0e-39



```
Seq. No.
                   165491
Seq. ID
                   LIB3177-090-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q4567202
BLAST score
                   675
E value
                   3.0e-71
Match length
                   136
% identity
                   98
                  (AC007168) putative myo-inositol 1-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165492
Seq. ID
                  LIB3177-090-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g2541876
BLAST score
                   214
E value
                   4.0e-17
                   98
Match length
                   53
% identity
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                  165493
Seq. ID
                  LIB3177-090-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g4510360
BLAST score
                  114
E value
                   3.0e-57
Match length
                   391
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  165494
Seq. ID
                  LIB3177-090-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4454036
BLAST score
                   538
E value
                   3.0e-55
Match length
                  108
% identity
                   94
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  165495
Seq. ID
                  LIB3177-090-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  414
E value
                  1.0e-40
Match length
                  116
% identity
                  73
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

Seq. No. 165496

Seq. ID LIB3177-090-P1-K1-F10

Method BLASTX



NCBI GI g4689474 BLAST score 554 3.0e-57E value Match length 112 99 % identity NCBI Description (AC007213) unknown protein [Arabidopsis thaliana] 165497 Seq. No. LIB3177-090-P1-K1-F11 Seq. ID

Method BLASTX
NCBI GI g3461819
BLAST score 212
E value 6.0e-17

Match length 132 % identity 44

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 165498

Seq. ID LIB3177-090-P1-K1-F12

Method BLASTX
NCBI GI 94206610
BLAST score 606
E value 4.0e-63
Match length 126
% identity 96

NCBI Description (AF066851) ATP synthase beta subunit [Trichilia emetica]

Seq. No. 165499

Seq. ID LIB3177-090-P1-K1-F4

Method BLASTX
NCBI GI g4741960
BLAST score 526
E value 1.0e-53
Match length 101
% identity 97

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 165500

Seq. ID LIB3177-090-P1-K1-F5

Method BLASTX
NCBI GI g2062158
BLAST score 747
E value 1.0e-79
Match length 144
% identity 50

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 165501

Seq. ID LIB3177-090-P1-K1-F6

Method BLASTX
NCBI GI g3080371
BLAST score 670
E value 1.0e-70
Match length 126
% identity 98

NCBI Description (AL022580) putative pectinacetylesterase protein



[Arabidopsis thaliana]

 Seq. No.
 165502

 Seq. ID
 LIB3177-090-P1-K1-F7

 Method
 BLASTX

NCBI GI g1532135 BLAST score 251 E value 2.0e-21 Match length 62 % identity 77

NCBI Description (U49442) chloroplast mRNA-binding protein CSP41 precursor

[Spinacia oleracea]

Seq. No. 165503

Seq. ID LIB3177-090-P1-K1-F8

Method BLASTX
NCBI GI 9430947
BLAST score 95
E value 3.0e-03
Match length 144
% identity 81

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 165504

Seq. ID LIB3177-090-P1-K1-F9

Method BLASTX
NCBI GI g4586255
BLAST score 280
E value 3.0e-25
Match length 70
% identity 80

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 165505

Seq. ID LIB3177-090-P1-K1-G1

Method BLASTN
NCBI GI g2980757
BLAST score 336
E value 0.0e+00
Match length 360
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18

(ESSAII project)

Seq. No. 165506

Seq. ID LIB3177-090-P1-K1-G10

Method BLASTX
NCBI GI g115385
BLAST score 574
E value 2.0e-59
Match length 112
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]



Seq. No. 165507

Seq. ID LIB3177-090-P1-K1-G11

Method BLASTX
NCBI GI g115767
BLAST score 775
E value 7.0e-83
Match length 147
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165508

Seq. ID LIB3177-090-P1-K1-G12

Method BLASTX
NCBI GI g4587525
BLAST score 294
E value 2.0e-26
Match length 146
% identity 40

NCBI Description (AC007060) Contains the PF_00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb Z25700 come from this gene.

[Arabidopsis thaliana]

Seq. No. 165509

Seq. ID LIB3177-090-P1-K1-G2

Method BLASTX
NCBI GI g4454051
BLAST score 585
E value 1.0e-60
Match length 117
% identity 94

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 165510

Seq. ID LIB3177-090-P1-K1-G3

Method BLASTX
NCBI GI g3608153
BLAST score 252
E value 2.0e-21
Match length 146
% identity 43

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 165511

Seq. ID LIB3177-090-P1-K1-G4

Method BLASTN
NCBI GI g4585952
BLAST score 143
E value 8.0e-75
Match length 232

E value

Match length

% identity

2.0e-53

131

82



```
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,
                  complete sequence
Seq. No.
                  165512
Seq. ID
                  LIB3177-090-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q166702
BLAST score
                  218
E value
                  6.0e-18
Match length
                  51
% identity
                  88
NCBI Description
                  (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit
                  [Arabidopsis thaliana]
Seq. No.
                  165513
Seq. ID
                  LIB3177-090-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q3334128
BLAST score
                  661
E value
                  2.0e-69
Match length
                  142
% identity
                  98
NCBI Description BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
                  PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA
                  carboxylase biotin-containing subunit [Arabidopsis
                  thaliana]
Seq. No.
                  165514
Seq. ID
                  LIB3177-090-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1916613
BLAST score
                  420
E value
                  3.0e-41
Match length
                  92
% identity
                  95
NCBI Description (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
Seq. No.
                  165515
Seq. ID
                  LIB3177-090-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g4159709
BLAST score
                  408
E value
                  0.0e+00
Match length
                  488
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
Seq. No.
                  165516
Seq. ID
                  LIB3177-090-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g421826
BLAST score
                  191
```



NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 165517

Seq. ID LIB3177-090-P1-K1-H1

Method BLASTX
NCBI GI g2160166
BLAST score 229
E value 4.0e-19
Match length 58
% identity 79

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 165518

Seq. ID LIB3177-090-P1-K1-H10

Method BLASTN
NCBI GI 94454587
BLAST score 100
E value 7.0e-49
Match length 288
% identity 84

NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 165519

Seq. ID LIB3177-090-P1-K1-H11

Method BLASTN
NCBI GI 94757392
BLAST score 199
E value 1.0e-108
Match length 207
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 165520

Seq. ID LIB3177-090-P1-K1-H12

Method BLASTN
NCBI GI g2707927
BLAST score 255
E value 1.0e-141
Match length 290
% identity 97

NCBI Description A.thaliana mRNA for outward rectifying potassium channel

KC01

Seq. No. 165521

Seq. ID LIB3177-090-P1-K1-H2

Method BLASTX
NCBI GI g1363489
BLAST score 713
E value 1.0e-75
Match length 131
% identity 100

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis

thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside



glucohydrolase [Arabidopsis thaliana]

```
Seq. No.
                   165522
                   LIB3177-090-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204266
BLAST score
                   425
E value
                   5.0e-42
Match length
                   119
% identity
                   77
NCBI Description
                  (AC005223) 52263 [Arabidopsis thaliana]
Seq. No.
                   165523
Seq. ID
                   LIB3177-090-P1-K1-H4
Method
                   BLASTX
                   g4835233
NCBI GI
BLAST score
                   730
E value
                   1.0e-77
Match length
                   150
                   97
% identity
NCBI Description
                   (AL049862) putative protein 1 photosystem II
                   oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                   165524
Seq. ID
                   LIB3177-090-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1669389
                   700
BLAST score
E value
                   4.0e-74
Match length
                   139
% identity
                   100
NCBI Description
                  (U42007) actin 8 [Arabidopsis thaliana]
Seq. No.
                   165525
Seq. ID
                   LIB3177-090-P1-K1-H8
Method
                   BLASTN
NCBI GI
                   q3176694
BLAST score
                   300
E value
                   1.0e-168
Match length
                   387
% identity
                   75
NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165526
Seq. ID
                   LIB3177-090-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q1172995
BLAST score
                   243
E value
                   2.0e-20
Match length
                   100
% identity
                   53
NCBI Description
                  60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]
```

22233

norvegicus]

>gi_1093952_prf__2105193A ribosomal protein L22 [Rattus



```
Seq. No.
                   165527
Seq. ID
                   LIB3177-091-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g2264306
BLAST score
                   321
E value
                   0.0e + 00
Match length
                   337
% identity
                   99
NCBI Description
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No. 165528 Seq. ID LIB3177-091-P1-K1-A10 Method BLASTX NCBI GI q4585900 BLAST score 342

E value 3.0e-32 Match length 101 71 % identity

NCBI Description (AC007133) putative histone H2A [Arabidopsis thaliana]

Seq. No. 165529

Seq. ID LIB3177-091-P1-K1-A11

Method BLASTX NCBI GI g115767 BLAST score 623 4.0e-65 E value Match length 120 99 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein $ab16\overline{5}$ - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165530

Seq. ID LIB3177-091-P1-K1-A12

Method BLASTX NCBI GI g3413717 BLAST score 437 E value 2.0e-43Match length 106 % identity 86

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

>gi 3643590 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 165531

Seq. ID LIB3177-091-P1-K1-A2

Method BLASTX NCBI GI g3386607 BLAST score 300 E value 3.0e-27 Match length 114

E value

Match length

3.0e-33



```
% identity
NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   165532
                   LIB3177-091-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3599491
BLAST score
                   168
E value
                   8.0e-12
Match length
                   42
% identity
                   81
                  (AF085149) putative aminotransferase [Capsicum chinense]
NCBI Description
Seq. No.
                  165533
Seq. ID
                  LIB3177-091-P1-K1-A4
Method
                  BLASTN
NCBI GI
                   q3241925
                   98
BLAST score
E value
                   1.0e-47
Match length
                   223
                   94
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOK9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165534
Seq. ID
                   LIB3177-091-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q544425
BLAST score
                   423
E value
                   8.0e-42
Match length
                  83
% identity
                   99
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                   >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                   - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                   glycine rich protein [Arabidopsis thaliana] >gi 166658
                   (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                   RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                   165535
Seq. ID
                  LIB3177-091-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  524
E value
                   2.0e-53
Match length
                  101
% identity
                  100
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  165536
Seq. ID
                  LIB3177-091-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4191785
BLAST score
                  351
```



% identity NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana] Seq. No. 165537 LIB3177-091-P1-K1-A9 Seq. ID Method BLASTX NCBI GI q3914658 BLAST score 625 3.0e-65 E value 122 Match length 99 % identity 50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR NCBI Description >gi 1694974 emb CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana] Seq. No. 165538 LIB3177-091-P1-K1-B1 BLASTX g1946690 493

Seq. ID Method NCBI GI BLAST score E value 5.0e-50 Match length 94 100 % identity

NCBI Description (U94495) glutathione peroxidase [Arabidopsis thaliana] >gi 4582452 gb AAD24836.1 AC007071 8 (AC007071) putative

glutathione peroxidase [Arabidopsis thaliana]

Seq. No. 165539

LIB3177-091-P1-K1-B10 Seq. ID

Method BLASTX NCBI GI g132074 BLAST score 639 E value 5.0e-67 Match length 116 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165540

Seq. ID LIB3177-091-P1-K1-B12

Method BLASTX NCBI GI g133872 BLAST score 289 E value 6.0e-26 Match length 73 % identity 82

30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) NCBI Description

>gi_282838_pir__S26494 ribosomal protein S1, chloroplast spinach >gi_322404_pir_ A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi 170143 (M82923) chloroplast ribosomal protein S1

[Spinacia oleracea]

Seq. No. 165541



```
Seq. ID
                  LIB3177-091-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  509
E value
                  6.0e-52
Match length
                  97
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
```

Seq. No. 165542

Seq. ID LIB3177-091-P1-K1-B3

Method BLASTN
NCBI GI g1769904
BLAST score 202
E value 1.0e-110
Match length 213
% identity 99

NCBI Description A.thaliana psbP gene

Seq. No. 165543

Seq. ID LIB3177-091-P1-K1-B6

Method BLASTX
NCBI GI g115767
BLAST score 526
E value 6.0e-54
Match length 103
% identity 98

a raelicity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165544

Seq. ID LIB3177-091-P1-K1-B7

Method BLASTN
NCBI GI g22564
BLAST score 128
E value 8.0e-66
Match length 215
% identity 97

NCBI Description A.thaliana tufA gene for elongation factor Tu

Seq. No. 165545

Seq. ID LIB3177-091-P1-K1-B8

Method BLASTX NCBI GI g4539292 BLAST score 435 E value 3.0e-43



```
Match length
                  85
% identity
NCBI Description
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
                  165546
Seq. No.
Seq. ID
                  LIB3177-091-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2702281
BLAST score
                  464
E value
                  9.0e-47
Match length
                  91
% identity
                  59
                  (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  165547
                  LIB3177-091-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                  468
E value
                  4.0e-47
Match length
                  92
% identity
                  95
NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                  165548
Seq. ID
                  LIB3177-091-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1850546
BLAST score
                  271
E value
                  7.0e-24
Match length
                  55
                  100
% identity
NCBI Description
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
                  thaliana]
Seq. No.
                  165549
Seq. ID
                  LIB3177-091-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  785
E value
                  4.0e-84
Match length
                  147
                  99
% identity
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  165550
```

Seq. ID LIB3177-091-P1-K1-C12

Method BLASTX
NCBI GI g3236259
BLAST score 413
E value 8.0e-41
Match length 91

Seq. No.

165556



```
% identity
NCBI Description
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
                   thaliana]
Seq. No.
                   165551
                   LIB3177-091-P1-K1-C2
Seq. ID
                                                                                4--,-
Method
                   BLASTX
NCBI GI
                   q4584527
BLAST score
                   223
E value
                   3.0e-18
Match length
                  105
% identity
                   39
NCBI Description
                 (AL049607) putative protein [Arabidopsis thaliana]
                  165552
Seq. No.
                  LIB3177-091-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  408
E value
                   5.0e-40
Match length
                  118
% identity
                   68
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                  165553
                  LIB3177-091-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4262156
BLAST score
                   551
E value
                   1.0e-56
Match length
                  133
% identity
                   81
                  (AC005275) putative component of cytochrome B6-F complex
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  165554
Seq. ID
                  LIB3177-091-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1321731
BLAST score
                  173
E value
                  2.0e-12
Match length
                  129
% identity
                   40
NCBI Description
                  (Z72439) major allergen Cor a 1 [Corylus avellana]
Seq. No.
                  165555
Seq. ID
                  LIB3177-091-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4741954
BLAST score
                  656
E value
                  6.0e-69
Match length
                  141
% identity
NCBI Description
                  (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
```

Method

NCBI GI

BLAST score



LIB3177-091-P1-K1-C8 Seq. ID Method BLASTN NCBI GI a3763915 BLAST score 151 2.0e-79 E value Match length 176 95 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165557 Seq. ID LIB3177-091-P1-K1-D1 Method BLASTX g421836 NCBI GI BLAST score 660 E value 2.0e-69 Match length 131 99 % identity NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >qi 553040 (M96855) GF14 [Arabidopsis thaliana] 165558 Seq. No. LIB3177-091-P1-K1-D10 Seq. ID Method BLASTX NCBI GI g4204274 BLAST score 755 1.0e-80 E value Match length 148 % identity 99 NCBI Description (AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] Seq. No. 165559 Seq. ID LIB3177-091-P1-K1-D11 Method BLASTX NCBI GI g4455359 BLAST score 637 E value 8.0e-67 Match length 133 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] Seq. No. 165560 Seq. ID LIB3177-091-P1-K1-D12 Method BLASTX NCBI GI q4417280 BLAST score 615 E value 4.0e-64 Match length 137 % identity NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana] Seq. No. 165561 Seq. ID LIB3177-091-P1-K1-D2

324

BLASTX

g132102



E value 9.0e-57 Match length 113 % identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165562

Seq. ID LIB3177-091-P1-K1-D4

Method BLASTX
NCBI GI g543841
BLAST score 536
E value 6.0e-55
Match length 106
% identity 98

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875

ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)

ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 165563

Seq. ID LIB3177-091-P1-K1-D6

Method BLASTN
NCBI GI g2454181
BLAST score 287
E value 1.0e-160
Match length 343
% identity 99

NCBI Description Arabidopsis thaliana pyruvate dehydrogenase E1 alpha

subunit mRNA, nuclear gene encoding plastid protein,

complete cds

Seq. No. 165564

Seq. ID LIB3177-091-P1-K1-D7

Method BLASTX
NCBI GI g115385
BLAST score 346
E value 7.0e-33
Match length 72
% identity 96

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165565

Seq. ID LIB3177-091-P1-K1-D8

Method BLASTX
NCBI GI g3785981
BLAST score 544
E value 8.0e-56
Match length 136
% identity 72



NCBI Description (AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No. 165566

Seq. ID LIB3177-091-P1-K1-D9

Method BLASTX
NCBI GI g4115379
BLAST score 466
E value 1.0e-46
Match length 111
% identity 79

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 165567

Seq. ID LIB3177-091-P1-K1-E10

Method BLASTX
NCBI GI g132074
BLAST score 786
E value 3.0e-84
Match length 151
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063 pir RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165568

Seq. ID LIB3177-091-P1-K1-E11

Method BLASTX
NCBI GI g2129755
BLAST score 482
E value 8.0e-49
Match length 96
% identity 100

NCBI Description tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis

thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp

synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 165569

Seq. ID LIB3177-091-P1-K1-E12

Method BLASTN
NCBI GI g1304412
BLAST score 50
E value 4.0e-20
Match length 54
% identity 98

NCBI Description Arabidopsis thaliana Rac-like protein (ARAC3) gene,

complete cds

Seq. No. 165570

Seq. ID LIB3177-091-P1-K1-E2

Method BLASTX
NCBI GI g3342249
BLAST score 306
E value 8.0e-32



Match length 106 % identity 75

NCBI Description (AF047719) GA3 [Arabidopsis thaliana] >gi_3342251

(AF047720) GA3 [Arabidopsis thaliana]

Seq. No. 165571

Seq. ID LIB3177-091-P1-K1-E3

Method BLASTN
NCBI GI 94454004
BLAST score 163
E value 1.0e-86
Match length 185
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 165572

Seq. ID LIB3177-091-P1-K1-E4

Method BLASTN
NCBI GI g2924729
BLAST score 406
E value 0.0e+00
Match length 426
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNA5, complete sequence [Arabidopsis thaliana]

Seq. No. 165573

Seq. ID LIB3177-091-P1-K1-E5

Method BLASTX
NCBI GI g1871181
BLAST score 175
E value 1.0e-12
Match length 110
% identity 48

NCBI Description (U90439) ring zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 165574

Seq. ID LIB3177-091-P1-K1-E6

Method BLASTX
NCBI GI g3096931
BLAST score 561
E value 8.0e-58
Match length 110
% identity 99

NCBI Description (AL023094) putative ribosomal protein S16 [Arabidopsis

thaliana]

Seq. No. 165575

Seq. ID LIB3177-091-P1-K1-E7

Method BLASTX
NCBI GI g2119846
BLAST score 625
E value 2.0e-65
Match length 118
% identity 100



NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 165576 LIB3177-091-P1-K1-E8 Seq. ID Method BLASTX NCBI GI g3522929 51 3.0e-21

BLAST score E value 55 Match length % identity 98

NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 165577 Seq. ID LIB3177-091-P1-K1-F10 Method BLASTX NCBI GI g3287695

BLAST score 415 E value 1.0e-40 Match length 111 % identity 67

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No. 165578

LIB3177-091-P1-K1-F11 Seq. ID

Method BLASTX NCBI GI q3212869 BLAST score 648 E value 4.0e-68 Match length 133 % identity 87

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 165579

Seq. ID LIB3177-091-P1-K1-F3

Method BLASTN NCBI GI q4757414 BLAST score 117 E value 2.0e-59 Match length 189 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 165580

Seq. ID LIB3177-091-P1-K1-F4

Method BLASTX NCBI GI g2642435



BLAST score 489 2.0e-49 E value 98 Match length 94 % identity

NCBI Description (AC002391) MYB-related protein [Arabidopsis thaliana]

Seq. No. 165581

LIB3177-091-P1-K1-F5 Seq. ID

Method BLASTX NCBI GI g3834312 BLAST score 594 E value 1.0e-61 Match length 135 % identity 85

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 qb L16983

Daucus carota and a member of S locus glycoprotein $\overline{\mathsf{f}}\mathsf{amily}$

PF 00954. ESTs gb AA067487, gb Z35737, gb Z30815, gb Z35350, gb AA713171, gb AI100553, gb Z34248,

gb_AA728536, gb_Z30816 an

Seq. No. 165582

Seq. ID LIB3177-091-P1-K1-F6

Method BLASTX NCBI GI g548653 BLAST score 42 E value 3.0e - 33Match length 104 % identity 82

NCBI Description 50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)

> >gi 541895 pir A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181 (X68046)

ribosomal protein L12 [Arabidopsis thaliana]

Seq. No. 165583

Seq. ID LIB3177-091-P1-K1-F7

Method BLASTN NCBI GI g1890129 BLAST score 386 E value 0.0e + 00Match length 406 % identity 99

NCBI Description Arabidopsis thaliana valyl tRNA synthetase (valRS) mRNA,

complete cds

Seq. No. 165584

Seq. ID LIB3177-091-P1-K1-F8

Method BLASTX NCBI GI q132863 BLAST score 708 E value 5.0e-75 Match length 136 % identity 97

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2

>gi 12214 emb CAA46568 (X65615) ribosomal protein L2

[Sinapis alba]

Seq. No. 165585



```
Seq. ID
                  LIB3177-091-P1-K1-F9
                  BLASTN
Method
NCBI GI
                  g405130
BLAST score
                  361
E value
                  0.0e + 00
Match length
                  373
                  99
% identity
NCBI Description
                  Arabidopsis thaliana nuclear-encoded chloroplast stromal
                  cyclophilin (ROC4) mRNA, complete cds
Seq. No.
                  165586
Seq. ID
                  LIB3177-091-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g730645
BLAST score
                  463
E value
                  2.0e-46
Match length
                  109
                  86
% identity
                 40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal
NCBI Description
                  protein S15 - Arabidopsis thaliana >qi 313152 emb CAA80679
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                  [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                  gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
                  165587
Seq. No.
Seq. ID
                  LIB3177-091-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2129577
                  335
BLAST score
                  2.0e-31
E value
Match length
                  76
                  88
% identity
NCBI Description
                  DnaJ homolog protein - Arabidopsis thaliana >gi_727357
                  (U22340) DnaJ homolog [Arabidopsis thaliana]
Seq. No.
                  165588
Seq. ID
                  LIB3177-091-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  732
E value
                  6.0e-78
Match length
                  138
% identity
                  99
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
```

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 165589

Seq. ID LIB3177-091-P1-K1-G2

Method BLASTX NCBI GI g4204274 BLAST score 681 E value 7.0e-72



Match length 133 % identity NCBI Description (AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] 165590 Seq. No. Seq. ID LIB3177-091-P1-K1-G3 Method BLASTX NCBI GI g4539335 BLAST score 215 E value 2.0e-17 Match length 86 % identity 53 NCBI Description (AL035539) putative protein [Arabidopsis thaliana] Seq. No. 165591 Seq. ID LIB3177-091-P1-K1-G4 Method BLASTX NCBI GI g1213442 BLAST score 747 E value 1.0e-79 Match length 146 99 % identity NCBI Description (U48961) isopentenyl pyrophosphate isomerase [Arabidopsis thaliana] Seq. No. 165592 LIB3177-091-P1-K1-G5 Seq. ID Method BLASTX NCBI GI g2244750 BLAST score 510 E value 6.0e-52Match length 113 % identity NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana] Seq. No. 165593 Seq. ID LIB3177-091-P1-K1-G6 Method BLASTX NCBI GI g140285 BLAST score 286 E value 1.0e-25 Match length 60 % identity NCBI Description HYPOTHETICAL 19 KD PROTEIN (ORF 168) >gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana tabacum]

Seq. No. 165594

Seq. ID LIB3177-091-P1-K1-G7

Method BLASTX NCBÌ GI g2829862 BLAST score 512 E value 4.0e-52 Match length 114



% identity NCBI Description (AC002396) Similar to glucosyltransferases [Arabidopsis thaliana] Seq. No. 165595 LIB3177-091-P1-K1-G8 Seq. ID Method BLASTX

NCBI GI g4741960 BLAST score 740 E value 7.0e-79 Match length 136 % identity 99

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 165596

Seq. ID LIB3177-091-P1-K1-G9

Method BLASTX NCBI GI q2865623 BLAST score 540 E value 2.0e-55 Match length 109 99 % identity

(AF045286) NCBI Description

GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase

[Arabidopsis thaliana]

Seq. No. 165597

LIB3177-091-P1-K1-H11 Seq. ID

Method BLASTN NCBI GI g4510360 BLAST score 33 E value 6.0e-09

Match length 65 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

165598 Seq. No.

Seq. ID LIB3177-091-P1-K1-H12

Method BLASTX NCBI GI g2507587 BLAST score 284 E value 2.0e-25 Match length 57 % identity 88

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)

>gi 1361998 pir S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A

metallothionein 1 [Arabidopsis thaliana]

Seq. No. 165599

Seq. ID LIB3177-091-P1-K1-H2

Method BLASTX NCBI GI g4262242 BLAST score 387 E value 5.0e-39



Match length 95 % identity 87

NCBI Description (AC006200) NADC homolog [Arabidopsis thaliana]

Seq. No. 165600

Seq. ID LIB3177-091-P1-K1-H3

Method BLASTX
NCBI GI g3004560
BLAST score 417
E value 5.0e-41
Match length 112
% identity 75

NCBI Description (AC003673) putative ATP binding protein [Arabidopsis

thaliana]

Seq. No. 165601

Seq. ID LIB3177-091-P1-K1-H4

Method BLASTN
NCBI GI g3046849
BLAST score 147
E value 6.0e-77
Match length 408
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18L3, complete sequence [Arabidopsis thaliana]

Seq. No. 165602

Seq. ID LIB3177-091-P1-K1-H5

Method BLASTX
NCBI GI g1172873
BLAST score 536
E value 5.0e-55
Match length 106
% identity 100

NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir_JN0719

drought-inducible cysteine proteinase ($\overline{\text{EC}}$ 3.4. $\overline{22}$.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 165603

Seq. ID LIB3177-091-P1-K1-H6

Method BLASTN
NCBI GI 9499159
BLAST score 313
E value 1.0e-176
Match length 345
% identity 98

NCBI Description A.thaliana mRNA Athb-5

Seq. No. 165604

Seq. ID LIB3177-091-P1-K1-H7

Method BLASTX
NCBI GI g3819164
BLAST score 451
E value 5.0e-53
Match length 116
% identity 88



NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine Seq. No. 165605 Seq. ID LIB3177-091-P1-K1-H8 Method BLASTX NCBI GI q2231312 BLAST score 462 E value 3.0e-46Match length 100 % identity 91 NCBI Description (U75603) AtRab18 [Arabidopsis thaliana] Seq. No. 165606 Seq. ID LIB3177-091-P1-K1-H9 Method BLASTX NCBI GI g2062158 BLAST score 376 E value 3.0e-36 Match length 82 % identity 44 NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana] Seq. No. 165607 Seq. ID LIB3177-092-P1-K1-A1 Method BLASTX NCBI GI q4455360 BLAST score 138 E value 1.0e-08 Match length 89 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] Seq. No. 165608 Seq. ID LIB3177-092-P1-K1-A10 Method BLASTX NCBI GI g2407314 BLAST score 143 E value 2.0e-26 Match length 81 67 % identity (AF017998) chlorophyll a/b binding protein [Tetraselmis sp. NCBI Description RG-15] Seq. No. 165609

Seq. ID LIB3177-092-P1-K1-A11

BLASTN Method NCBI GI g3297806 BLAST score 224 E value 1.0e-123 Match length 224 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5

(ESSA project)

Seq. No. 165610

BLAST score

E value

427

3.0e-42



```
LIB3177-092-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4455262
BLAST score
                  351
E value
                  0.0e + 00
                  351
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
Seq. No.
                  165611
                  LIB3177-092-P1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1769904
BLAST score
                  149
E value
                  2.0e-78
Match length
                  153
% identity
                  99
NCBI Description A.thaliana psbP gene
                  165612
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3892722
BLAST score
                  44
E value
                  4.0e-51
Match length
                  104
                  100
% identity
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                  165613
                  LIB3177-092-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617013
BLAST score
                  225
E value
                  1.0e-18
Match length
                  49
                  90
% identity
NCBI Description (Y07745) histone H2B like protein [Arabidopsis thaliana]
Seq. No.
                  165614
Seq. ID
                  LIB3177-092-P1-K1-A7
Method
                  BLASTX
                  g4455223
NCBI GI
BLAST score
                  296
E value
                  1.0e-26
Match length
                  101
% identity
                  38
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  165615
Seq. ID
                  LIB3177-092-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1169201
```



Match length 129 % identity 70

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis

thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 165616

Seq. ID LIB3177-092-P1-K1-A9

Method BLASTX NCBI GI g132074 BLAST score 532 E value 2.0e-58 Match length 114 % identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC $4.\overline{1.1.39}$) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165617

Seq. ID LIB3177-092-P1-K1-B1

Method BLASTX NCBI GI g115767 BLAST score 643 E value 8.0e-70 Match length 140 % identity 96

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165618

Seq. ID LIB3177-092-P1-K1-B10

Method BLASTN NCBI GI q4589436 BLAST score 320 E value 1.0e-180 Match length 340 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPA22, complete sequence

Seq. No. 165619

Seq. ID LIB3177-092-P1-K1-B11

Method BLASTX NCBI GI q3915865 BLAST score 343 1.0e-32 E value Match length 67 % identity 99

NCBI Description 40S RIBOSOMAL PROTEIN S4

Seq. No. 165620



```
Seq. ID
                   LIB3177-092-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1762584
BLAST score
                   270
                   7.0e-24
E value
Match length
                   76
                   67
% identity
NCBI Description
                  (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
Seq. No.
                   165621
                   LIB3177-092-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586256
BLAST score
                   56
E value
                   5.0e-47
Match length
                   153
% identity
                   69
                  (AL049640) probable photosystem I chain XI precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165622
Seq. ID
                   LIB3177-092-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   q1483149
BLAST score
                   209
E value
                   1.0e-114
Match length
                   258
% identity
                   95
NCBI Description Arabidopsis thaliana mRNA for monodehydroascorbate
                   reductase, complete cds
Seq. No.
                   165623
Seq. ID
                   LIB3177-092-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g421929
BLAST score
                   61
E value
                   5.0e-43
Match length
                   114
% identity
NCBI Description
                  ubiquitin - tomato >gi 312160 emb CAA51679 (X73156)
                   ubiquitin [Lycopersicon esculentum]
Seq. No.
                   165624
Seq. ID
                   LIB3177-092-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g114122
BLAST score
                   373
E value
                   6.0e-36
Match length
                   87
                   84
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 2 >gi 423228 pir A45422
                   ADP-ribosylation factor 2 - bovine >\overline{g}i_2\overline{13}7127_{pir}
                   ADP-ribosylation factor type 2 - mouse >gi 162682 (J03794)
                   ADP-ribosylation factor protein [Bos taurus] >gi 163668
```

(M88292) ADP-ribosylation factor 2 [Bos taurus] >gi_304249 (M88287) ADP-ribosylation factor 2 [Bos taurus] >gi_438864



(L12381) ADP-ribosylation factor 2 [Rattus norvegicus] >gi_1565209_dbj_BAA13491_ (D87899) ARF2 [Mus musculus] >gi_740260_prf__2004472B phospholipase D-activating factor [Bos taurus]

 Seq. No.
 165625

 Seq. ID
 LIB3177-092-P1-K1-B7

 Method
 BLASTN

 NCBI GI
 g2337888

 BLAST score
 228

 E value
 1.0e-125

E value 1.0e-1
Match length 420
% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 165626

Seq. ID LIB3177-092-P1-K1-B8

Method BLASTX
NCBI GI g4544393
BLAST score 88
E value 3.0e-34
Match length 102
% identity 78

NCBI Description (AC007047) putative ribosomal protein S25 [Arabidopsis

thaliana]

Seq. No. 165627

Seq. ID LIB3177-092-P1-K1-B9

Method BLASTX
NCBI GI g4454032
BLAST score 437
E value 3.0e-43
Match length 137
% identity 64

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 165628

Seq. ID LIB3177-092-P1-K1-C1

Method BLASTN
NCBI GI g3641835
BLAST score 124
E value 3.0e-63
Match length 164
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20

(ESSAII project)

Seq. No. 165629

Seq. ID LIB3177-092-P1-K1-C10

Method BLASTN
NCBI GI g975645
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

NCBI Description A.thaliana cor47 gene



Seq. No. 165630

Seq. ID LIB3177-092-P1-K1-C11

Method BLASTX
NCBI GI 94678924
BLAST score 50
E value 2.0e-70
Match length 139
% identity 96

NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 165631

Seq. ID LIB3177-092-P1-K1-C12

Method BLASTX
NCBI GI g3377835
BLAST score 314
E value 5.0e-29
Match length 108
% identity 60

NCBI Description (AF075598) contains similarity to Arabidopsis thaliana

downy mildew resistance protein RPP5 (GB:U97106)

[Arabidopsis thaliana]

Seq. No. 165632

Seq. ID LIB3177-092-P1-K1-C3

Method BLASTX
NCBI GI g2119846
BLAST score 654
E value 9.0e-69
Match length 125
% identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165633

Seq. ID LIB3177-092-P1-K1-C4

Method BLASTN
NCBI GI g4757405
BLAST score 85
E value 6.0e-40

Match length 423 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOJ10, complete sequence

Seq. No. 165634

Seq. ID LIB3177-092-P1-K1-C5

Method BLASTX
NCBI GI g2129637
BLAST score 384
E value 5.0e-37
Match length 98



% identity 64

NCBI Description low temperature-induced protein cor47 - Arabidopsis thaliana >gi_975646_emb_CAA62449_ (X90959) dehydrin

[Arabidopsis thaliana]

Seq. No. 165635

Seq. ID LIB3177-092-P1-K1-C6

Method BLASTX
NCBI GI g4741950
BLAST score 608
E value 2.0e-63
Match length 126
% identity 92

NCBI Description (AF134125) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 165636

Seq. ID LIB3177-092-P1-K1-C7

Method BLASTX
NCBI GI g1143511
BLAST score 812
E value 3.0e-87
Match length 149
% identity 98

NCBI Description (Z47076) Ser/Thr protein phosphatase homologous to PPX

[Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein

phosphatase [Malus domestica]

Seq. No. 165637

Seq. ID LIB3177-092-P1-K1-C9

Method BLASTX
NCBI GI g4583542
BLAST score 297
E value 7.0e-27
Match length 136
% identity 53

NCBI Description (Y16847) 16 kDa polypeptide of oxygen-evolving complex

[Arabidopsis thaliana]

Seq. No. 165638

Seq. ID LIB3177-092-P1-K1-D10

Method BLASTX
NCBI GI g2119846
BLAST score 598
E value 3.0e-62
Match length 116
% identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165639

Seq. ID LIB3177-092-P1-K1-D12

Method BLASTN



NCBI GI g4159701 BLAST score 373 E value 0.0e+00420 Match length 97 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence

165640 Seq. No.

LIB3177-092-P1-K1-D3 Seq. ID

Method BLASTX NCBI GI g3367515 BLAST score 727 E value 3.0e-77Match length 147 98 % identity

(AC004392) Similar to NCBI Description

glucose-6-phosphate/phosphate-translocator (GPT)

gb AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 165641

LIB3177-092-P1-K1-D4 Seq. ID

Method BLASTX NCBI GI g4454036 BLAST score 369 E value 1.0e-75Match length 137

% identity 90

(AL035394) putative major latex protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 165642

LIB3177-092-P1-K1-D5 Seq. ID

Method BLASTX NCBI GI q1351272 BLAST score 435 E value 4.0e-43Match length 86 % identity 98

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550

(U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 165643

Seq. ID LIB3177-092-P1-K1-D6

Method BLASTX NCBI GI g1168609 BLAST score 531 E value 2.0e-54 Match length 120 % identity 88

AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir S35071 NCBI Description

auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana]



>gi_448755_prf__1917337A ubiquitin-activating enzyme E1
[Arabidopsis thaliana]

Seq. No. 165644

Seq. ID LIB3177-092-P1-K1-D7

Method BLASTN
NCBI GI g166645
BLAST score 102
E value 4.0e-50
Match length 152
% identity 94

NCBI Description Arabidopsis thaliana light-harvesting chlorophyll

a/b-binding protein (Cab4) mRNA, complete cds

Seq. No. 165645

Seq. ID LIB3177-092-P1-K1-D8

Method BLASTX
NCBI GI g126766
BLAST score 654
E value 1.0e-68
Match length 142
% identity 89

NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate

synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150
(J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No. 165646

Seq. ID LIB3177-092-P1-K1-D9

Method BLASTX
NCBI GI g282865
BLAST score 465
E value 8.0e-47
Match length 97
% identity 69

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 165647

Seq. ID LIB3177-092-P1-K1-E1

Method BLASTX
NCBI GI g1169476
BLAST score 624
E value 3.0e-65
Match length 123
% identity 98

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 165648

Seq. ID LIB3177-092-P1-K1-E10

Method BLASTX NCBI GI g2244750



BLAST score 643 E value 2.0e-67 Match length 124 % identity 99

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 165649

Seq. ID LIB3177-092-P1-K1-E11

Method BLASTX
NCBI GI g115783
BLAST score 607
E value 3.0e-63
Match length 114
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 165650

Seq. ID LIB3177-092-P1-K1-E2

Method BLASTX
NCBI GI g231586
BLAST score 617
E value 2.0e-64
Match length 132
% identity 92

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82027_pir__S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree
>gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

Seq. No. 165651

Seq. ID LIB3177-092-P1-K1-E3

Method BLASTN
NCBI GI g3128142
BLAST score 300
E value 1.0e-168
Match length 316
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No. 165652

Seq. ID LIB3177-092-P1-K1-E4

Method BLASTX
NCBI GI g480450
BLAST score 62
E value 1.0e-51
Match length 108
% identity 89

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis

thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]



```
Seq. No.
                  165653
Seq. ID
                  LIB3177-092-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1145699
BLAST score
                  605
E value
                  6.0e-63
Match length
                  126
% identity
                  97
                  (U39486) delta tonoplast integral protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165654
                  LIB3177-092-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q166834
BLAST score
                  56
E value
                  9.0e-59
                  128
Match length
% identity
                  93
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
Seq. No.
                  165655
                  LIB3177-092-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  100
                  2.0e-49
E value
                  128
Match length
                  94
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  165656
Seq. ID
                  LIB3177-092-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4574208
BLAST score
                  446
E value
                  1.0e-44
Match length
                  92
% identity
                  99
NCBI Description (AF093108) histone H3 [Tortula ruralis]
Seq. No.
                  165657
Seq. ID
                  LIB3177-092-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4455253
BLAST score
                  569
E value
                  7.0e-59
Match length
                  122
% identity
                  89
NCBI Description
                  (AL035523) superoxide dismutase (EC 1.15.1.1)
```

Seq. No. 165658

(Fe)(fragment) [Arabidopsis thaliana]



Seq. ID LIB3177-092-P1-K1-F10

Method BLASTX
NCBI GI g4469408
BLAST score 459
E value 8.0e-46
Match length 133
% identity 71

NCBI Description (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis

thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box

protein FLOWERING LOCUS F [Arabidopsis thaliana]

Seq. No. 165659

Seq. ID LIB3177-092-P1-K1-F11

Method BLASTX
NCBI GI g4741952
BLAST score 703
E value 2.0e-74
Match length 136
% identity 70

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 165660

Seq. ID LIB3177-092-P1-K1-F12

Method BLASTX
NCBI GI g132110
BLAST score 581
E value 3.0e-60
Match length 112
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165661

Seq. ID LIB3177-092-P1-K1-F2

Method BLASTN
NCBI GI g166695
BLAST score 34
E value 1.0e-09
Match length 226
% identity 86

NCBI Description Arabidopsis thaliana recombination and DNA-damage

resistance protein (DRT112) mRNA, complete cds

Seq. No. 165662

Seq. ID LIB3177-092-P1-K1-F3

Method BLASTX
NCBI GI g3036805
BLAST score 657
E value 4.0e-69
Match length 127
% identity 98

NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]

% identity

NCBI Description

99

fragment No



```
Seq. No.
                    165663
Seq. ID
                    LIB3177-092-P1-K1-F4
Method
                    BLASTX
NCBI GI
                    q3420008
BLAST score
                    240
E value
                    4.0e-20
Match length
                    123
% identity
                    38
NCBI Description (AF000307) steroid sulfotransferase 3 [Brassica napus]
Seq. No.
                    165664
                    LIB3177-092-P1-K1-F5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3157944
BLAST score
                    548
E value
                    3.0e-56
Match length
                   109
% identity
                    95
NCBI Description
                   (AC002131) Very strong similarity to aminomethyltransferase
                   precursor gb U79769 from Mesembryanthemum crystallinum.
                   ESTs gb_T43167, gb T21076, gb H36999, qb T22773,
                    gb_{380\overline{3}8}, gb_{137\overline{4}2}, gb_{2265\overline{4}5}, gb_{12075\overline{3}} and gb_{43123}
                   come from this ge
Seq. No.
                   165665
                   LIB3177-092-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115783
BLAST score
                   568
E value
                   1.0e-58
Match length
                   112
% identity
                   95
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-140) (LHCP) >gi_16376 emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   165666
Seq. ID
                   LIB3177-092-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2970034
BLAST score
                   202
E value
                   2.0e-16
Match length
                   50
% identity
                   70
NCBI Description (D88536) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                   165667
Seq. ID
                   LIB3177-092-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g2244950
BLAST score
                   325
E value
                   0.0e+00
Match length
                   341
```

22262

Arabidopsis thaliana DNA chromosome 4, ESSA I contig

% identity

NCBI Description

99



```
Seq. No.
                  165668
Seq. ID
                  LIB3177-092-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3123188
BLAST score
                   685
                   2.0e-72
E value
Match length
                  140
% identity
                   95
                  CATALASE 3 > gi_2347178 (U43147) catalase 3 [Arabidopsis
NCBI Description
                   thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis
                   thaliana]
                   165669
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-G12
Method
                  BLASTX
                  g116343
NCBI GI
BLAST score
                   321
E value
                  1.0e-29
Match length
                  138
% identity
                  43
NCBI Description BASIC ENDOCHITINASE PRECURSOR
Seq. No.
                  165670
Seq. ID
                  LIB3177-092-P1-K1-G2
Method
                  BLASTN
                  g11244
NCBI GI
BLAST score
                  38
E value
                   6.0e-13
Match length
                  54
% identity
                  93
NCBI Description A.thaliana chloroplast DNA for transfer RNA-Ile and
                  ribosomal protein
Seq. No.
                  165671
Seq. ID
                  LIB3177-092-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g625977
BLAST score
                  531
E value
                  2.0e-54
Match length
                  108
% identity
                  96
NCBI Description p40 protein homolog - Arabidopsis thaliana >gi 402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
                  165672
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  500
                  7.0e-51
E value
Match length
                  97
```

(CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

NCBI Description



thaliana]

```
Seq. No.
                   165673
                   LIB3177-092-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4741952
BLAST score
                   430
E value
                   1.0e-42
Match length
                   98
% identity
                   83
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   165674
Seq. ID
                   LIB3177-092-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g2583125
BLAST score
                   77
E value
                   1.1e-01
Match length
                   54
% identity
                   65
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
                   thaliana]
Seq. No.
                   165675
Seq. ID
                   LIB3177-092-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q2244750
BLAST score
                   543
E value
                   9.0e-56
Match length
                   113
% identity
                   96
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   165676
Seq. ID
                   LIB3177-092-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q3080415
BLAST score
                   514
E value
                   2.0e-52
Match length
                  111
% identity
                   82
NCBI Description
                  (AL022604) cysteine proteinase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   165677
Seq. ID
                  LIB3177-092-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  459
E value
                   5.0e-46
Match length
                  117
% identity
                  74
```

22264

CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_



(D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 165678 Seq. ID LIB3177-092-P1-K1-H1 Method BLASTX NCBI GI g687844 BLAST score 292 E value 2.0e-26 Match length 119 % identity 50

NCBI Description (U21320) contains TPR domain-like repeats [Caenorhabditis

elegans]

Seq. No. 165679

Seq. ID LIB3177-092-P1-K1-H10

Method BLASTX
NCBI GI g3913733
BLAST score 734
E value 4.0e-78
Match length 141
% identity 97

NCBI Description HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME

(GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644_ (Y08357) hydroxyacylglutathione hydrolase [Arabidopsis thaliana]

Seq. No. 165680

Seq. ID LIB3177-092-P1-K1-H11

Method BLASTX
NCBI GI g132110
BLAST score 594
E value 9.0e-62
Match length 112
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165681

Seq. ID LIB3177-092-P1-K1-H2

Method BLASTX
NCBI GI g3688173
BLAST score 384
E value 6.0e-46
Match length 133
% identity 65

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 165682

Seq. ID LIB3177-092-P1-K1-H3

Method BLASTX
NCBI GI g3550519
BLAST score 493
E value 7.0e-50
Match length 113



% identity 80

NCBI Description (AJ007630) oxygenase [Nicotiana tabacum]

Seq. No. 165683

Seq. ID LIB3177-092-P1-K1-H4

Method BLASTN
NCBI GI 94678315
BLAST score 150
E value 9.0e-79
Match length 173
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15

(ESSA project)

Seq. No. 165684

Seq. ID LIB3177-092-P1-K1-H5

Method BLASTX
NCBI GI g2119846
BLAST score 666
E value 2.0e-71
Match length 138
% identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165685

Seq. ID LIB3177-092-P1-K1-H6

Method BLASTX
NCBI GI g3319347
BLAST score 305
E value 3.0e-28
Match length 72

% identity 82

NCBI Description (AF077407) No definition line found [Arabidopsis thaliana]

Seq. No. 165686

Seq. ID LIB3177-092-P1-K1-H7

Method BLASTX
NCBI GI g4006934
BLAST score 411
E value 2.0e-40
Match length 100
% identity 76

NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No. 165687

Seq. ID LIB3177-092-P1-K1-H8

Method BLASTN
NCBI GI g3985952
BLAST score 340
E value 0.0e+00
Match length 372



% identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MRC8, complete sequence [Arabidopsis thaliana] Seq. No. 165688 Seq. ID LIB3177-092-P1-K1-H9 Method BLASTX NCBI GI g2199574 BLAST score 394 E value 1.0e-38 Match length 76 % identity 99 NCBI Description (AF004293) aquaporin [Brassica rapa] Seq. No. 165689 Seq. ID LIB3177-093-P1-K1-A1 Method BLASTN NCBI GI g3738088 BLAST score 363 E value 0.0e + 00Match length 425 % identity 96 NCBI Description Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165690 LIB3177-093-P1-K1-A10 Seq. ID Method BLASTX NCBI GI q2129583 BLAST score 329 E value 1.0e-30 Match length 84 % identity 82 NCBI Description ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_ (X94248) ferritin [Arabidopsis thaliana] Seq. No. 165691 Seq. ID LIB3177-093-P1-K1-A11 Method BLASTN NCBI GI g3341671 BLAST score 273 E value 1.0e-152 Match length 431 99 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165692 Seq. ID LIB3177-093-P1-K1-A12

Method BLASTX NCBI GI q3695023 BLAST score 242 2.0e-20 E value Match length 96 % identity 51

NCBI Description (AF055850) unknown [Arabidopsis thaliana]



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Seq. No.
                   165693
                   LIB3177-093-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1710780
BLAST score
                   501
E value
                   9.0e-51
                   131
Match length
% identity
                   74
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                    (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   165694
Seq. No.
Seq. ID
                   LIB3177-093-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g4584351
                   302
BLAST score
E value
                   1.0e-169
Match length
                   357
                   96
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T12H3 genomic
                   sequence, complete sequence
Seq. No.
                   165695
                   LIB3177-093-P1-K1-A4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2351073
BLAST score
                   175
E value
                   1.0e-93
Match length
                   400
                   98
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165696
Seq. ID
                   LIB3177-093-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   q3004543
BLAST score
                   55
E value
                   5.0e-22
Match length
                   280
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F19F24 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165697
Seq. ID
                   LIB3177-093-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g232031
BLAST score
                   336
E value
                   2.0e-31
Match length
                   116
% identity
                   54
NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_ S29224 translation elongation factor eEF-1 beta' chain - rice
```

22268

[Oryza sativa]

>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'



Seq. No. 165698 Seq. ID LIB3177-093-P1-K1-A7 Method BLASTX NCBI GI q4538963 BLAST score 66 E value 1.0e-57 111 Match length 75 % identity NCBI Description (AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb AAD28776.1 AF134129 1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] Seq. No. 165699 LIB3177-093-P1-K1-A8 Seq. ID Method BLASTX NCBI GI q131770 BLAST score 271 E value 6.0e-24Match length 94 % identity 56 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) NCBI Description (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353 emb CAA29844 (X06636) rp1024 protein [Dictyostelium discoideum] Seq. No. 165700 Seq. ID LIB3177-093-P1-K1-B1 Method BLASTN NCBI GI q166879 BLAST score 197 E value 1.0e-107 Match length 232 97 % identity NCBI Description A.thaliana gene sequence, exon Seq. No. 165701 Seq. ID LIB3177-093-P1-K1-B10 Method BLASTX NCBI GI g132110 BLAST score 716 E value 5.0e-76 Match length 134 % identity 99 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165702

Seq. ID LIB3177-093-P1-K1-B11

Method BLASTX NCBI GI g4335745 BLAST score 406



E value 1.0e-39
Match length 142
% identity 55
NCBI Description (AC0062

(AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 165703

Seq. ID LIB3177-093-P1-K1-B12

Method BLASTX
NCBI GI g4512655
BLAST score 401
E value 4.0e-39
Match length 74
% identity 99

NCBI Description (AC007048) putative protein phosphatase 2C [Arabidopsis

thaliana]

Seq. No. 165704

Seq. ID LIB3177-093-P1-K1-B2

Method BLASTX
NCBI GI g1351271
BLAST score 666
E value 4.0e-70
Match length 144
% identity 90

NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)

>gi_1084309_pir__S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

Seq. No. 165705

Seq. ID LIB3177-093-P1-K1-B3

Method BLASTX
NCBI GI 94454036
BLAST score 807
E value 1.0e-86
Match length 148
% identity 100

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 165706

Seq. ID LIB3177-093-P1-K1-B4

Method BLASTX
NCBI GI g115385
BLAST score 615
E value 4.0e-64
Match length 123
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165707

Seq. ID LIB3177-093-P1-K1-B5



Method BLASTN
NCBI GI g2645198
BLAST score 45
E value 5.0e-16
Match length 162
% identity 83

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165708

Seq. ID LIB3177-093-P1-K1-B6

Method BLASTX
NCBI GI g115767
BLAST score 734
E value 4.0e-78
Match length 142
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165709

Seq. ID LIB3177-093-P1-K1-B7

Method BLASTN
NCBI GI g4115352
BLAST score 77
E value 3.0e-35
Match length 168
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T15J14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165710

Seq. ID LIB3177-093-P1-K1-B8

Method BLASTX
NCBI GI g1082054
BLAST score 150
E value 1.0e-09
Match length 136
% identity 30

NCBI Description (Z49859) copper transporter protein [Arabidopsis thaliana]

Seq. No. 165711

Seq. ID LIB3177-093-P1-K1-B9

Method BLASTN
NCBI GI g2673901
BLAST score 251
E value 1.0e-139
Match length 449
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Match length

% identity

73

49



```
Seq. No.
                  165712
Seq. ID
                  LIB3177-093-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  745
E value
                  2.0e-79
Match length
                  143
                  99
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165713
                  LIB3177-093-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757392
BLAST score
                  83
E value
                  9.0e-39
Match length
                  219
% identity
                  85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
Seq. No.
                  165714
Seq. ID
                  LIB3177-093-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g3241923
BLAST score
                  361
E value
                  0.0e+00
Match length
                  361
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165715
Seq. ID
                  LIB3177-093-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3600058
BLAST score
                  526
E value
                  1.0e-53
Match length
                  110
% identity
                  98
NCBI Description
                  (AF080120) similar to vacuolar ATPases [Arabidopsis
                  thaliana]
Seq. No.
                  165716
Seq. ID
                  LIB3177-093-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1171642
BLAST score
                  188
E value
                  5.0e-14
```



NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK

>gi_481206_pir__S38326 protein kinase - Arabidopsis
thaliana >gi_166809 (L07248) protein kinase [Arabidopsis

thaliana]

Seq. No. 165717

Seq. ID LIB3177-093-P1-K1-C5

Method BLASTX
NCBI GI g132102
BLAST score 724
E value 6.0e-77
Match length 137
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165718

Seq. ID LIB3177-093-P1-K1-C6

Method BLASTN
NCBI GI 94757392
BLAST score 68
E value 3.0e-30
Match length 116
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 165719

Seq. ID LIB3177-093-P1-K1-C8

Method BLASTX
NCBI GI g99696
BLAST score 801
E value 5.0e-86
Match length 144
% identity 99

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor,

chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453 prf 1804333A Gln

synthetase [Arabidopsis thaliana]

Seq. No. 165720

Seq. ID LIB3177-093-P1-K1-C9

Method BLASTX
NCBI GI g2244863
BLAST score 174
E value 2.0e-12
Match length 132
% identity 38

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 165721



```
Seq. ID
                    LIB3177-093-P1-K1-D11
Method
                    BLASTX
NCBI GI
                    q4115925
BLAST score
                    690
E value
                    5.0e-73
Match length
                    135
% identity
                    60
NCBI Description
                   (AF118222) contains similarity to RNA recognition motifs
                    (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                    >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                    [Arabidopsis thaliana]
Seq. No.
                   165722
Seq. ID
                   LIB3177-093-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g4006898
BLAST score
                   304
E value
                   8.0e-28
Match length
                   58
% identity
                   98
NCBI Description
                  (Z99708) splicing factor-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   165723
Seq. ID
                   LIB3177-093-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g2829871
BLAST score
                   792
E value
                   7.0e-85
Match length
                   150
% identity
                   99
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   165724
Seq. ID
                   LIB3177-093-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q132102
BLAST score
                   639
E value
                   5.0e-67
Match length
                   128
% identity
                   95
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana?
Seq. No.
                   165725
Seq. ID
                   LIB3177-093-P1-K1-D4
Method
                   BLASTX
```

NCBI GI g2956690 BLAST score 443 E value 1.0e-48 Match length 135

% identity

NCBI Description (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928

Match length

% identity

279

98



(AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No. 165726 Seq. ID LIB3177-093-P1-K1-D6 Method BLASTX NCBI GI g132090 BLAST score 208 E value 7.0e-17 Match length 50 % identity 84 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Bl precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana] Seq. No. 165727 Seq. ID LIB3177-093-P1-K1-D7 Method BLASTX NCBI GI q4678259 BLAST score 555 E value 4.0e-57 Match length 144 % identity 78 NCBI Description (AL049657) putative protein [Arabidopsis thaliana] Seq. No. 165728 Seq. ID LIB3177-093-P1-K1-D8 Method BLASTX NCBI GI g2062164 BLAST score 403 E value 1.0e-39 Match length 76 % identity 99 (AC001645) jasmonate inducible protein isolog [Arabidopsis NCBI Description thaliana] Seq. No. 165729 Seq. ID LIB3177-093-P1-K1-E1 Method BLASTX NCBI GI g4581146 BLAST score 734 E value 4.0e-78 Match length 152 % identity 93 NCBI Description (AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana] Seq. No. 165730 Seq. ID LIB3177-093-P1-K1-E10 Method BLASTN NCBI GI g3236234 BLAST score 148 1.0e-77 E value



NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165731

Seq. ID LIB3177-093-P1-K1-E11

Method BLASTX
NCBI GI g3377797
BLAST score 336
E value 2.0e-31
Match length 67
% identity 99

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 165732

Seq. ID LIB3177-093-P1-K1-E12

Method BLASTX
NCBI GI g166834
BLAST score 662
E value 9.0e-70
Match length 128
% identity 98

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase

activase [Arabidopsis thaliana] >gi 2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 165733

Seq. ID LIB3177-093-P1-K1-E2

 Method
 BLASTN

 NCBI GI
 g4309719

 BLAST score
 294

 E value
 1.0e-164

 Match length
 400

Match length 400 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165734

Seq. ID LIB3177-093-P1-K1-E3

Method BLASTX
NCBI GI g4678332
BLAST score 150
E value 1.0e-09
Match length 85
% identity 41

NCBI Description (AL049658) putative peptide transporter [Arabidopsis

thaliana]

Seq. No. 165735

Seq. ID LIB3177-093-P1-K1-E6

Method BLASTX
NCBI GI g2119846
BLAST score 618
E value 1.0e-64



Match length 119 % identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165736

Seq. ID LIB3177-093-P1-K1-E7

Method BLASTX
NCBI GI g401169
BLAST score 262
E value 5.0e-23
Match length 53
% identity 94

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No. 165737

Seq. ID LIB3177-093-P1-K1-E8

Method BLASTX
NCBI GI g4218123
BLAST score 441
E value 1.0e-43
Match length 143
% identity 65

NCBI Description (AL035353) photosystem I subunit PSI-E-like protein

[Arabidopsis thaliana]

Seq. No. 165738

Seq. ID LIB3177-093-P1-K1-E9

Method BLASTX
NCBI GI g1709825
BLAST score 663
E value 9.0e-70
Match length 134
% identity 100

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 165739

Seq. ID LIB3177-093-P1-K1-F1

Method BLASTN
NCBI GI g2088638
BLAST score 232
E value 1.0e-127
Match length 465
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165740

Seq. ID LIB3177-093-P1-K1-F10

Method BLASTX NCBI GI g3288821



BLAST score 505
E value 2.0e-51
Match length 113
% identity 86
NCBI Description (AF06390

(AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

>gi_4733989_gb_AAD28669.1 AC007209 5 (AC007209)

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 165741

Seq. ID LIB3177-093-P1-K1-F11

Method BLASTN
NCBI GI g2264317
BLAST score 55
E value 5.0e-22
Match length 196
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 165742

Seq. ID LIB3177-093-P1-K1-F12

Method BLASTN
NCBI GI g3297806
BLAST score 39
E value 1.0e-12
Match length 288

% identity 87
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1715

(ESSA project)

Seq. No. 165743

Seq. ID LIB3177-093-P1-K1-F3

Method BLASTN
NCBI GI g4454022
BLAST score 210
E value 1.0e-115
Match length 230

Match length 230 % identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16

(ESSAII project)

Seq. No. 165744

Seq. ID LIB3177-093-P1-K1-F4

Method BLASTX
NCBI GI g4678935
BLAST score 637
E value 2.0e-69
Match length 152
% identity 89

NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 165745

Seq. ID LIB3177-093-P1-K1-F6

Method BLASTX NCBI GI g2245144 BLAST score 449



```
E value 1.0e-44
Match length 138
% identity 64
NCBI Description (Y10846)
Seq. No. 165746
Seq. ID LIB3177-0
```

(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Method BLASTY

Method BLASTX
NCBI GI g2415406
BLAST score 150
E value 1.0e-09
Match length 84
% identity 37

NCBI Description (AF015775) YodT [Bacillus subtilis]

>gi_2634366_emb_CAB13865_ (Z99114) similar to

adenosylmethionine-8-amino-7-oxononanoate aminotransferase

[Bacillus subtilis]

Seq. No. 165747

Seq. ID LIB3177-093-P1-K1-F8

Method BLASTN
NCBI GI g2244950
BLAST score 184
E value 4.0e-99
Match length 313
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 165748

Seq. ID LIB3177-093-P1-K1-F9

Method BLASTX
NCBI GI g548604
BLAST score 483
E value 6.0e-49
Match length 102
% identity 86

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_1076728_pir__S51813 photosystem-I PSI-F chain precursor
- barley >gi_469560 (U08135) photosystem-I PSI-F subunit

precursor [Hordeum vulgare]

Seq. No. 165749

Seq. ID LIB3177-093-P1-K1-G1

Method BLASTX
NCBI GI g4539316
BLAST score 633
E value 4.0e-69
Match length 144
% identity 98

NCBI Description (AL035679) putative fructose-bisphosphate aldolase

[Arabidopsis thaliana]

Seq. No. 165750

Seq. ID LIB3177-093-P1-K1-G10

Method BLASTX



```
NCBI GI
                   q4454036
BLAST score
                   492
E value
                   5.0e-50
Match length
                   91
% identity
                   99
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  165751
                  LIB3177-093-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3108025
BLAST score
                  309
E value
                  1.0e-174
Match length
                  317
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T13D8, complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  165752
                  LIB3177-093-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135860
BLAST score
                  576
E value
                  1.0e-59
Match length
                  116
% identity
                  100
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                   (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi_445129_prf__1908432B tonoplast intrinsic protein gamma
                   [Arabidopsis thaliana]
Seq. No.
                  165753
Seq. ID
                  LIB3177-093-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  504
E value
                  4.0e-51
Match length
                  118
                  83
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  165754
Seq. ID
                  LIB3177-093-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q66618
BLAST score
                  622
                  6.0e-65
E value
```

Match length 141 % identity 87

NCBI Description 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)

precursor - Arabidopsis thaliana



Seq. No. 165755 Seq. ID LIB3177-093-P1-K1-G4 Method BLASTX NCBI GI q1169599 BLAST score 574 E value 2.0e-59 Match length 125 % identity 86 NCBI Description OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR $>gi_541883_pir_JQ2336$ omega-3 fatty acid desaturase (EC 1.14.99.-) CFD - Arabidopsis thaliana $>gi_408481$ (L22961) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid desaturase [Arabidopsis thaliana] >gi_541653_dbj BAA03106 (D14007) omega-3-desaturase [Arabidopsis thaliana] Seq. No. 165756 Seq. ID LIB3177-093-P1-K1-G5 Method BLASTN NCBI GI q2673901 BLAST score 255 E value 1.0e-141 Match length 423 % identity 99 NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165757 Seq. ID LIB3177-093-P1-K1-G6 Method BLASTN NCBI GI q4741184 BLAST score 321 E value 0.0e+00Match length 347 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project) Seq. No. 165758 Seq. ID LIB3177-093-P1-K1-G7 Method BLASTX NCBI GI g4210334 BLAST score 150 E value 1.0e-09

29 Match length % identity 97

NCBI Description (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit

[Arabidopsis thaliana]

Seq. No. 165759

Seq. ID LIB3177-093-P1-K1-G9

Method BLASTN NCBI GI q4468801 BLAST score 290

E value 1.0e-162 Match length 294 % identity 100



NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project) Seq. No. 165760 Seq. ID LIB3177-093-P1-K1-H10 Method BLASTX NCBI GI g2129729 BLAST score 633 E value 3.0e-66 Match length 124 % identity 98 NCBI Description senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046270 (U26945) senescence-associated protein [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein senl [Arabidopsis thaliana] >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated protein sen [Arabidopsis thaliana] Seq. No. 165761 Seq. ID LIB3177-093-P1-K1-H11 Method BLASTX NCBI GI q1931655 BLAST score 181 E value 1.0e-13 Match length 36 % identity 97 NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana] Seq. No. 165762 Seq. ID LIB3177-093-P1-K1-H12 Method BLASTX NCBI GI g4539405 BLAST score 287 E value 2.0e-26 73 Match length % identity 81 NCBI Description (AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana] Seq. No. 165763 LIB3177-093-P1-K1-H2 Seq. ID Method BLASTX NCBI GI g2257743 BLAST score 232 E value 1.0e-19 Match length 58 % identity

NCBI Description (U62020) lysine-sensitive aspartate kinase [Arabidopsis

thaliana]

Seq. No. 165764

Seq. ID LIB3177-093-P1-K1-H3

Method BLASTX
NCBI GI g1703108
BLAST score 414
E value 1.0e-71
Match length 146



% identity 97

NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 165765

Seq. ID LIB3177-093-P1-K1-H4

Method BLASTN
NCBI GI g2275194
BLAST score 254
E value 1.0e-141
Match length 262
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165766

Seq. ID LIB3177-093-P1-K1-H5

Method BLASTX
NCBI GI g4587525
BLAST score 210
E value 5.0e-17
Match length 90
% identity 48

NCBI Description (AC007060) Contains the PF_00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene.

[Arabidopsis thaliana]

Seq. No. 165767

Seq. ID LIB3177-093-P1-K1-H6

Method BLASTX
NCBI GI g3738261
BLAST score 284
E value 2.0e-25
Match length 97
% identity 68

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 165768

Seq. ID LIB3177-093-P1-K1-H7

Method BLASTX
NCBI GI g2257743
BLAST score 241
E value 1.0e-20
Match length 58
% identity 84

NCBI Description (U62020) lysine-sensitive aspartate kinase [Arabidopsis

thaliana]

Seq. No. 165769

Seq. ID LIB3177-093-P1-K1-H8

Method BLASTX NCBI GI g126766



BLAST score E value 2.0e-71 Match length 139 % identity 97

NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi 167150

(J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No. 165770

Seq. ID LIB3177-093-P1-K1-H9

Method BLASTX NCBI GI g3023216 BLAST score 505 E value 3.0e-51Match length 105 98 % identity

NCBI Description 14-3-3-LIKE PROTEIN GF14 MU >gi 1531629 (U60444) GF14 mu

[Arabidopsis thaliana]

Seq. No. 165771

Seq. ID LIB3177-094-P1-K1-A1

Method BLASTX NCBI GI q3025205 BLAST score 157 E value 1.0e-10 Match length 103 % identity 33

NCBI Description HYPOTHETICAL 65.1 KD PROTEIN SLR1919

>gi_1652223_dbj_BAA17147_ (D90903) ABC1-like [Synechocystis

sp.]

Seq. No. 165772

Seq. ID LIB3177-094-P1-K1-A10

Method BLASTX NCBI GI g126985 BLAST score 643 E value 2.0e-67 Match length 126 % identity 98

NCBI Description MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis

thaliana]

Seq. No. 165773

Seq. ID LIB3177-094-P1-K1-A11

Method BLASTX NCBI GI g2062158 BLAST score 592 E value 2.0e-61 Match length 122 47 % identity

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 165774

Seq. ID LIB3177-094-P1-K1-A12

Method BLASTX NCBI GI g1370188



```
BLAST score 404
E value 1.0e-39
Match length 96
% identity 84
```

NCBI Description (Z73943) RAB7D [Lotus japonicus]

Seq. No. 165775

Seq. ID LIB3177-094-P1-K1-A2

Method BLASTX
NCBI GI g2497733
BLAST score 570
E value 7.0e-59
Match length 118
% identity 95

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein

[Arabidopsis thaliana] >gi 3786018 (AC005499) unknown

protein [Arabidopsis thaliana]

Seq. No. 165776

Seq. ID LIB3177-094-P1-K1-A3

Method BLASTN
NCBI GI g3600062
BLAST score 122
E value 2.0e-62
Match length 215
% identity 68

NCBI Description Arabidopsis thaliana BAC T25C13

Seq. No. 165777

Seq. ID LIB3177-094-P1-K1-A4

Method BLASTX
NCBI GI g4827050
BLAST score 357
E value 6.0e-34
Match length 121
% identity 55

NCBI Description ubiquitin specific protease 14 (tRNA-quanine

transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine

Transglycosylase [Homo sapiens]

Seq. No. 165778

Seq. ID LIB3177-094-P1-K1-A5

Method BLASTX
NCBI GI 94586256
BLAST score 365
E value 4.0e-35
Match length 83
% identity 88

NCBI Description (AL049640) probable photosystem I chain XI precursor

[Arabidopsis thaliana]

Seq. No. 165779

Seq. ID LIB3177-094-P1-K1-A6

Method BLASTX



```
NCBI GI
                   q4538963
BLAST score
                   141
E value
                   5.0e-09
Match length
                   30
% identity
                   97
                   (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                   165780
                  LIB3177-094-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1076366
BLAST score
                   678
E value
                   1.0e-71
Match length
                   130
% identity
                   98
                  peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
NCBI Description
                  thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans
                  isomerase [Arabidopsis thaliana] >gi_992643 (U32186)
                   cyclophilin [Arabidopsis thaliana]
                  >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase
                   [Arabidopsis thaliana]
Seq. No.
                  165781
Seq. ID
                  LIB3177-094-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q1076440
BLAST score
                  375
E value
                   4.0e-36
Match length
                  84
% identity
NCBI Description
                  acyl-CoA binding protein - rape >gi_1076441_pir_ S49102
                  acyl-CoA binding protein - rape >gi_509265_emb CAA54390
                  (X77134) acyl-CoA binding protein [Brassica napus]
Seq. No.
                  165782
Seq. ID
                  LIB3177-094-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g3413696
BLAST score
                  386
E value
                  0.0e+00
Match length
                  425
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T19L18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165783
Seq. ID
                  LIB3177-094-P1-K1-B1
Method
                  BLASTX
```

NCBI GI g4584110
BLAST score 306
E value 5.0e-28
Match length 119
% identity 50

NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]

% identity

41



```
Seq. No.
                   165784
Seq. ID
                   LIB3177-094-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g3023848
BLAST score
                   462
E value
                   2.0e-46
Match length
                   111
% identity
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thaliana]
Seq. No.
                   165785
Seq. ID
                   LIB3177-094-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   464
E value
                   1.0e-46
Match length
                   90
% identity
                   100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   165786
Seq. ID
                   LIB3177-094-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g973313
BLAST score
                   538
E value
                   4.0e-55
Match length
                   111
% identity
                   93
NCBI Description
                 (U30250) myo-inositol 1-phosphate synthase isozyme-2
                   [Arabidopsis thaliana]
Seq. No.
                   165787
Seq. ID
                  LIB3177-094-P1-K1-B3
Method
                  BLASTX
NCBI GI
                   g4753655
BLAST score
                   407
E value
                   8.0e-40
Match length
                  115
% identity
                   65
NCBI Description
                  (AL049751) pectate lyase like protein [Arabidopsis
                   thaliana]
Seq. No.
                  165788
Seq. ID
                  LIB3177-094-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g2264316
BLAST score
                  46
E value
                  8.0e-17
Match length
                  304
```

22287

MRO11, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Seq. ID

Method



```
Seq. No.
                   165789
Seq. ID
                   LIB3177-094-P1-K1-B6
Method
                   BLASTX
                   g2651314
NCBI GI
BLAST score
                   379
E value
                   1.0e-36
Match length
                   109
% identity
                   70
NCBI Description
                  (AC002336) putative ribosomal protein S26 [Arabidopsis
                   thaliana]
                   165790
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2052379
BLAST score
                   632
E value
                   3.0e-66
Match length
                   120
% identity
NCBI Description (U66343) calreticulin [Arabidopsis thaliana]
Seq. No.
                  165791
Seq. ID
                  LIB3177-094-P1-K1-B8
Method
                  BLASTN
                  g2618602
NCBI GI
BLAST score
                   359
E value
                  0.0e + 00
Match length
                   445
% identity
                   96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165792
Seq. ID
                  LIB3177-094-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g4584351
BLAST score
                   303
E value
                  1.0e-170
Match length
                   342
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
Seq. No.
                  165793
Seq. ID
                  LIB3177-094-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2393775
BLAST score
                  286
E value
                  1.0e-25
                  58
Match length
% identity
NCBI Description (U82230) prolamin box binding factor [Zea mays]
Seq. No.
                  165794
```

22288

LIB3177-094-P1-K1-C11

BLASTX



```
NCBI GI
                   q3122724
BLAST score
                   351
E value
                   3.0e - 33
Match length
                   69
% identity
                   100
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal
                   protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                   165795
                   LIB3177-094-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4587641
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   422
% identity
                   96
NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic
                   sequence, complete sequence
Seq. No.
                   165796
Seq. ID
                   LIB3177-094-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g4263525
BLAST score
                   590
E value
                   3.0e-61
Match length
                   138
% identity
                   84
NCBI Description (AC004044) putative photosystem I reaction center subunit
                   II precursor [Arabidopsis thaliana]
Seq. No.
                   165797
Seq. ID
                   LIB3177-094-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q3786014
BLAST score
                   435
E value
                   4.0e-43
Match length
                   130
% identity
                   81
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   165798
Seq. ID
                   LIB3177-094-P1-K1-C4
Method
                  BLASTX
                   g3885511
                   431
                   1.0e-42
Match length
                  109
% identity
                   80
                  (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
```

NCBI GI BLAST score E value

barley [Medicago sativa]

Seq. No. 165799

Seq. ID LIB3177-094-P1-K1-C6

Method BLASTN NCBI GI g4455348 BLAST score 358 E value 0.0e+00



Match length 457 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8

(ESSAII project)

Seq. No. 165800

Seq. ID LIB3177-094-P1-K1-C7

Method BLASTX
NCBI GI g119975
BLAST score 516
E value 1.0e-52
Match length 119
% identity 89

NCBI Description FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin

[2Fe-2S] precursor - Arabidopsis thaliana

>gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A

[Arabidopsis thaliana]

Seq. No. 165801

Seq. ID LIB3177-094-P1-K1-C8

Method BLASTN
NCBI GI g3241927
BLAST score 165
E value 6.0e-88
Match length 215
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 165802

Seq. ID LIB3177-094-P1-K1-C9

Method BLASTX
NCBI GI g132102
BLAST score 454
E value 2.0e-45
Match length 92
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165803

Seq. ID LIB3177-094-P1-K1-D10

Method BLASTX
NCBI GI g3929651
BLAST score 583
E value 2.0e-60
Match length 116
% identity 100

NCBI Description (AJ131206) microbody NAD-dependent malate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 165804



Seq. ID LIB3177-094-P1-K1-D11 Method BLASTN NCBI GI q3985952 BLAST score 458 E value 0.0e+00Match length 470 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana] Seq. No. 165805 Seq. ID LIB3177-094-P1-K1-D12 Method BLASTX NCBI GI q4097567 BLAST score 164 E value 8.0e-12 Match length 34 97 % identity NCBI Description (U64921) ATGP4 [Arabidopsis thaliana] Seq. No. 165806 Seq. ID LIB3177-094-P1-K1-D2 Method BLASTX NCBI GI g2055273 BLAST score 582 E value 2.0e-60 Match length 131 % identity NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana] Seq. No. 165807 Seq. ID LIB3177-094-P1-K1-D3 Method BLASTX NCBI GI q115767 BLAST score 693 E value 2.0e-73 Match length 131 % identity 99 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368 emb CAA27540 (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi 16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 165808

Seq. ID LIB3177-094-P1-K1-D4

Method BLASTX NCBI GI g1490554 738 BLAST score E value 2.0e-78 Match length 157

% identity 92

NCBI Description (U63633) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]



Seq. No. 165809

Seq. ID LIB3177-094-P1-K1-D5

Method BLASTX
NCBI GI g115767
BLAST score 758
E value 7.0e-81
Match length 144
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165810

Seq. ID LIB3177-094-P1-K1-D7

Method BLASTX
NCBI GI 94531437
BLAST score 591
E value 2.0e-61
Match length 121
% identity 98

NCBI Description (AC006224) putative isopropylmalate dehydratase

[Arabidopsis thaliana]

Seq. No. 165811

Seq. ID LIB3177-094-P1-K1-D8

Method BLASTX
NCBI GI g2911085
BLAST score 181
E value 9.0e-20
Match length 122
% identity 56

NCBI Description (AL021960) photosystem II oxygen-evolving complex protein

3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3

- like [Arabidopsis thaliana]

Seq. No. 165812

Seq. ID LIB3177-094-P1-K1-D9

Method BLASTN
NCBI GI g3367567
BLAST score 262
E value 1.0e-145
Match length 292
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20

(ESSAII project)

Seq. No. 165813

Seq. ID LIB3177-094-P1-K1-E1

Method BLASTX
NCBI GI g3776578
BLAST score 157
E value 1.0e-10



Match length 66 % identity 50

NCBI Description (AC005388) ESTs gb_F13915 and gb_F13916 come from this

gene. [Arabidopsis thaliana]

Seq. No. 165814

Seq. ID LIB3177-094-P1-K1-E11

Method BLASTX
NCBI GI g1169201
BLAST score 391
E value 4.0e-38
Match length 108
% identity 77

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

>gi_421830_pir__S33707 DRT112 protein - Arabidopsis

thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 165815

Seq. ID LIB3177-094-P1-K1-E2

Method BLASTN
NCBI GI 94581103
BLAST score 29
E value 8.0e-07
Match length 173
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T24I21 genomic

sequence, complete sequence

Seq. No. 165816

Seq. ID LIB3177-094-P1-K1-E3

Method BLASTX
NCBI GI g1709687
BLAST score 495
E value 3.0e-50
Match length 104
% identity 91

NCBI Description PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)

REDUCTASE) >gi_2129643_pir_S71275 methionine sulfoxide reductase - Arabidopsis thaliana >gi_1279212 emb_CAA65991_(X97326) methionine sulfoxide reductase - Arabidopsis thaliana >gi_1279212 emb_CAA65991_

(X97326) methionine sulfoxide reductase [Arabidopsis

thaliana]

Seq. No. 165817

Seq. ID LIB3177-094-P1-K1-E4

Method BLASTX
NCBI GI g2947062
BLAST score 152
E value 7.0e-10
Match length 141
% identity 32

NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]

Seq. No. 165818

Seq. ID LIB3177-094-P1-K1-E5

Method BLASTX NCBI GI g132074 BLAST score 653



```
E value
                    1.0e-68
Match length
                    123
% identity
                    99
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                    (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   165819
Seq. ID
                   LIB3177-094-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q4490732
BLAST score
                   201
E value
                   5.0e-16
Match length
                   43
% identity
                   93
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   165820
Seq. ID
                   LIB3177-094-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g4757404
BLAST score
                   259
E value
                   1:0e-144
Match length
                   266
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MLJ15, complete sequence
Seq. No.
                   165821
Seq. ID
                   LIB3177-094-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q4454051
BLAST score
                   500
E value
                   9.0e-51
Match length
                   99
% identity
                   98
                   (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165822
Seq. ID
                   LIB3177-094-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g125576
BLAST score
                   640
E value
                   4.0e-67
Match length
                   136
% identity
                   92
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana
```

>gi 16441_emb CAA41155_ (X58149) Ribulose-5-phosphate

kinase [Arabidopsis thaliana]

Seq. No. 165823

Seq. ID LIB3177-094-P1-K1-F10



```
Method
                  BLASTX
NCBI GI
                   q4567207
BLAST score
                   773
E value
                   1.0e-82
Match length
                  148
                   98
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  165824
Seq. ID
                  LIB3177-094-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q132102
BLAST score
                  61
E value
                   9.0e-35
Match length
                  78
```

% identity 96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
(RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

 Seq. No.
 165825

 Seq. ID
 LIB3177-094-P1-K1-F12

 Method
 BLASTX

 NCBI GI
 g132090

 BLAST score
 707

 E value
 5.0e-75

BLAST score 707
E value 5.0e-75
Match length 135
% identity 97
NCRI Description BIBLIOS

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR

(RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165826

Seq. ID LIB3177-094-P1-K1-F3

Method BLASTX
NCBI GI g2583134
BLAST score 445
E value 3.0e-44
Match length 83
% identity 100

NCBI Description (AC002387) putative proline-rich protein [Arabidopsis

thaliana]

Seq. No. 165827

Seq. ID LIB3177-094-P1-K1-F4

Method BLASTX
NCBI GI g2494175
BLAST score 819
E value 5.0e-88
Match length 160
% identity 98



NCBI Description GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665)

glutamate decarboxylase 2 [Arabidopsis thaliana]

>gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis

thaliana]

Seq. No. 165828

Seq. ID LIB3177-094-P1-K1-F5

Method BLASTX NCBI GI g2252825 BLAST score 627 E value 2.0e-65 Match length 119 % identity 100

NCBI Description (AF013293) Similar to transmembrane protein; coded for by

A. thaliana cDNA H37637; coded for by A. thaliana cDNA T41850; coded for by A. thaliana cDNA T13717; coded for by A. thaliana cDNA T04371; coded for by A. thaliana cDNA

T43789; coded

Seq. No. 165829

Seq. ID LIB3177-094-P1-K1-F6

Method BLASTX NCBI GI q115767 BLAST score 771 E value 2.0e-82 Match length 146 % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165830

Seq. ID LIB3177-094-P1-K1-F7

Method BLASTX NCBI GI q1657617 BLAST score 585 E value 1.0e-60 Match length 117 % identity 99

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)

putative nuclear DNA-binding protein G2p [Arabidopsis

thaliana]

Seq. No. 165831

Seq. ID LIB3177-094-P1-K1-F9

Method BLASTX NCBI GI g3885511 BLAST score 390 E value 7.0e - 38Match length 99 % identity

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]



 Seq. No.
 165832

 Seq. ID
 LIB3177-094-P1-K1-G1

 Method
 BLASTX

 NCBI GI
 g2501555

 BLAST score
 528

 E value
 5.0e-54

 Match length
 122

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 165833

% identity

Seq. ID LIB3177-094-P1-K1-G10

78

Method BLASTX
NCBI GI g132110
BLAST score 561
E value 6.0e-58
Match length 105
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165834

Seq. ID LIB3177-094-P1-K1-G11

Method BLASTX
NCBI GI 94587989
BLAST score 651
E value 1.0e-68
Match length 114
% identity 98

NCBI Description (AF085279) hypothetical Cys-3-His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 165835

Seq. ID LIB3177-094-P1-K1-G12

Method BLASTN
NCBI GI 94589437
BLAST score 457
E value 0.0e+00
Match length 480
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 165836

Seq. ID LIB3177-094-P1-K1-G2

Method BLASTX
NCBI GI 94164473
BLAST score 191
E value 1.0e-14
Match length 55
% identity 69



NCBI Description (AF061157) negatively light-regulated protein [Vernicia fordii] Seq. No. 165837 Seq. ID LIB3177-094-P1-K1-G3 Method BLASTX NCBI GI g4056494 BLAST score 421 E value 1.0e-41 Match length 98 % identity 84 NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana] Seq. No. 165838 Seq. ID LIB3177-094-P1-K1-G4 Method BLASTN NCBI GI q4678219 BLAST score 183 E value 8.0e-99 Match length 190 99 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence Seq. No. 165839 Seq. ID LIB3177-094-P1-K1-G5 Method BLASTX NCBI GI q3885331 BLAST score 367 E value 2.0e-35 Match length 98 % identity 68 (AC005623) putative cytochrome p450 protein [Arabidopsis NCBI Description thaliana] Seq. No. 165840 Seq. ID LIB3177-094-P1-K1-G6 Method BLASTX NCBI GI g2688824 BLAST score 254 E value 6.0e-24 Match length 88 72 % identity NCBI Description (U93273) putative auxin-repressed protein [Prunus armeniaca] Seq. No. 165841 Seq. ID LIB3177-094-P1-K1-G7

Method BLASTX NCBI GI g2244990 BLAST score 312 E value 6.0e-29 Match length 116 % identity 69

NCBI Description (Z97340) similarity to LIM homeobox protein -

Caenorhabditis [Arabidopsis thaliana]



165842

BLASTX

g4741952

LIB3177-094-P1-K1-G8

Seq. No.

Seq. ID

Method

NCBI GI

```
BLAST score
                   607
E value
                   3.0e-63
Match length
                   113
% identity
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   165843
Seq. ID
                   LIB3177-094-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   a2795803
BLAST score
                   378
E value
                   1.0e-36
Match length
                   106
% identity
                   68
NCBI Description
                   (AC003674) putative beta-1,3-endoglucanase [Arabidopsis
                   thaliana] >gi_3355491 (AC004218) putative
                  beta-1,3-endoglucanase [Arabidopsis thaliana]
Seq. No.
                   165844
Seq. ID
                  LIB3177-094-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  g4557061
BLAST score
                   98
E value
                   8.0e-48
Match length
                  252
% identity
                   97
NCBI Description Arabidopsis thaliana chromosome II BAC F23M2 genomic
                  sequence, complete sequence
Seq. No.
                  165845
Seq. ID
                  LIB3177-094-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1709825
BLAST score
                  527
E value
                  6.0e-54
Match length
                  115
% identity
                  95
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  165846
Seq. ID
                  LIB3177-094-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1362078
BLAST score
                  391
E value
                  6.0e-38
Match length
                  97
% identity
                  73
NCBI Description
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
                  - common nasturtium >gi_311835_emb_CAA48324_ (X68254)
                  cellulase [Tropaeolum majus]
```

% identity

NCBI Description



```
Seq. No.
                   165847
                  LIB3177-094-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4662640
BLAST score
                   353
E value
                   0.0e + 00
Match length
                   374
                   98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
                   sequence, complete sequence
                  165848
Seq. No.
                  LIB3177-094-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335366
BLAST score
                   306
E value
                   6.0e-28
Match length
                  115
% identity
                   47
NCBI Description
                  (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  165849
                  LIB3177-094-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1076366
BLAST score
                   738
E value
                  1.0e-78
Match length
                  137
                   99
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
                   thaliana >gi 460968 (U07276) peptidyl-prolyl cis-trans
                   isomerase [Arabidopsis thaliana] >gi 992643 (U32186)
                   cyclophilin [Arabidopsis thaliana]
                   >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase
                   [Arabidopsis thaliana]
Seq. No.
                   165850
Seq. ID
                  LIB3177-094-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4210334
BLAST score
                   286
E value
                   1.0e-25
Match length
                  59
% identity
                   93
NCBI Description
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
                   [Arabidopsis thaliana]
Seq. No.
                  165851
Seq. ID
                  LIB3177-094-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4678353
BLAST score
                   678
E value
                   2.0e-71
Match length
                  128
                   98
```

[Arabidopsis thaliana]

(AL049659) cysteine endopeptidase precursor-like protein

Match length

% identity

99

88

```
Seq. No.
                  165852
Seq. ID
                  LIB3177-094-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4049350
BLAST score
                  601
E value
                  1.0e-62
Match length
                  115
% identity
                  99
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  165853
                  LIB3177-094-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  a4581084
BLAST score
                  257
E value
                  1.0e-142
Match length
                  332
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
                  sequence, complete sequence
Seq. No.
                  165854
Seq. ID
                  LIB3177-095-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  504
E value
                  2.0e-51
Match length
                  98
                   98
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165855
Seq. ID
                  LIB3177-095-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g4558521
BLAST score
                  146
E value
                  1.0e-76
Match length
                  250
% identity
                  98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
Seq. No.
                  165856
Seq. ID
                  LIB3177-095-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2160168
BLAST score
                  471
E value
                  2.0e-47
```



NCBI Description (AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb X70652). ESTs gb T41853, gb T76648 come from this gene. [Arabidopsis Seq. No. 165857 Seq. ID LIB3177-095-P1-K1-A2 Method BLASTX NCBI GI q2980771 BLAST score 481 E value 1.0e-48 Match length 93 % identity 91 NCBI Description (AL022198) chloroplast omega-6 fatty acid desaturase (fad6) [Arabidopsis thaliana] Seq. No. 165858 Seq. ID LIB3177-095-P1-K1-A4 Method BLASTX NCBI GI q4490303 BLAST score 450 E value 4.0e-45 Match length 98 % identity 91 NCBI Description (AL035678) putative protein [Arabidopsis thaliana] Seq. No. 165859 Seq. ID LIB3177-095-P1-K1-A5 Method BLASTN NCBI GI g4185120 BLAST score 139 E value 1.0e-72 Match length 166 % identity 49 NCBI Description Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165860 Seq. ID LIB3177-095-P1-K1-A9 Method BLASTN NCBI GI g4454022 BLAST score 39 E value 1.0e-12 Match length 99 % identity 91 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project) Seq. No. 165861 Seq. ID LIB3177-095-P1-K1-B1 Method BLASTX g1769907

NCBI GI BLAST score 464 E value 2.0e-46 Match length 89 % identity

NCBI Description (X92975) xyloglucan endo-transglycosylase [Arabidopsis



thaliana]

Seq. No. 165862 Seq. ID LIB3177-095-P1-K1-B10 Method BLASTX NCBI GI g115385 BLAST score 153 E value 1.0e-10 35 Match length % identity 86 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165863

Seq. ID LIB3177-095-P1-K1-B6

Method BLASTN
NCBI GI g1107482
BLAST score 211
E value 1.0e-115
Match length 242
% identity 97

NCBI Description A.thaliana mRNA for 30S ribosomal protein S13

Seq. No. 165864

Seq. ID LIB3177-095-P1-K1-C1

Method BLASTX
NCBI GI g2062158
BLAST score 610
E value 1.0e-63
Match length 132
% identity 47

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 165865

Seq. ID LIB3177-095-P1-K1-C10

Method BLASTN
NCBI GI g3510340
BLAST score 301
E value 1.0e-169
Match length 354
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDN11, complete sequence [Arabidopsis thaliana]

Seq. No. 165866

Seq. ID LIB3177-095-P1-K1-C11

Method BLASTN
NCBI GI g4220627
BLAST score 90
E value 7.0e-43
Match length 332
% identity 8

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K20J1, complete sequence [Arabidopsis thaliana]



165867

LIB3177-095-P1-K1-C12

Seq. No.

Seq. ID

```
Method
                   BLASTX
NCBI GI
                   g2494174
BLAST score
                   53
E value
                   9.0e-75
Match length
                   146
% identity
                   99
NCBI Description
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
                   glutamate decarboxylase [Arabidopsis Thaliana]
Seq. No.
                   165868
Seq. ID
                   LIB3177-095-P1-K1-C2
Method
                   BLASTX
NCBI GI
                  q1071913
BLAST score
                   462
E value
                   3.0e-46
Match length
                   125
% identity
                   70
NCBI Description
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                   - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                   165869
Seq. ID
                  LIB3177-095-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3819710
BLAST score
                  473
E value
                  1.0e-47
Match length
                  87
% identity
                  99
                  (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165870
Seq. ID
                  LIB3177-095-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q3510340
BLAST score
                  184
E value
                  3.0e-99
Match length
                  233
% identity
                  94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDN11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165871
Seq. ID
                  LIB3177-095-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  66
E value
                  4.0e-29
Match length
                  132
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  165872
```



```
Seq. ID
                   LIB3177-095-P1-K1-C9
 Method
                  BLASTN
NCBI GI
                   g1167960
BLAST score
                   38
E value
                   7.0e-12
Match length
                   455
% identity
                   22
NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds
Seq. No.
                   165873
Seq. ID
                   LIB3177-095-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1353163
BLAST score
                   202
E value
                   5.0e-16
Match length
                   67
% identity
                   57
NCBI Description HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHROMOSOME III
                   PRECURSOR >gi_1055071 (U39851) C23G10.2 gene product
                   [Caenorhabditis elegans]
Seq. No.
                   165874
Seq. ID
                   LIB3177-095-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g445612
BLAST score
                   387
E value
                   1.0e-37
Match length
                   86
% identity
                   88
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   165875
Seq. ID
                  LIB3177-095-P1-K1-D11
Method
                  BLASTN
NCBI GI
                   g2832611
BLAST score
                   275
E value
                   1.0e-153
Match length
                  308
% identity
                   98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
                   (ESSAII project)
Seq. No.
                  165876
                  LIB3177-095-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432863
BLAST score
                  567
E value
                  1.0e-58
Match length
                  116
% identity
NCBI Description
                  (AC006300) putative phosphate/phosphoenolpyruvate
                  translocator protein [Arabidopsis thaliana]
```

Seq. No. 165877

Seq. ID LIB3177-095-P1-K1-D3

Method BLASTX NCBI GI g4210334

```
BLAST score
                  179
E value
                  1.0e-13
Match length
                  63
                  67
% identity
NCBI Description
                  (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
                  [Arabidopsis thaliana]
                  165878
Seq. No.
                  LIB3177-095-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170203
BLAST score
                  432
E value
                  6.0e-43
Match length
                  109
                  81
% identity
NCBI Description GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >qi 454359
                  (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
                  165879
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-D5
Method
                  BLASTN
                  g4587641
NCBI GI
BLAST score
                  284
E value
                  1.0e-159
Match length
                  300
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  165880
Seq. ID
                  LIB3177-095-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                  377
E value
                  1.0e-36
Match length
                  79
% identity
                  95
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165881
Seq. ID
                  LIB3177-095-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g4587641
BLAST score
                  386
E value
                  0.0e+00
Match length
                  402
```

99 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Seq. No. 165882

Seq. ID LIB3177-095-P1-K1-D9



Method BLASTN
NCBI GI g1737217
BLAST score 195
E value 1.0e-105
Match length 270
% identity 93

NCBI Description Arabidopsis thaliana vacuolar sorting receptor homolog

mRNA, complete cds

Seq. No. 165883

Seq. ID LIB3177-095-P1-K1-E1

Method BLASTX
NCBI GI g2501188
BLAST score 560
E value 1.0e-57
Match length 135
% identity 85

NCBI Description THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750 pir S71191 TH14

protein homolog - Arabidopsis thaliana >gi 1113783 (U17589)

Thil protein [Arabidopsis thaliana]

Seq. No. 165884

Seq. ID LIB3177-095-P1-K1-E10

Method BLASTX
NCBI GI g2499811
BLAST score 566
E value 2.0e-58
Match length 109
% identity 98

NCBI Description PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis

thaliana] >gi 1353772 (U43326) profilin 2 [Arabidopsis

thaliana]

Seq. No. 165885

Seq. ID LIB3177-095-P1-K1-E12

Method BLASTX
NCBI GI g2119848
BLAST score 646
E value 9.0e-68
Match length 121
% identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 165886

Seq. ID LIB3177-095-P1-K1-E2

Method BLASTN
NCBI GI g3420043
BLAST score 237
E value 1.0e-131
Match length 279



```
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F23F1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165887
Seq. ID
                  LIB3177-095-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q1709446
BLAST score
                  468
                  4.0e-47
E value
Match length
                  115
                  90
% identity
NCBI Description
                  PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
                  PRECURSOR (PDHE1-A) >gi 2117533 pir JC4358 pyruvate
                  dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha
                  chain - Arabidopsis thaliana mitochondrion >gi 710400
                   (U21214) pyruvate dehydrogenase El alpha subunit
                   [Arabidopsis thaliana]
                  165888
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  q4741944
BLAST score
                  273
                  1.0e-24
E value
Match length
                  60
                  90
% identity
NCBI Description (AF134122) Lhcb2 protein [Arabidopsis thaliana]
                  165889
Seq. No.
                  LIB3177-095-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  494
                  4.0e-50
E value
                  124
Match length
% identity
                  75
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  165890
                  LIB3177-095-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760168
BLAST score
                  59
E value
                  9.0e-25
Match length
                  162
                  75
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 165891

Seq. ID LIB3177-095-P1-K1-E8

Method BLASTN
NCBI GI g4159706
BLAST score 228
E value 1.0e-125
Match length 263

BLAST score

Match length

% identity

E value

607

115

99

3.0e-63



```
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence
                   165892
Seq. No.
                   LIB3177-095-P1-K1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q457403
                   54
BLAST score
                   4.0e-22
E value
Match length
                   88
% identity
                   92
                   Arabidopsis thaliana mRNA for MAP kinase, complete cds
NCBI Description
Seq. No.
                   165893
Seq. ID
                   LIB3177-095-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g3738275
BLAST score
                   271
                   1.0e-151
E value
Match length
                   435
% identity
                   98
                   Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   165894
Seq. No.
                   LIB3177-095-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g119975
BLAST score
                   638
                   7.0e-67
E value
                   145
Match length
                   90
% identity
                  FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
NCBI Description
                   [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754 (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                    [Arabidopsis thaliana]
                   165895
Seq. No.
                   LIB3177-095-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4755189
BLAST score
                   417
E value
                   6.0e-41
Match length
                   147
% identity
                   57
NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   165896
                   LIB3177-095-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115783
```



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 165897

Seq. ID LIB3177-095-P1-K1-F4

Method BLASTN
NCBI GI g1209241
BLAST score 114
E value 2.0e-57
Match length 230

% identity 87

NCBI Description Arabidopsis thaliana metallothionein mRNA sequence

Seq. No. 165898

Seq. ID LIB3177-095-P1-K1-F6

Method BLASTX
NCBI GI g115783
BLAST score 646
E value 8.0e-68
Match length 127
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 165899

Seq. ID LIB3177-095-P1-K1-F7

Method BLASTX
NCBI GI g1172977
BLAST score 56
E value 9.0e-41
Match length 105
% identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 165900

Seq. ID LIB3177-095-P1-K1-F8

Method BLASTN
NCBI GI g4314354
BLAST score 76
E value 2.0e-35
Match length 79
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T9I22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165901

Seq. ID LIB3177-095-P1-K1-F9

Method BLASTX
NCBI GI g132074
BLAST score 701
E value 3.0e-74
Match length 133



% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165902

Seq. ID LIB3177-095-P1-K1-G10

Method BLASTX
NCBI GI g3953473
BLAST score 625
E value 2.0e-65
Match length 126
% identity 100

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 165903

Seq. ID LIB3177-095-P1-K1-G11

Method BLASTX
NCBI GI 94741960
BLAST score 540
E value 2.0e-55
Match length 102
% identity 62

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 165904

Seq. ID LIB3177-095-P1-K1-G2

Method BLASTX
NCBI GI g132074
BLAST score 785
E value 4.0e-84
Match length 147
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 165905

Seq. ID LIB3177-095-P1-K1-G4

Method BLASTX
NCBI GI g115783
BLAST score 654
E value 9.0e-69
Match length 126
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seg. No. 165906

Seq. ID LIB3177-095-P1-K1-G5

Method BLASTX
NCBI GI g4049341
BLAST score 152

BLAST score

E value

721

1.0e-76



```
3.0e-10
 E value
 Match length
                    58
                    48
 % identity
 NCBI Description
                   (AL034567) putative protein [Arabidopsis thaliana]
                   165907
Seq. No.
                   LIB3177-095-P1-K1-G6
 Seq. ID
 Method
                   BLASTN
                   g4455290
 NCBI GI
 BLAST score
                    57
                    2.0e-23
 E value
                    94
 Match length
 % identity
                    66
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5
 NCBI Description
                    (ESSAII project)
 Seq. No.
                    165908
                    LIB3177-095-P1-K1-G7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3869251
 BLAST score
                    297
                    5.0e-27
 E value
 Match length
                    95
 % identity
                    (U39287) ferredoxin-dependent glutamate synthase precursor
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    165909
 Seq. ID
                   LIB3177-095-P1-K1-G8
 Method
                   BLASTX
                    q120675
· NCBI GI
                    43
 BLAST score
                    7.0e-49
 E value
 Match length
                    125
                    89
 % identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 NCBI Description
                    >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                    dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                    >gi_21143 emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                    alba]
                    165910
 Seg. No.
                    LIB3177-095-P1-K1-G9
 Seq. ID
 Method
                    BLASTX
                    g2462840
 NCBI GI
 BLAST score
                    605
 E value
                    5.0e-63
 Match length
                    114
 % identity
 NCBI Description (AF000657) cytochrome C [Arabidopsis thaliana]
 Seq. No.
                    165911
 Seq. ID
                    LIB3177-095-P1-K1-H12
                    BLASTX
 Method
 NCBI GI
                    q4567207
```



```
Match length
                  135
                  99
% identity
NCBI Description
                 (AC007168) unknown protein [Arabidopsis thaliana]
                  165912
Seq. No.
                  LIB3177-095-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3249094
BLAST score
                  228
E value
                  1.0e-125
Match length
                  315
% identity
                  99
                  Arabidopsis thaliana chromosome 1 BAC T12M4 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  165913
                  LIB3177-095-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q114654
BLAST score
                  46
                  1.0e-16
E value
Match length
                  55
                  95
% identity
NCBI Description
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                  >gi 67898 pir LWNTA H+-transporting ATP synthase (EC
                  3.6.1.34) lipid-binding protein - common tobacco
                  chloroplast >gi 11812 emb CAA77343 (Z00044) ATPase III
                  subunit [Nicotiana tabacum] >gi 343484 (M10124) ATPase
                  subunit III [Nicotiana tabacum] >gi 224347 prf 1102209A
                  ATPase III, H translocating [Nicotiana sp.]
                  >gi 225272 prf 1211235G ATPase III [Nicotiana tabacum]
Seq. No.
                  165914
                  LIB3177-095-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4755189
BLAST score
                  381
E value
                  1.0e-36
Match length
                  138
% identity
                  57
NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  165915
                  LIB3177-095-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350965
BLAST score
                  551
E value
                  1.0e-56
Match length
                  108
                  97
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12)
```

Seq. No. 165916

Seq. ID LIB3177-095-P1-K1-H8

MethodBLASTXNCBI GIg99696BLAST score246



E value 4.0e-21 Match length 77 66 % identity NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >qi 240070 bbs 69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln synthetase [Arabidopsis thaliana] Seq. No. 165917 Seq. ID LIB3177-095-P1-K1-H9 Method BLASTX q282865 354

NCBI GI BLAST score 2.0e-38 E value Match length 93 87 % identity

chlorophyll a/b-binding protein - Arabidopsis thaliana NCBI Description >qi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >qi 166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 165918

LIB3177-096-P1-K1-A1 Seq. ID

Method BLASTX NCBI GI q2529665 BLAST score 421 E value 1.0e-41 Match length 110 79 % identity

(AC002535) putative ribosomal protein L7A [Arabidopsis NCBI Description

thaliana]

165919 Seq. No.

Seq. ID LIB3177-096-P1-K1-A10

Method BLASTX NCBI GI g2764941 478 BLAST score 3.0e-48E value Match length 86 % identity 99

(X98255) transcriptionally stimulated by gibberellins; NCBI Description

expressed in meristematic region, and style [Arabidopsis

thaliana]

Seq. No. 165920

LIB3177-096-P1-K1-A12 Seq. ID

Method BLASTN NCBI GI q4587641 BLAST score 212 E value 1.0e-115 Match length 372 99 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic



sequence, complete sequence

Seq. No. 165921

Seq. ID LIB3177-096-P1-K1-A2

Method BLASTX
NCBI GI g3212869
BLAST score 551
E value 7.0e-57
Match length 108
% identity 98

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 165922

Seq. ID LIB3177-096-P1-K1-A4

Method BLASTX
NCBI GI g2129600
BLAST score 57
E value 1.0e-68
Match length 139
% identity 99

NCBI Description glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana

(fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione synthetase [Arabidopsis thaliana] >gi 1585560 prf 2201360A

glutathione synthetase [Arabidopsis thaliana]

Seq. No. 165923

Seq. ID LIB3177-096-P1-K1-A5

Method BLASTX
NCBI GI g2119846
BLAST score 565
E value 2.0e-58
Match length 107
% identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165924

Seq. ID LIB3177-096-P1-K1-A6

Method BLASTX
NCBI GI g2708740
BLAST score 153
E value 6.0e-10
Match length 140
% identity 35

NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

>gi_4406824_gb_AAD20132_ (AC006201) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 165925

Seq. ID LIB3177-096-P1-K1-A7

Method BLASTN NCBI GI g4263762

Match length

% identity

143

86



```
BLAST score
                   51
                   4.0e-20
E value
                   75
Match length
                   92
% identity
                  Arabidopsis thaliana chromosome II BAC F17L24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  165926
Seq. No.
                  LIB3177-096-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170159
BLAST score
                  308
E value
                   3.0e-28
Match length
                  62
% identity
                  100
NCBI Description HISTONE H2B
Seq. No.
                  165927
                  LIB3177-096-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351071
BLAST score
                  353
E value
                  0.0e+00
Match length
                  387
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MVA3, complete sequence [Arabidopsis thaliana]
                  165928
Seq. No.
                  LIB3177-096-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                  473
E value
                  1.0e-47
Match length
                  94
% identity
                  100
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
                  165929
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-B10
Method
                  BLASTX
                  g2062161
NCBI GI
BLAST score
                  700
E value
                   4.0e-74
Match length
                  132
% identity
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  165930
Seq. ID
                  LIB3177-096-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4263525
BLAST score
                  622
E value
                  5.0e-65
```



```
(AC004044) putative photosystem I reaction center subunit
NCBI Description
                  II precursor [Arabidopsis thaliana]
                  165931
Seq. No.
                  LIB3177-096-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128228
BLAST score
                  620
E value
                  9.0e-65
Match length
                  125
% identity
                  92
NCBI Description
```

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 165932

Seq. ID LIB3177-096-P1-K1-B3

Method BLASTX
NCBI GI g4324967
BLAST score 768
E value 4.0e-82
Match length 151
% identity 99

NCBI Description (AF114796) ADP-ribosylation factor [Glycine max]

Seq. No. 165933

Seq. ID LIB3177-096-P1-K1-B4

Method BLASTX
NCBI GI g115385
BLAST score 695
E value 2.0e-73
Match length 135
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165934

Seq. ID LIB3177-096-P1-K1-B5

Method BLASTX
NCBI GI g3786324
BLAST score 436
E value 4.0e-43
Match length 147
% identity 54

NCBI Description (AB015139) chlorophyll a oxygenase [Chlamydomonas

reinhardtii]

Seq. No. 165935

Seq. ID LIB3177-096-P1-K1-B6

Method BLASTX
NCBI GI 94097549
BLAST score 319
E value 2.0e-29
Match length 116
% identity 62

NCBI Description (U64907) ATFP4 [Arabidopsis thaliana]

```
Seq. No.
                   165936
Seq. ID
                   LIB3177-096-P1-K1-B7
                   BLASTX
Method
NCBI GI
                   g3746062
BLAST score
                   322
E value
                   5.0e-30
Match length
                   90
                   71
% identity
NCBI Description
                  (AC005311) hypothetical protein [Arabidopsis thaliana]
                   165937
Seq. No.
Seq. ID
                   LIB3177-096-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q2160166
BLAST score
                   155
E value
                   2.0e-10
Match length
                   85
% identity
                   45
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   165938
Seq. ID
                   LIB3177-096-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q3420050
BLAST score
                   608
E value
                   2.0e-63
Match length
                   119
% identity
                   92
NCBI Description
                  (AC004680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   165939
                   LIB3177-096-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1363489
BLAST score
                   700
                   4.0e-74
E value
Match length
                   128
% identity
                   100
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                   thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
                   165940
Seq. No.
                  LIB3177-096-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4704730
BLAST score
                  263
E value
                   7.0e-23
Match length
                  125
```

% identity 41

NCBI Description (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No. 165941

LIB3177-096-P1-K1-C2 Seq. ID

Method BLASTX NCBI GI g2407802



```
BLAST score
                  426
E value
                  5.0e-42
Match length
                  87
% identity
                  100
NCBI Description (Y12576) histone H2B [Arabidopsis thaliana]
Seq. No.
                  165942
Seq. ID
                  LIB3177-096-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g119975
BLAST score
                  353
E value
                  8.0e-34
Match length
                  75
                  95
% identity
NCBI Description
                  FERREDOXÍN PRECURSOR > gi 99692 pir S09979 ferredoxin
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
                  [Arabidopsis thaliana] >gi 166698 (M35868) ferrodoxin A
                  [Arabidopsis thaliana]
Seq. No.
                  165943
Seq. ID
                  LIB3177-096-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4572669
BLAST score
                  514
E value
                  3.0e-52
Match length
                  142
% identity
NCBI Description
                  (AC006954) putative glucosyltransferase [Arabidopsis
                  thaliana]
                  165944
Seq. No.
                  LIB3177-096-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757399
BLAST score
                  440
                  0.0e+00
E value
Match length
                  452
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MEE13, complete sequence
Seq. No.
                  165945
                  LIB3177-096-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589440
```

BLAST score 241 E value 1.0e-133 Match length 368 91 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:

MSD21, complete sequence

Seq. No. 165946

LIB3177-096-P1-K1-C8 Seq. ID

Method BLASTN NCBI GI g4589440



BLAST score 394 E value 0.0e+00 Match length 442 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSD21, complete sequence

Seq. No. 165947

Seq. ID LIB3177-096-P1-K1-C9

Method BLASTX
NCBI GI g4587513
BLAST score 212
E value 7.0e-17
Match length 114
% identity 42

NCBI Description (AC007060) Contains eukaryotic protein kinase domain

PF 00069. [Arabidopsis thaliana]

Seq. No. 165948

Seq. ID LIB3177-096-P1-K1-D1

Method BLASTX
NCBI GI g3892048
BLAST score 717
E value 4.0e-76
Match length 142
% identity 100

NCBI Description (AC002330) putative tryptophan synthase alpha 1-like

protein [Arabidopsis thaliana]

Seq. No. 165949

Seq. ID LIB3177-096-P1-K1-D10

Method BLASTX
NCBI GI g2160183
BLAST score 500
E value 1.0e-50
Match length 130
% identity 78

NCBI Description (AC000132) Identical to A. thaliana U2 SnRNP-specific A'

protein (gb_X69137). ESTs gb ATTS0705, gb ATTS0339 come

from this gene. [Arabidopsis thaliana]

Seq. No. 165950

Seq. ID LIB3177-096-P1-K1-D11

Method BLASTX
NCBI GI g4678354
BLAST score 756
E value 1.0e-80
Match length 146
% identity 99

NCBI Description (AL049659) cysteine endopeptidase-like protein [Arabidopsis

thaliana]

Seq. No. 165951

Seq. ID LIB3177-096-P1-K1-D12

Method BLASTX NCBI GI g3193289 BLAST score 646



E value 9.0e-68 Match length 150 87

NCBI Description (AF069298) similar to several small proteins (~100 aa) that

are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG

(SW:32292) [Arabidopsis thaliana]

Seq. No. 165952

Seq. ID LIB3177-096-P1-K1-D2

Method BLASTX
NCBI GI g1145697
BLAST score 490
E value 2.0e-64
Match length 133
% identity 60

NCBI Description (U39485) delta tonoplast integral protein [Arabidopsis

thaliana]

Seq. No. 165953

Seq. ID LIB3177-096-P1-K1-D3

Method BLASTN
NCBI GI g2852453
BLAST score 260
E value 1.0e-144
Match length 281
% identity 98

NCBI Description Arabidopsis thaliana gene for cystathionine gamma-synthase,

complete cds

Seq. No. 165954

Seq. ID LIB3177-096-P1-K1-D4

Method BLASTX
NCBI GI g4006934
BLAST score 636
E value 1.0e-66
Match length 120
% identity 99

NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No. 165955

Seq. ID LIB3177-096-P1-K1-D5

Method BLASTX
NCBI GI g4587515
BLAST score 614
E value 5.0e-64
Match length 151
% identity 77

NCBI Description (AC007060) EST gb_Z37678 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 165956

Seq. ID LIB3177-096-P1-K1-D6

Method BLASTN
NCBI GI g3869069
BLAST score 214
E value 1.0e-117



413 Match length % identity 100 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MEB5, complete sequence [Arabidopsis thaliana] 165957 Seq. No. LIB3177-096-P1-K1-D9 Seq. ID Method BLASTN NCBI GI g4263774 BLAST score 233 E value 1.0e-128 312 Match length 99 % identity Arabidopsis thaliana chromosome II BAC T20F21 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165958 LIB3177-096-P1-K1-E10 Seq. ID Method BLASTN NCBI GI g3805755 BLAST score 215 E value 1.0e-117 259 Match length 96 % identity Arabidopsis thaliana chromosome II BAC T25N22 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165959 LIB3177-096-P1-K1-E12 Seq. ID Method BLASTX NCBI GI g1883006 BLAST score 409 E value 5.0e-40 Match length 129 23 % identity NCBI Description (Y11483) jasmonate inducible protein [Brassica napus] Seq. No. 165960 LIB3177-096-P1-K1-E2 Seq. ID Method BLASTN NCBI GI q3046849 BLAST score 183 E value 2.0e-98 Match length 456 50 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K18L3, complete sequence [Arabidopsis thaliana]

Seq. No. 165961

Seq. ID LIB3177-096-P1-K1-E4

Method BLASTX
NCBI GI g4585995
BLAST score 229
E value 4.0e-19
Match length 60
% identity 78

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

BLAST score

Match length

E value

413

92

1.0e-40



```
Seq. No.
                  165962
                  LIB3177-096-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  67
E value
                  5.0e-63
Match length
                  143
                  69
% identity
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi_4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  165963
                  LIB3177-096-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3608126
BLAST score
                  230
E value
                  1.0e-126
                  412
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  165964
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g232033
BLAST score
                  184
                  1.0e-13
E value
Match length
                  58
% identity
                  64
NCBI Description
                  ELONGATION FACTOR 1 BETA' >gi_479830_pir_ $35501
                  translation elongation factor eEF-1 beta chain - wheat
                  >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'
                   [Triticum aestivum]
Seq. No.
                  165965
Seq. ID
                  LIB3177-096-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q232033
BLAST score
                  194
E value
                  8.0e-15
Match length
                  58
% identity
                  66
NCBI Description
                  ELONGATION FACTOR 1 BETA' >gi_479830_pir__$35501
                  translation elongation factor eEF-1 beta chain - wheat
                  >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'
                   [Triticum aestivum]
Seq. No.
                  165966
Seq. ID
                  LIB3177-096-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4835233
```



% identity (AL049862) putative protein 1 photosystem II NCBI Description oxygen-evolving complex [Arabidopsis thaliana] 165967 Seq. No. LIB3177-096-P1-K1-F10 Seq. ID Method BLASTX g4115918 NCBI GI 254 BLAST score 5.0e-22 E value 58 Match length % identity 84 (AF118222) similar to nascent polypeptide associated NCBI Description complex alpha chain [Arabidopsis thaliana] Seq. No. 165968 LIB3177-096-P1-K1-F11 Seq. ID Method BLASTN q3293583 NCBI GI BLAST score 32 E value 3.0e-08 Match length 171 % identity 87 NCBI Description Arabidopsis thaliana BAC T27D20 Seq. No. 165969 LIB3177-096-P1-K1-F2 Seq. ID Method BLASTN NCBI GI g2708736 416 BLAST score 0.0e + 00E value 439 Match length % identity 99 NCBI Description Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 cM, complete sequence [Arabidopsis thaliana] Seq. No. 165970 Seq. ID LIB3177-096-P1-K1-F3 Method BLASTX NCBI GI g4454037 BLAST score 701 3.0e-74E value Match length 128 100 % identity (AL035394) putative major latex protein [Arabidopsis NCBI Description thaliana] Seq. No. 165971 Seq. ID LIB3177-096-P1-K1-F5 Method BLASTX NCBI GI g294845 BLAST score 299

3.0e-27 E value Match length 131 % identity 44

NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar

H65-7052]



```
165972
Seq. No.
Seq. ID
                   LIB3177-096-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q1175011
BLAST score
                   507
E value
                   1.0e-51
Match length
                   98
% identity
                   99
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
                   A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)
                   plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
Seq. No.
                   165973
                   LIB3177-096-P1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q119143
BLAST score
                   208
E value
                   8.0e-17
Match length
                   88
                   53
% identity
NCBI Description
                 ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_81606_pir__S06724 translation elongation factor eEF-1
                   alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
                   (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1369927_emb CAA34454 (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                   (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                   >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                   >gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                   165974
Seq. ID
                   LIB3177-096-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q99688
BLAST score
                   428
E value
                   3.0e-42
Match length
                   141
% identity
                   65
NCBI Description
                  translation elongation factor eEF-1 alpha chain (gene A4) -
                   Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                   elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                   165975
Seq. ID
                   LIB3177-096-P1-K1-F9
```

Method BLASTX
NCBI GI g1592681
BLAST score 486
E value 5.0e-49
Match length 97
% identity 98

NCBI Description (X91917) LEA D113 homologue type2 [Arabidopsis thaliana]

>gi_3668076 (AC004667) LEA D113 type2 protein [Arabidopsis

thaliana]



```
Seq. No.
                   165976
Seq. ID
                  LIB3177-096-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  q246255
                  65
BLAST score
É value
                   5.0e-28
Match length
                  158
                  90
% identity
NCBI Description Bcg4-4=acyl carrier protein [Brassica rapa, Genomic, 3898
                  nt]
                  165977
Seq. No.
                  LIB3177-096-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4835233
BLAST score
                   727
                  3.0e-77
E value
Match length
                  142
% identity
                  99
NCBI Description
                  (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  165978
Seq. ID
                  LIB3177-096-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  q4371278
BLAST score
                  325
E value
                  0.0e + 00
Match length
                  442
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165979
Seq. ID
                  LIB3177-096-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g4586098
BLAST score
                  254
E value
                  1.0e-141
Match length
                  383
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                   (ESSA project)
Seq. No.
                  165980
Seq. ID
                  LIB3177-096-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4322346
BLAST score
                  183
E value
                  2.0e-13
Match length
                  67
                  45
% identity
NCBI Description (AF081825) sodium-dependent high-affinity dicarboxylate
                  transporter [Rattus norvegicus]
```

Seq. ID LIB3177-096-P1-K1-G3

Seq. No.



Method BLASTN
NCBI GI 94757405
BLAST score 147
E value 6.0e-77
Match length 398
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOJ10, complete sequence

Seq. No. 165982

Seq. ID LIB3177-096-P1-K1-G4

Method BLASTX
NCBI GI g4835235
BLAST score 241
E value 3.0e-20
Match length 102
% identity 43

NCBI Description (AL049862) putative protein [Arabidopsis thaliana]

Seq. No. 165983

Seq. ID LIB3177-096-P1-K1-G5

Method BLASTN
NCBI GI g2244747
BLAST score 431
E value 0.0e+00
Match length 443
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 165984

Seq. ID LIB3177-096-P1-K1-G6

Method BLASTX
NCBI GI g266839
BLAST score 142
E value 2.0e-10
Match length 62
% identity 63

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir__S29240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha

chain - Arabidopsis thaliana >gi_16445_emb_CAA47298_ (X66825) proteosome alpha subunit [Arabidopsis thaliana]

>gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
proteasome:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 165985

Seq. ID LIB3177-096-P1-K1-G7

Method BLASTX
NCBI GI g99696
BLAST score 517
E value 9.0e-53
Match length 108
% identity 95

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor,

chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana



>gi 240070 bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No. 165986 Seq. ID LIB3177-096-P1-K1-G8 Method BLASTX NCBI GI q99696 BLAST score 643 E value 2.0e-67 Match length 131 % identity

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor,

chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070 bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln

synthetase [Arabidopsis thaliana]

Seq. No. 165987

Seq. ID LIB3177-096-P1-K1-G9

Method BLASTN NCBI GI q2264310 BLAST score 208 E value 1.0e-113 Match length 440 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MKP11, complete sequence [Arabidopsis thaliana]

Seq. No. 165988

Seq. ID LIB3177-096-P1-K1-H1

Method BLASTX NCBI GI g2911044 BLAST score 602 E value 1.0e-62 Match length 114 % identity 99

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 165989

Seq. ID LIB3177-096-P1-K1-H11

Method BLASTX NCBI GI g232033 BLAST score 152 E value 7.0e-10 Match length 38 % identity 74

NCBI Description ELONGATION FACTOR 1 BETA' >gi_479830_pir__S35501 translation elongation factor eEF-1 beta' chain - wheat >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'

[Triticum aestivum]

Seq. No. 165990

Seq. ID LIB3177-096-P1-K1-H12

Method BLASTX



```
NCBI GI
                   g2213600
BLAST score
                   335
E value
                   3.0e - 31
Match length
                   101
% identity
                   40
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
                   165991
Seq. No.
Seq. ID
                   LIB3177-096-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g1176658
BLAST score
                   244
E value
                   1.0e-20
Match length
                   76
                   63
% identity
NCBI Description
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                   >gi_726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
Seq. No.
                   165992
                   LIB3177-096-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4741952
BLAST score
                   686
E value
                   2.0e-72
Match length
                   134
% identity
                   67
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   165993
Seq. ID
                  LIB3177-096-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   629
E value
                   8.0e-66
Match length
                   120
% identity
                   98
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                             (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   165994
Seq. ID
                  LIB3177-096-P1-K1-H6
Method
                  BLASTN
NCBI GI
                   g4757400
BLAST score
                   48
E value
                   4.0e-18
Match length
                  83
% identity
                   90
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MFJ20, complete sequence
Seq. No.
                   165995
```

LIB3177-096-P1-K1-H7 Seq. ID

BLASTX Method

NCBI GI g4827253



BLAST score 154 E value 3.0e-10 Match length 35 % identity 83

NCBI Description (AB027002) plastidic aldolase [Nicotiana paniculata]

Seq. No. Seq. ID

165996

Method

LIB3177-096-P1-K1-H8 BLASTX

NCBI GI g1781348 BLAST score 154 E value 3.0e-10 Match length 35 83 % identity

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No.

165997

Seq. ID

LIB3177-096-P1-K1-H9

Method BLASTX g132110 NCBI GI BLAST score 666 E value 4.0e-70 Match length 122 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060 pir RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No.

165998

Seq. ID LIB3177-097-P1-K1-A1

Method BLASTX NCBI GI g1169201 BLAST score 239 E value 1.0e-27 Match length 98

% identity 65

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

>gi_421830_pir__S33707 DRT112 protein - Arabidopsis

thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 165999

Seq. ID LIB3177-097-P1-K1-A10

Method BLASTX NCBI GI g1169476 BLAST score 645 E value 1.0e-67 Match length 123 % identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 166000



Seq. ID LIB3177-097-P1-K1-A11 Method BLASTX

NCBI GI g2501188 BLAST score 692 E value 4.0e-73 Match length 155 % identity 90

NCBI Description THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14

protein homolog - Arabidopsis thaliana >gi_1113783 (U17589)

Thil protein [Arabidopsis thaliana]

Seq. No. 166001

Seq. ID LIB3177-097-P1-K1-A12

Method BLASTN
NCBI GI g2191126
BLAST score 77
E value 3.0e-35
Match length 173
% identity 86

NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 166002

Seq. ID LIB3177-097-P1-K1-A2

Method BLASTX
NCBI GI g3273743
BLAST score 610
E value 2.0e-63
Match length 118
% identity 99

NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis

thaliana] >gi 3786019 (AC005499) unknown protein

[Arabidopsis thaliana]

Seq. No. 166003

Seq. ID LIB3177-097-P1-K1-A3

Method BLASTX
NCBI GI g4689386
BLAST score 406
E value 7.0e-40
Match length 88
% identity 86

NCBI Description (AF139468) photosystem I reaction center subunit III [Viqna

radiata]

Seq. No. 166004

Seq. ID LIB3177-097-P1-K1-A4

Method BLASTX
NCBI GI g120667
BLAST score 537
E value 6.0e-55
Match length 137
% identity 78

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi_166706 (M64116) cystolic

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis



thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No. 166005 LIB3177-097-P1-K1-A5 Seq. ID Method BLASTX NCBI GI q3413700 BLAST score 620 E value 9.0e-65 Match length 145 % identity 87 NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 166006

Seq. ID LIB3177-097-P1-K1-A6
Method BLASTX
NCBI GI g132110
BLAST score 668
E value 2.0e-70

Match length 124 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 166007

Seq. ID LIB3177-097-P1-K1-A8

Method BLASTX
NCBI GI g3885511
BLAST score 473
E value 2.0e-47
Match length 115

% identity 82

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 166008

Seq. ID LIB3177-097-P1-K1-A9

Method BLASTN
NCBI GI g3510336
BLAST score 314
E value 1.0e-176

Match length 457 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 166009

Seq. ID LIB3177-097-P1-K1-B1

Method BLASTN
NCBI GI g3883125
BLAST score 406
E value 0.0e+00
Match length 461



% identity Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA, NCBI Description complete cds Seq. No. 166010 LIB3177-097-P1-K1-B10 . Seq. ID Method BLASTX g1709534 NCBI GI BLAST score 573 E value 3.0e-59 Match length 135 % identity 85 NCBI Description DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir__\$66637 delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis thaliana >gi_829100_emb_CAA60740_ (X87330) pyrroline-5-carboxylate synthetase [Arabidopsis thaliana] >gi_870866_emb_CAA60446_ (X86777) pyrroline-5-carboxylate synthetase A [Arabidopsis thaliana] >gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate synthase [Arabidopsis thaliana] >gi_2642162 (AC003000) delta-1-pyrroline 5-carboxylase synthetase, P5C1 [Arabidopsis thaliana] Seq. No. 166011 LIB3177-097-P1-K1-B11 Seq. ID Method BLASTX NCBI GI g4455198 BLAST score 737 E value 2.0e-78 Match length 143 % identity 100 NCBI Description (AL035440) putative protein [Arabidopsis thaliana] Seq. No. 166012 Seq. ID LIB3177-097-P1-K1-B12 Method BLASTX NCBI GI q3288821 BLAST score 630 E value 7.0e-66 Match length 139 % identity 88 NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989 gb AAD28669.1 AC007209 5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana] Seq. No. 166013 Seq. ID LIB3177-097-P1-K1-B2 Method BLASTN NCBI GI g2245377

BLAST score 477

E value 0.0e+00477 Match length



% identity 100

NCBI Description Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA,

complete cds

Seq. No. 166014

Seq. ID LIB3177-097-P1-K1-B3

Method BLASTN
NCBI GI g4510360
BLAST score 33
E value 7.0e-09
Match length 65
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 166015

Seq. ID LIB3177-097-P1-K1-B4

Method BLASTX
NCBI GI g2827559
BLAST score 265
E value 5.0e-23
Match length 67
% identity 79

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

>gi_3292808_emb_CAA19798_ (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 166016

Seq. ID LIB3177-097-P1-K1-B6

Method BLASTX
NCBI GI g2695703
BLAST score 634
E value 2.0e-66
Match length 149
% identity 81

NCBI Description (Y10555) CONSTANS [Arabidopsis thaliana]

>gi_2695705_emb_CAA71588_ (Y10556) CONSTANS [Arabidopsis

thalianal

Seq. No. 166017

Seq. ID LIB3177-097-P1-K1-B8

Method BLASTX
NCBI GI g132110
BLAST score 662
E value 1.0e-69
Match length 127
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 166018

Seq. ID LIB3177-097-P1-K1-B9

Method BLASTN



```
NCBI GI
                   g3985932
BLAST score
                   134
E value
                   3.0e-69
Match length
                   354
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K22J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166019
Seq. ID
                  LIB3177-097-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  q259446
BLAST score
                  147
E value
                   5.0e-77
Match length
                  168
                  100
% identity
                  glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,
NCBI Description
                  C24, mRNA, 680 nt]
Seq. No.
                  166020
                  LIB3177-097-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113024
BLAST score
                   712
E value
                   2.0e-75
Match length
                  136
% identity
                  99
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]
Seq. No.
                  166021
Seq. ID
                  LIB3177-097-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1171993
BLAST score
                  654
E value
                  8.0e-69
Match length
                  128
% identity
                  98
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE 2 >gi_1076370_pir__$52991
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis
                   thaliana >gi 497421 (L33678) phenylalanine ammonia lyase
                   [Arabidopsis thaliana]
Seq. No.
                  166022
Seq. ID
                  LIB3177-097-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q2342687
BLAST score
                  800
E value
                  8.0e-86
Match length
                  154
% identity
                  98
NCBI Description
                  (AC000106) Similar to Beta integral membrane protein
                   (gb U43629). EST qb W43122 comes from this gene.
                   [Arabidopsis thaliana]
```

Seq. No. 166023

Seq. ID LIB3177-097-P1-K1-C6



```
Method
                  BLASTX
NCBI GI
                  q4507433
BLAST score
                  240
E value
                  4.0e-20
Match length
                  129
                  42
% identity
NCBI Description testis enhanced gene transcript
                  >gi_1729891_sp_P55061_TEGT_HUMAN TEGT PROTEIN (TESTIS
                  ENHANCED GENE TRANSCRIPT) >gi_2136254_pir__138334 TEGT
                  (testis enhanced gene transcript) - human
                  >gi_458545_emb_CAA53472_ (X75861) TEGT [Homo sapiens]
                  166024
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4567208
BLAST score
                  192
E value
                  2.0e-14
Match length
                  81
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166025
Seq. ID
                  LIB3177-097-P1-K1-C8
Method
                  BLASTX
```

NCBI GI g2245110 BLAST score 274 E value 3.0e-24Match length 54 % identity 100

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 166026 Seq. ID LIB3177-097-P1-K1-C9 Method BLASTX NCBI GI g2119846 BLAST score 408 E value 5.0e-40

Match length 80 97 % identity

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 166027

LIB3177-097-P1-K1-D1 Seq. ID

Method BLASTN NCBI GI q3492855 BLAST score 355 E value 0.0e + 00Match length 395 % identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2,



complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  166028
Seq. ID
                  LIB3177-097-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3046703
BLAST score
                  201
E value
                  5.0e-18
Match length
                  56
% identity
NCBI Description
                  (AL021749) protein kinase ADK1-like protein [Arabidopsis
                  thaliana]
                  166029
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  q3228389
BLAST score
                  259
E value
                  1.0e-143
Match length
                  447
                  98
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,
                  complete sequence [Arabidopsis thaliana]
                  166030
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  449
E value
                  1.0e-44
Match length
                  145
% identity
                  58
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp_AJ001449_2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                  166031
Seq. ID
                  LIB3177-097-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g4309683
BLAST score
                  460
E value
                  0.0e+00
Match length
                  480
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166032
Seq. ID
                  LIB3177-097-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q3893081
BLAST score
                  652
E value
                  2.0e-68
Match length
                  157
% identity
                  77
```

22337

NCBI Description (AJ012747) MLH1 protein [Arabidopsis thaliana]



Seq. No. 166033

Seq. ID LIB3177-097-P1-K1-D4

Method BLASTX
NCBI GI g119143
BLAST score 711
E value 2.0e-75
Match length 140
% identity 98

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_(X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 166034

Seq. ID LIB3177-097-P1-K1-D6

Method BLASTX
NCBI GI g3522954
BLAST score 572
E value 4.0e-59
Match length 137
% identity 82

NCBI Description (AC004411) IAA20 [Arabidopsis thaliana]

Seq. No. 166035

Seq. ID LIB3177-097-P1-K1-D7

Method BLASTX
NCBI GI g119975
BLAST score 505
E value 2.0e-51
Match length 118
% identity 88

NCBI Description FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin

[2Fe-2S] precursor - Arabidopsis thaliana

>gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A

[Arabidopsis thaliana]

Seq. No. 166036

Seq. ID LIB3177-097-P1-K1-D8

98

Method BLASTX
NCBI GI g2119846
BLAST score 615
E value 3.0e-64
Match length 118

% identity

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I

Method

BLASTX



chlorophyll a/b binding protein [Arabidopsis thaliana]

```
166037
Seq. No.
Seq. ID
                      LIB3177-097-P1-K1-D9
Method
                      BLASTX
NCBI GI
                      q4467137
BLAST score
                      332
                      4.0e-32
E value
Match length
                      149
% identity
                      45
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                      166038
Seq. ID
                      LIB3177-097-P1-K1-E1
Method
                      BLASTX
NCBI GI
                      q115470
BLAST score
                      380
E value
                      1.0e-36
Match length
                      143
% identity
                      57
NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                      DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                      (EC 4.2.1.1) precursor - Arabidopsis thaliana
                      >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                      [Arabidopsis thaliana].
Seq. No.
                      166039
                      LIB3177-097-P1-K1-E10
Seq. ID
Method
                      BLASTX
NCBI GI
                      q1076708
BLAST score
                      587
E value
                      7.0e-61
Match length
                      120
% identity
                      27
NCBI Description
                      seed tetraubiquitin - common sunflower
                      >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                      putative polyubiquitin [Arabidopsis thaliana]
                      >gi 1096513 prf 2111434A tetraubiquitin [Helianthus
                      annuus]
Seq. No.
                      166040
Seq. ID
                      LIB3177-097-P1-K1-E11
Method
                      BLASTX
NCBI GI
                      g3915826
BLAST score
                      650
E value
                      3.0e-68
Match length
                      152
                      82
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                      166041
Seq. ID
                      LIB3177-097-P1-K1-E12
```



NCBI GI g1145699
BLAST score 546
E value 4.0e-56
Match length 111
% identity 99

NCBI Description (U39486) delta tonoplast integral protein [Arabidopsis

thaliana]

Seq. No. 166042

Seq. ID LIB3177-097-P1-K1-E2

Method BLASTX
NCBI GI g4263525
BLAST score 574
E value 2.0e-59
Match length 135
% identity 84

NCBI Description (AC004044) putative photosystem I reaction center subunit

II precursor [Arabidopsis thaliana]

Seq. No. 166043

Seq. ID LIB3177-097-P1-K1-E3

Method BLASTX
NCBI GI g4160280
BLAST score 313
E value 9.0e-29
Match length 95
% identity 61

NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No. 166044

Seq. ID LIB3177-097-P1-K1-E4

Method BLASTN
NCBI GI 94263774
BLAST score 189
E value 1.0e-102
Match length 475
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T20F21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166045

Seq. ID LIB3177-097-P1-K1-E7

Method BLASTX
NCBI GI g100525
BLAST score 624
E value 3.0e-65
Match length 135
% identity 25

NCBI Description ubiquitin precursor UbB2 - common sunflower (fragment)

>gi 18803 emb CAA40323 (X57003) polyubiquitin protein

[Helianthus annuus]

Seq. No. 166046

Seq. ID LIB3177-097-P1-K1-E8

Method BLASTX NCBI GI g1363489 BLAST score 630



```
E value
                   6.0e-66
Match length
                   115
                   100
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                   thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  166047
Seq. ID
                  LIB3177-097-P1-K1-E9
Method
                  BLASTX
                  g166834
NCBI GI
BLAST score
                   445
E value
                   3.0e-44
Match length
                  103
% identity
                  87
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                   activase [Arabidopsis thaliana] >qi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
Seq. No.
                  166048
Seq. ID
                  LIB3177-097-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  421
E value
                  2.0e-41
Match length
                  92
% identity
                  93
NCBI Description
                  (AF007269) A_IG002N01.18 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  166049
Seq. ID
                  LIB3177-097-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1762584
BLAST score
                  744
                  3.0e-79
E value
Match length
                  144
                  74
% identity
NCBI Description
                  (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
Seq. No.
                  166050
Seq. ID
                  LIB3177-097-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2244759
                  588
BLAST score
E value
                  5.0e-61
Match length
                  125
% identity
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
```

Seq. No. 166051

Seq. ID LIB3177-097-P1-K1-F12

Method BLASTX NCBI GI g4587564 BLAST score 727 E value 3.0e-77



Match length 152 % identity 91

NCBI Description (AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,

gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No. 166052

Seq. ID LIB3177-097-P1-K1-F2

Method BLASTX
NCBI GI g2529663
BLAST score 618
E value 1.0e-64
Match length 125
% identity 98

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis

thaliana] >gi 3738277 (AC005309) putative lysophospholipase

[Arabidopsis thaliana]

Seq. No. 166053

Seq. ID LIB3177-097-P1-K1-F3

Method BLASTX
NCBI GI g2529663
BLAST score 482
E value 8.0e-55
Match length 135
% identity 84

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis

thaliana] >gi 3738277 (AC005309) putative lysophospholipase

[Arabidopsis thaliana]

Seq. No. 166054

Seq. ID LIB3177-097-P1-K1-F4

Method BLASTX
NCBI GI g3182982
BLAST score 68
E value 5.6e+00
Match length 105

Match length 105 % identity 87

NCBI Description CELL ELONGATION PROTEIN DIMINUTO (CELL ELONGATION PROTEIN

DWARF1) >gi_602302 (L38520) diminuto [Arabidopsis thaliana]

Seq. No. 166055

Seq. ID LIB3177-097-P1-K1-F5

Method BLASTX
NCBI GI g3980383
BLAST score 440
E value 1.0e-43
Match length 83
% identity 100

NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]

Seq. No. 166056

Seq. ID LIB3177-097-P1-K1-F7

Method BLASTN MCBI GI g2062153

BLAST score 36



E value 1.0e-10 Match length 36 % identity 100

NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166057

Seq. ID LIB3177-097-P1-K1-F8

Method BLASTX
NCBI GI g3738291
BLAST score 470
E value 4.0e-47
Match length 117
% identity 83

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 166058

Seq. ID LIB3177-097-P1-K1-F9

Method BLASTX
NCBI GI g132102
BLAST score 692
E value 3.0e-73
Match length 134
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 166059

Seq. ID LIB3177-097-P1-K1-G1

Method BLASTX
NCBI GI g113617
BLAST score 644
E value 2.0e-67
Match length 128
% identity 99

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68199_pir__ADMU fructose-bisphosphate aldolase (EC
4.1.2.13) - Arabidopsis thaliana >gi_16284_emb_CAA37226_
(X53058) fructose 1,6-diphosphate aldolase [Arabidopsis

thaliana]

Seq. No. 166060

Seq. ID LIB3177-097-P1-K1-G10

Method BLASTX
NCBI GI 94567268
BLAST score 456
E value 1.0e-45
Match length 102
% identity 96

NCBI Description (AC006841) putative fructose biphosphate aldolase

[Arabidopsis thaliana]

Seq. No. 166061



```
Seq. ID
                   LIB3177-097-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q1145699
BLAST score
                   511
E value
                   3.0e-52
Match length
                   104
% identity
NCBI Description
                  (U39486) delta tonoplast integral protein [Arabidopsis
                   thaliana]
Seq. No.
                   166062
Seq. ID
                   LIB3177-097-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q2119846
BLAST score
                   260
E value
                   4.0e-23
Match length
                   51
                   100
% identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790 (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   166063
Seq. ID
                   LIB3177-097-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g114591
BLAST score
                   643
E value
                   2.0e-67
Match length
                   132
% identity
                   98
NCBI Description ATP SYNTHASE EPSILON CHAIN >gi_81663_pir__S01903
                   H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain -
                   Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_
                   (X12889) Cf1 ATPase epsilon subunit (AA 1 \overline{\phantom{a}} 13\overline{\phantom{a}})
                   [Arabidopsis thaliana]
Seq. No.
                   166064
Seq. ID
                   LIB3177-097-P1-K1-G3
                   BLASTN
                   g2739359
                   171
                   2.0e-91
                   178
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T9J22 genomic
```

Method NCBI GI BLAST score E value Match length

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166065

Seq. ID LIB3177-097-P1-K1-G5

Method BLASTX q3122724 NCBI GI BLAST score 184 E value 6.0e-14



```
Match length
                  50
                  76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  166066
Seq. ID
                  LIB3177-097-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q3913379
BLAST score
                  479
E value
                  2.0e-48
Match length
                  98
                  91
% identity
                  CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
                  >gi 1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis
                  thaliana]
Seq. No.
                  166067
Seq. ID
                  LIB3177-097-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4572671
BLAST score
                  206
E value
                  3.0e-16
Match length
                  104
% identity
                  41
NCBI Description
                 (AC006954) putative cyclic nucleotide regulated ion channel
                  [Arabidopsis thaliana]
Seq. No.
                  166068
Seq. ID
                  LIB3177-097-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2853090
BLAST score
                  344
E value
                  1.0e-32
Match length
                  70
% identity
                  100
                  (AL021768) small GTP-binding protein-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166069
Seq. ID
                  LIB3177-097-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4490737
BLAST score
                  525
E value
                  1.0e-53
Match length
                  118
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                  166070
Seq. No.
```

Seq. ID LIB3177-097-P1-K1-H11 Method BLASTN

NCBI GI g2335089
BLAST score 235
E value 1.0e-129
Match length 302
% identity 99



NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166071

Seq. ID LIB3177-097-P1-K1-H12

98

Method BLASTX
NCBI GI g2119846
BLAST score 435
E value 2.0e-43
Match length 83

% identity

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 166072

Seq. ID LIB3177-097-P1-K1-H2

Method BLASTN
NCBI GI g3046856
BLAST score 405
E value 0.0e+00
Match length 441
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 166073

Seq. ID LIB3177-097-P1-K1-H3

Method BLASTX
NCBI GI g2119848
BLAST score 668
E value 2.0e-70
Match length 126
% identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789 (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 166074

Seq. ID LIB3177-097-P1-K1-H4

Method BLASTX
NCBI GI g4455336
BLAST score 721
E value 1.0e-76
Match length 142

% identity 96

NCBI Description (AL035525) pectinesterase-like protein [Arabidopsis

thalianal

% identity

NCBI Description



```
Seq. No.
                   166075
Seq. ID
                   LIB3177-097-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1363489
BLAST score
                   563
E value
                   3.0e-58
Match length
                   104
% identity
                   98
NCBI Description
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   166076
Seq. ID
                   LIB3177-097-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g3560243
BLAST score
                   236
E value
                   2.0e-23
Match length
                   144
% identity
                   47
NCBI Description (AL031532) putative hydrolase [Schizosaccharomyces pombe]
Seq. No.
                   166077
Seq. ID
                   LIB3177-097-P1-K1-H8
Method
                  BLASTX
NCBI GI
                   q4249379
BLAST score
                   733
E value
                   5.0e-78
Match length
                   146
% identity
                   69
NCBI Description
                  (AC005966) Strong similarity to gb_X82030 chloroplast RNA
                   binding protein (RNP1) from Phaseolus vulgaris.
                   [Arabidopsis thaliana]
                   166078
Seq. No.
Seq. ID
                   LIB3177-097-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   g2760316
BLAST score
                   315
E value
                   1.0e-177
Match length
                   460
                   100
% identity
NCBI Description
                  The sequence of BAC F1N21 from Arabidopsis thaliana
                  chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166079
                  LIB3177-098-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g584794
BLAST score
                   527
E value
                  7.0e-54
Match length
                  135
```

>gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
- curled-leaved tobacco >gi_170289 (M80489) plasma membrane

PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)



166080

H+ ATPase [Nicotiana plumbaginifolia]

Seq. ID LIB3177-098-P1-K1-A10 Method BLASTX NCBI GI g421826 BLAST score 523 E value 2.0e-53 Match length 123 % identity 80

Seq. No.

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 166081

Seq. ID LIB3177-098-P1-K1-A11

Method BLASTX
NCBI GI g2388578
BLAST score 562
E value 4.0e-58
Match length 114
% identity 99

NCBI Description (AC000098) Similar to Mycobacterium RlpF (gb Z84395). ESTs

gb_T75785,gb_R30580,gb_T04698 come from this gene.

[Arabidopsis thaliana]

Seq. No. 166082

Seq. ID LIB3177-098-P1-K1-A12

Method BLASTX
NCBI GI g132102
BLAST score 710
E value 3.0e-75
Match length 136
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 166083

Seq. ID LIB3177-098-P1-K1-A2

Method BLASTX
NCBI GI g3335378
BLAST score 299
E value 4.0e-27
Match length 66
% identity 83

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 166084

Seq. ID LIB3177-098-P1-K1-A3

Method BLASTX NCBI GI g2335100 BLAST score 789



E value 2.0e-84 Match length 152 % identity 97

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

166085 Seq. No.

LIB3177-098-P1-K1-A5 Seq. ID

Method BLASTX NCBI GI g417148 BLAST score 422 E value 2.0e-41 Match length 144 % identity 56

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)

(G2-4) >gi_99912_pir__A33654 heat shock protein 26A soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]

166086 Seq. No.

LIB3177-098-P1-K1-A6 Seq. ID

Method BLASTX NCBI GI g3122753 BLAST score 539 E value 3.0e-55 Match length 104 95 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_

(Z97336) ribosomal protein [Arabidopsis thaliana]

166087 Seq. No.

Seq. ID LIB3177-098-P1-K1-A7

Method BLASTX NCBI GI g3885511 BLAST score 504 E value 4.0e-51 Match length 127 % identity

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 166088

Seq. ID LIB3177-098-P1-K1-B10

Method BLASTX g4454036 NCBI GI BLAST score 754 E value 2.0e-80 Match length 139 % identity 99

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 166089

Seq. ID LIB3177-098-P1-K1-B11

Method BLASTX NCBI GI g1076287 BLAST score 570 E value 6.0e-59 Match length 130



```
% identity
NCBI Description
                  amine acid permease - Arabidopsis thaliana
                  >gi_510236_emb_CAA50672 (X71787) amine acid permease
                  [Arabidopsis thaliana]
Seq. No.
                  166090
Seq. ID
                  -LIB3177-098-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4218123
BLAST score
                  165
E value
                  2.0e-31
Match length
                  95
% identity
                  82
NCBI Description (AL035353) photosystem I subunit PSI-E-like protein
                  [Arabidopsis thaliana]
                  166091
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q4106388
BLAST score
                  249
E value
                  3.0e-21
Match length
                  154
% identity
                  44
NCBI Description (AF074849) unknown [Arabidopsis thaliana]
                  166092
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2651314
BLAST score
                  384
E value
                  5.0e-37
Match length
                  110
% identity
                  70
NCBI Description (AC002336) putative ribosomal protein S26 [Arabidopsis
                  thaliana
                  166093
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3355463
BLAST score
                  66
E value
                  1.0e-28
Match length
                  134
% identity
                  87
NCBI Description Arabidopsis thaliana chromosome II BAC F12L6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166094
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g266463
```

Method BLASTX
NCBI GI g266463
BLAST score 644
E value 1.0e-67
Match length 137
% identity 91

NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM



166095

DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__\$25670 3-isopropylmalate dehydrogenase (EC $\overline{1.1.1.85}$) $\overline{\text{precursor}}$ potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi 445064 prf 1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No. Seq. ID LIB3177-098-P1-K1-B8 Method BLASTN NCBI GI g2351070 BLAST score 34 E value 2.0e-09 Match length 58 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH12, complete sequence [Arabidopsis thaliana]

166096 Seq. No.

LIB3177-098-P1-K1-B9 Seq. ID

Method BLASTX NCBI GI g2392021 BLAST score 522 E value 3.0e-53 Match length 147 % identity 63

NCBI Description (D63425) phopholipid hydroperoxide glutathione

peroxidase-like protein [Spinacia oleracea]

166097 Seq. No.

Seq. ID LIB3177-098-P1-K1-C1

Method BLASTX NCBI GI g3935164 BLAST score 72 E value 4.0e-17 Match length 82 % identity

NCBI Description (AC004557) F17L21.7 [Arabidopsis thaliana]

Seq. No. 166098

Seq. ID LIB3177-098-P1-K1-C10

Method BLASTX NCBI GI g585536 BLAST score 707 E value 5.0e-75 Match length 129 % identity 100

MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) NCBI Description

> >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -Arabidopsis thaliana >gi 304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)

thioglucosidase [Arabidopsis thaliana]

Seq. No. 166099

Seq. ID LIB3177-098-P1-K1-C11

Method BLASTX NCBI GI g3482975 BLAST score 634



```
E value
                   2.0e-66
Match length
                  146
                   87
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166100
Seq. ID
                  LIB3177-098-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  798
E value
                  1.0e-85
Match length
                  147
% identity
                  65
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  166101
Seq. ID
                  LIB3177-098-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g421826
BLAST score
                  770
E value
                  2.0e-82
Match length
                  149
% identity
                  100
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana
                  166102
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g4159704
                  200
BLAST score
E value
                  1.0e-108
Match length
                  425
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MCB17, complete sequence
Seq. No.
                  166103
Seq. ID
                  LIB3177-098-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  709
                  4.0e-75
E value
Match length
                  131
% identity
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  166104
Seq. ID
                  LIB3177-098-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2244800
```

Method BLASTX
NCBI GI g2244800
BLAST score 553
E value 5.0e-57
Match length 112
% identity 96

NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. ID

Method



```
Seq. No.
                  166105
Seq. ID
                  LIB3177-098-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2062158
BLAST score
                  677
E value
                  2.0e-71
Match length
                  143
% identity
                  47
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  166106
Seq. ID
                  LIB3177-098-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2832641
BLAST score
                  358
E value
                  5.0e-34
Match length
                  124
% identity
NCBI Description
                  (AL021710) glycolate oxidase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  166107
Seq. ID
                  LIB3177-098-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2290528
BLAST score
                  451
E value
                  4.0e-45
Match length
                  114
                  77
% identity
NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]
Seq. No.
                  166108
Seq. ID
                  LIB3177-098-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g4159704
BLAST score
                  95
E value
                  6.0e-46
Match length
                  306
                  92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                  MCB17, complete sequence
Seq. No.
                  166109
Seq. ID
                  LIB3177-098-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  g2529229
BLAST score
                  510
E value
                  8.0e-52
Match length
                  120
% identity
                  78
NCBI Description (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
Seq. No.
                  166110
```

22353

LIB3177-098-P1-K1-D11

BLASTX



g3688799 NCBI GI BLAST score 637 E value 1.0e-66 Match length 129 % identity 98 NCBI Description

(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis

thaliana]

Seq. No. 166111

LIB3177-098-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI g3096939 BLAST score 539 E value 3.0e-55 Match length 117 % identity 87

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 166112

Seq. ID LIB3177-098-P1-K1-D2

Method BLASTX NCBI GI g2462741 BLAST score 664 E value 6.0e-70133 Match length % identity

NCBI Description (AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 166113

Seq. ID LIB3177-098-P1-K1-D3

Method BLASTN NCBI GI q4662609 BLAST score 150 E value 1.0e-78 Match length 469

% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 166114

Seq. ID LIB3177-098-P1-K1-D5

Method BLASTX NCBI GI g4006858 BLAST score 390 E value 9.0e-38Match length 132 58 % identity

NCBI Description (Z99707) cold acclimation protein homolog [Arabidopsis

thaliana]

Seq. No. 166115

Seq. ID LIB3177-098-P1-K1-D6

BLASTN Method NCBI GI g14342 BLAST score 234 E value 1.0e-129



Match length 332 % identity 99

NCBI Description A.thaliana mRNA for carbonic anhydrase

166116 Seq. No.

LIB3177-098-P1-K1-D7 Seq. ID

Method BLASTX NCBI GI q132110 BLAST score 632 4.0e-66 E value Match length 119 97 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 166117

Seq. ID LIB3177-098-P1-K1-D8

Method BLASTX NCBI GI q3879734 BLAST score 158 E value 1.0e-10 Match length 89 47 % identity

NCBI Description (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912

> comes from this gene; cDNA EST EMBL: D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST

EMBL:D74229 comes from this gene; cDNA EST EMBL:D727

Seq. No. 166118

Seq. ID LIB3177-098-P1-K1-E1

Method BLASTX NCBI GI g3236237 BLAST score 417 E value 6.0e-41 137 Match length 59 % identity

NCBI Description (AC004684) putative ribotol dehydrogenase [Arabidopsis

thaliana]

166119 Seq. No.

Seq. ID LIB3177-098-P1-K1-E10

89

BLASTX Method NCBI GI g2501188 BLAST score 633 E value 3.0e-66 Match length 144

NCBI Description THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14

protein homolog - Arabidopsis thaliana >gi_1113783 (U17589)

Thil protein [Arabidopsis thaliana]

Seq. No. 166120

% identity

LIB3177-098-P1-K1-E11 Seq. ID

Seq. No.

Seq. ID

166125

LIB3177-098-P1-K1-E5



```
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  394
E value
                  2.0e-38
Match length
                  79
                  97
% identity
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  166121
Seq. ID
                  LIB3177-098-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q99735
BLAST score
                  384
E value
                  5.0e-37
Match length
                  108
                  72
% identity
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                  Arabidopsis thaliana (fragment)
Seq. No.
                  166122
Seq. ID
                  LIB3177-098-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  673
E value
                  5.0e-71
Match length
                  122
% identity
                  100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  166123
Seq. ID
                  LIB3177-098-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4008012
BLAST score
                  494
E value
                  6.0e-50
Match length
                  154
% identity
                  68
NCBI Description (AF084037) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  166124
Seq. ID
                  LIB3177-098-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q4589444
BLAST score
                  313
E value
                  1.0e-176
Match length
                  328
% identity
                  54
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWF20, complete sequence
```

NCBI GI BLAST score

E value

637

1.0e-66



```
Method
                  BLASTX
NCBI GI
                  g3201613
BLAST score
                  52
E value
                  1.0e-40
Match length
                  89
% identity
                  93
NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.
                  166126
                  LIB3177-098-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204274
BLAST score
                  708
E value
                  5.0e-75
Match length
                  128
% identity
                  99
                  (AC004146) ribulose bisphosphate carboxylase, small subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  166127
                  LIB3177-098-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2842482
BLAST score
                  310
E value
                  2.0e-28
Match length
                  96
% identity
                  61
                  (AL021749) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  166128
Seq. No.
                  LIB3177-098-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341698
BLAST score
                  594
E value
                  1.0e-61
                  125
Match length
                  90
% identity
NCBI Description (AC003672) blue copper-binding protein II [Arabidopsis
                  thaliana]
                  166129
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  439
                  2.0e-43
E value
                  135
Match length
% identity
                  63
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  166130
Seq. ID
                  LIB3177-098-P1-K1-F11
Method
                  BLASTX
                  q3599491
```



150 Match length % identity 76 NCBI Description (AF085149) putative aminotransferase [Capsicum chinense] Seq. No. 166131 Seq. ID LIB3177-098-P1-K1-F12 Method BLASTX NCBI GI g3142295 BLAST score 412 E value 2.0e-40 Match length 110 % identity 68 NCBI Description (AC002411) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. [Arabidopsis thaliana] Seq. No. 166132 LIB3177-098-P1-K1-F2 Seq. ID Method BLASTX NCBI GI g4678328 BLAST score 385 E value 4.0e-37 Match length 127 % identity 57 NCBI Description (AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana] Seq. No. 166133 Seq. ID LIB3177-098-P1-K1-F3 Method BLASTX NCBI GI g4371284 BLAST score 69 E value 4.0e-64 Match length 127 % identity 99 NCBI Description (AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana] Seq. No. 166134 LIB3177-098-P1-K1-F4 Seq. ID Method BLASTN NCBI GI g4662640 BLAST score 402 E value 0.0e+00Match length 414 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F15K19 genomic

sequence, complete sequence

Seq. No. 166135

Seq. ID LIB3177-098-P1-K1-F5

Method BLASTX
NCBI GI g1350720
BLAST score 553
E value 7.0e-57
Match length 111
% identity 96



NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 166136

Seq. ID LIB3177-098-P1-K1-F6

Method BLASTX NCBI GI g132074 BLAST score 741 E value 6.0e-79Match length 135 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 166137

Seq. ID LIB3177-098-P1-K1-F7

Method BLASTN NCBI GI q4757401 BLAST score 302 E value 1.0e-169 Match length 448 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 166138

Seq. ID LIB3177-098-P1-K1-F8

Method BLASTX NCBI GI g1169861 BLAST score 470 E value 4.0e-47 Match length 112 79 % identity

NCBI Description G-BOX BINDING FACTOR 2 >gi_81616_pir__ S20884 G-box-binding factor 2 - Arabidopsis thaliana >gi_16288_emb_CAA45357_ (X63895) G-box binding factor 2 [Arabidopsis thaliana] >gi 3319286 (AF053228) G-box binding factor 2 [Arabidopsis

thaliana]

Seq. No. 166139

Seq. ID LIB3177-098-P1-K1-F9

Method BLASTX NCBI GI g2980770 BLAST score 681 E value 5.0e-73Match length 141 % identity 95

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

166140 Seq. No.

Seq. ID LIB3177-098-P1-K1-G1

Method BLASTX NCBI GI g4455253 BLAST score 685 E value 2.0e-72 Match length 148

NCBI Description



```
% identity
                   88
NCBI Description
                  (AL035523) superoxide dismutase (EC 1.15.1.1)
                   (Fe)(fragment) [Arabidopsis thaliana]
                  166141
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q3695023
BLAST score
                  472
                   4.0e-64
E value
Match length
                  144
% identity
                  89
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
Seq. No.
                  166142
                  LIB3177-098-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3927830
BLAST score
                   583
E value
                  2.0e-60
                  150
Match length
% identity
                  25
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  166143
Seq. ID
                  LIB3177-098-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q2809253
BLAST score
                   662
E value
                   9.0e-70
Match length
                  127
                   98
% identity
NCBI Description (AC002560) F21B7.22 [Arabidopsis thaliana]
Seq. No.
                   166144
Seq. ID
                  LIB3177-098-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3386597
BLAST score
                  576
E value
                  1.0e-59
Match length
                  109
                   98
% identity
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
                  >gi 3702347 (AC005397) putative permease [Arabidopsis
                  thaliana]
Seq. No.
                   166145
Seq. ID
                  LIB3177-098-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1707412
BLAST score
                  367
E value
                   5.0e-35
Match length
                  152
% identity
                   48
```

22360

protein [Bos taurus]

(X95906) Cleavage and Polyadenylation Specifity Factor



 Seq. No.
 166146

 Seq. ID
 LIB3177-098-P1-K1-G4

 Method
 BLASTN

 NCBI GI
 g2351063

 NCBI GI
 308

 NCBI GI
 g2351063

 BLAST score
 208

 E value
 1.0e-113

 Match length
 454

 % identity
 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCL19, complete sequence [Arabidopsis thaliana]

Seq. No. 166147

Seq. ID LIB3177-098-P1-K1-G5

Method BLASTX
NCBI GI g2864617
BLAST score 523
E value 2.0e-53
Match length 132
% identity 82

NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like

protein [Arabidopsis thaliana]

Seq. No. 166148

Seq. ID LIB3177-098-P1-K1-G6

Method BLASTX
NCBI GI g544018
BLAST score 613
E value 7.0e-64
Match length 153
% identity 78

NCBI Description NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772 nitrate-inducible nitrate transporter - Arabidopsis

thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs

gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688, gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from

this gene. [Arabidopsis thaliana]

Seq. No. 166149

Seq. ID LIB3177-098-P1-K1-G7

Method BLASTX
NCBI GI g512400
BLAST score 562
E value 6.0e-58
Match length 153
% identity 71

NCBI Description (X74947) annexin [Medicago sativa]

Seq. No. 166150

Seq. ID LIB3177-098-P1-K1-G8

Method BLASTX
NCBI GI g3915847
BLAST score 293
E value 1.0e-26
Match length 76
% identity 80



```
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  166151
Seq. ID
                  LIB3177-098-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  748
E value
                  1.0e-79
Match length
                  136
                  100
% identity
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 166152 Seq. ID LIB3177-098-P1-K1-H1 Method BLASTX NCBI GI g3643610 BLAST score 520 E value 5.0e-53

Match length 103 % identity 94

NCBI Description (AC005395) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 166153

Seq. ID LIB3177-098-P1-K1-H11

Method BLASTX NCBI GI g1710530 BLAST score 331 E value 3.0e-31 Match length 83 % identity 75

NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256

ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No. 166154

Seq. ID LIB3177-098-P1-K1-H12

Method BLASTX NCBI GI g99696 BLAST score 490 E value 1.0e-49 Match length 117 % identity 83

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor,

chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi 240070 bbs 69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf 1804333A Gln

synthetase [Arabidopsis thaliana]

Seq. No. 166155

Seq. ID LIB3177-098-P1-K1-H2



```
Method
                    BLASTX
NCBI GI
                    g1732572
BLAST score
                    601
E value
                    2.0e-66
Match length
                    133
% identity
                    92
NCBI Description (U72154) beta-glucosidase [Brassica nigra]
Seq. No.
                    166156
Seq. ID
                    LIB3177-098-P1-K1-H3
Method
                    BLASTN
NCBI GI
                    q2392762
BLAST score
                   147
E value
                    4.0e-77
Match length
                    294
% identity
                    98
NCBI Description Arabidopsis thaliana BAC T32N15 from chromsome III near 54
                    cM, complete sequence
Seq. No.
                    166157
                    LIB3177-098-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                    g2499810
BLAST score
                    684
E value
                    3.0e-72
Match length
                    131
% identity
                    99
NCBI Description PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1
                    profilin isoform 1 [Arabidopsis thaliana, Columbia,
```

[Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi 3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No. 166158

Seq. ID LIB3177-098-P1-K1-H5

Method BLASTX NCBI GI q3913525 BLAST score 120 E value 1.0e-26 Match length 110 71 % identity

NCBI Description DNA POLYMERASE DELTA CATALYTIC CHAIN >gi 2895198 (AF020193)

DNA polymerase delta [Glycine max]

Seq. No. 166159

Seq. ID LIB3177-098-P1-K1-H6

Method BLASTX NCBI GI q3757516 BLAST score 405 2.0e-39 E value Match length 143 % identity

NCBI Description (AC005167) putative TMV resistance protein [Arabidopsis

thaliana]



```
Seq. No.
                   166160
Seq. ID
                   LIB3177-098-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4490737
BLAST score
                   516
E value
                   3.0e-60
Match length
                   140
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   166161
                  LIB3177-098-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3834302
BLAST score
                  57
E value
                   6.0e-52
Match length
                  113
% identity
                   93
NCBI Description
                  (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
                   from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                   166162
Seq. ID
                  LIB3177-099-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q3193311
BLAST score
                  259
E value
                   1.0e-144
Match length
                  453
% identity
                   100
NCBI Description Arabidopsis thaliana BAC F6N15
Seq. No.
                   166163
Seq. ID
                  LIB3177-099-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q2983203
BLAST score
                  145
E value
                   5.0e-09
Match length
                  57
                  42
% identity
NCBI Description (AE000696) polypeptide deformylase [Aquifex aeolicus]
Seq. No.
                   166164
Seq. ID
                  LIB3177-099-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4056477
BLAST score
                  555
E value
                  4.0e-57
Match length
                  127
% identity
```

% identity 64
NCBI Description (AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 166165

Seq. ID LIB3177-099-P1-K1-A2

Method BLASTX NCBI GI g3386609



```
BLAST score
                  190
E value
                  1.0e-14
Match length
                  90
% identity
                  49
NCBI Description (AC004665) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  166166
Seq. ID
                  LIB3177-099-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2443751
BLAST score
                  677
E value
                  2.0e-71
Match length
                  135
% identity
                  99
NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
                  (AC002535) putative fumarase [Arabidopsis thaliana]
                  166167
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2160182
BLAST score
                  160
E value
                  8.0e-11
Match length
                  129
% identity
NCBI Description (AC000132) ESTs qb ATTS1236,qb T43334,qb N97019,qb AA395203
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  166168
Seq. ID
                  LIB3177-099-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2462840
BLAST score
                  168
E value
                  5.0e-12
Match length
                  34
                  97
% identity
NCBI Description (AF000657) cytochrome C [Arabidopsis thaliana]
Seq. No.
                  166169
Seq. ID
                  LIB3177-099-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g1934741
BLAST score
                  73
E value
                  9.1e-01
                  55
Match length
% identity
                  11
NCBI Description (Y10013) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  166170
Seq. ID
                  LIB3177-099-P1-K1-A8
```

Method BLASTX NCBI GI g4512655 BLAST score 363 E value 5.0e-35 Match length 69



```
% identity
                  (AC007048) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  166171
Seq. No.
                  LIB3177-099-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2118220
BLAST score
                  244
                  6.0e-21
E value
Match length
                  68
% identity
                  76
NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                  (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                  >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
                  166172
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-B1
Method
                  BLASTX
                  q2982464
NCBI GI
BLAST score
                  240
E value
                  3.0e-20
Match length
                  130
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                  166173
Seq. ID
                  LIB3177-099-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  618
E value
                  2.0e-64
Match length
                  116
                  100
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  166174
```

 Seq. No.
 166174

 Seq. ID
 LIB3177-099-P1-K1-B2

 Method
 BLASTX

NCBI GI g166410 BLAST score 220 E value 6.0e-18 Match length 85 % identity 52

NCBI Description (L07291) Alfin-1 [Medicago sativa]



Seq. No. 166175

Seq. ID LIB3177-099-P1-K1-B7

Method BLASTX
NCBI GI 94741950
BLAST score 738
E value 1.0e-78
Match length 138
% identity 100

NCBI Description (AF134125) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 166176

Seq. ID LIB3177-099-P1-K1-B8

Method BLASTX
NCBI GI g3288823
BLAST score 676
E value 3.0e-71
Match length 133
% identity 100

NCBI Description (AF063852) FUS5 [Arabidopsis thaliana]

Seq. No. 166177

Seq. ID LIB3177-099-P1-K1-B9

Method BLASTN
NCBI GI g2645198
BLAST score 45
E value 5.0e-16
Match length 162
% identity 83

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166178

Seq. ID LIB3177-099-P1-K1-C1

Method BLASTN
NCBI GI g4490324
BLAST score 115
E value 4.0e-58
Match length 131
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 166179

Seq. ID LIB3177-099-P1-K1-C10

Method BLASTX
NCBI GI g3549669
BLAST score 677
E value 2.0e-71
Match length 136
% identity 98

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 166180

Seq. ID LIB3177-099-P1-K1-C11

Method BLASTN
NCBI GI g2564050
BLAST score 424



E value 0.0e + 00Match length 428 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana] Seq. No. 166181 Seq. ID LIB3177-099-P1-K1-C12 Method BLASTX NCBI GI g2507281 BLAST score 702 E value 2.0e-74Match length 129 % identity 98 NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No. 166182 Seq. ID LIB3177-099-P1-K1-C2 Method BLASTX NCBI GI g3355480

BLAST score 325 E value 3.0e-30 Match length 100 % identity 59

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No. 166183

Seq. ID LIB3177-099-P1-K1-C3

Method BLASTX NCBI GI q282865 BLAST score 348 E value 3.0e - 3374 Match length 88 % identity

chlorophyll a/b-binding protein - Arabidopsis thaliana NCBI Description >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >gi 166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 166184

Seq. ID LIB3177-099-P1-K1-C4

Method BLASTX NCBI GI g3318617 BLAST score 742 E value 4.0e-79 Match length 139 % identity

NCBI Description (AB016066) mitochondrial phosphate transporter [Arabidopsis

thaliana]

Seq. No. 166185

Seq. ID LIB3177-099-P1-K1-C5

Method BLASTX



```
NCBI GI
                  q3445209
BLAST score
                  787
E value
                  2.0e-84
Match length
                  148
% identity
                  99
NCBI Description
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
Seq. No.
                  166186
Seq. ID
                  LIB3177-099-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  422
E value
                  0.0e + 00
Match length
                  446
% identity
                  36
NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166187
Seq. ID
                  LIB3177-099-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4455253
BLAST score
                  368
E value
                  3.0e-35
Match length
                  87
% identity
                  80
NCBI Description (AL035523) superoxide dismutase (EC 1.15.1.1)
                  (Fe) (fragment) [Arabidopsis thaliana]
Seq. No.
                  166188
Seq. ID
                  LIB3177-099-P1-K1-C8
Méthod
                  BLASTX
NCBI GI
                  g585536
BLAST score
                  51
E value
                  3.0e-79
Match length
                  146
                  96
% identity
NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                  >gi 1362006 pir__S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi 304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                  thioglucosidase [Arabidopsis thaliana]
Seq. No.
                  166189
Seq. ID
                  LIB3177-099-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g441490
BLAST score
                  80
E value
                  3.0e-37
Match length
                  80
                  100
% identity
NCBI Description S.alba chloroplast trnR gene
```

Seq. No. 166190

Seq. ID LIB3177-099-P1-K1-D1

Method BLASTN



```
NCBI GI
                   g2828182
                   370
BLAST score
E value
                   0.0e+00
                   374
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166191
Seq. ID
                  LIB3177-099-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g729479
                  394
BLAST score
E value
                  3.0e-38
Match length
                  100
                  73
% identity
NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
                   (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.
                  166192
Seq. ID
                  LIB3177-099-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  q1946354
BLAST score
                  165
E value
                  5.0e-88
Match length
                  169
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic
                  sequence, complete sequence
Seq. No.
                  166193
Seq. ID
                  LIB3177-099-P1-K1-D2
Method
                  {\tt BLASTX}
NCBI GI
                  q1769968
BLAST score
                  217
E value
                  1.0e-17
Match length
                  84
% identity
                  56
NCBI Description (Y10156) myrosinase-associated protein [Brassica napus]
Seq. No.
                  166194
                  LIB3177-099-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741954
BLAST score
                  561
E value
                  6.0e-58
Match length
                  119
% identity
NCBI Description (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                  166195
Seq. ID
                  LIB3177-099-P1-K1-D4
```

Method BLASTX
NCBI GI g4337175
BLAST score 669
E value 2.0e-70
Match length 134



```
% identity
NCBI Description
                    (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
                    gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                    166196
Seq. ID
                    LIB3177-099-P1-K1-D5
Method
                    BLASTX
NCBI GI
                    g2119846
BLAST score
                    731
E value
                    9.0e-78
Match length
                    139
% identity
                    99
NCBI Description
                    chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                    Arabidopsis thaliana >gi_16364_emb_CAA45790 (X64460)
                    photosystem II type I chlorophyll a /b binding protein
                    [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                    II type I chlorophyll a/b binding protein [Arabidopsis
                    thaliana] >gi_3337371 (AC004481) photosystem II type I
                    chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                    166197
Seq. ID
                    LIB3177-099-P1-K1-D6
Method
                    BLASTN
NCBI GI
                    g4490324
BLAST score
                    222
E value
                    1.0e-121
Match length
                    455
% identity
                    100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                    (ESSA project)
Seq. No.
                    166198
Seq. ID
                    LIB3177-099-P1-K1-D7
Method
                   BLASTX
NCBI GI
                    g4218123
BLAST score
                    239
E value
                    3.0e-20
Match length
                    101
% identity
                    52
NCBI Description (AL035353) photosystem I subunit PSI-E-like protein
                    [Arabidopsis thaliana]
Seq. No.
                    166199
Seq. ID
                    LIB3177-099-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    q2130028
```

Method BLASTX
NCBI GI g2130028
BLAST score 352
E value 2.0e-33
Match length 86
% identity 73

NCBI Description B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb CAA70936 (Y09805)

B12Dg1 [Hordeum vulgare]

Seq. No. 166200



LIB3177-099-P1-K1-D9 Seq. ID Method BLASTX NCBI GI g4454036 BLAST score 514 E value 2.0e-52 Match length 94. % identity 100 NCBI Description (AL035394) putative major latex protein [Arabidopsis thaliana] 166201 Seq. No. Seq. ID LIB3177-099-P1-K1-E1 Method BLASTX NCBI GI g2920839 BLAST score 299 E value 4.0e-27 101 Match length % identity 53 NCBI Description (U95136) Os-FIERG2 gene product [Oryza sativa] Seq. No. 166202 Seq. ID LIB3177-099-P1-K1-E10 Method BLASTX NCBI GI q3885943 BLAST score 483 E value 7.0e-49Match length 98 98 % identity NCBI Description (AF095455) PII protein [Arabidopsis thaliana] >gi_4558559 gb_AAD22652.1_AC007138 16 (AC007138) P II nitrogen sensing protein GLB I [Arabidopsis thaliana] Seq. No. 166203 Seq. ID LIB3177-099-P1-K1-E11 Method BLASTN NCBI GI g3386593 BLAST score 155 E value 1.0e-81 Match length 452 97 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 166204 Seq. ID LIB3177-099-P1-K1-E2 Method BLASTX q2213595 NCBI GI

Method BLASTX
NCBI GI g221359
BLAST score 535
E value 7.0e-55
Match length 121
% identity 87

NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No. 166205

Seq. ID LIB3177-099-P1-K1-E3

Method BLASTX NCBI GI g2446981



```
BLAST score 167
E value 4.0e-54
Match length 126
% identity 83
```

NCBI Description (AB005560) AtGDI2 [Arabidopsis thaliana]

>gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis

thaliana]

Seq. No. 166206

Seq. ID LIB3177-099-P1-K1-E5

Method BLASTX
NCBI GI g3257003
BLAST score 170
E value 6.0e-12
Match length 88
% identity 39

NCBI Description (AP000002) 376aa long hypothetical dehydrogenase

[Pyrococcus horikoshii]

Seq. No. 166207

Seq. ID LIB3177-099-P1-K1-E6

Method BLASTX
NCBI GI g1169278
BLAST score 305
E value 7.0e-28
Match length 75
% identity 84

NCBI Description DEHYDRIN ERD14 >qi 556474 dbj BAA04569 (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 166208

Seq. ID LIB3177-099-P1-K1-E7

Method BLASTX
NCBI GI g544134
BLAST score 191
E value 7.0e-16
Match length 77
% identity 57

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR

>gi_99720_pir__S22863 hypothetical protein - Arabidopsis
thaliana >gi_421844_pir__A46260 RecA functional analog

DRT100 - Arabidopsis thaliana (fragment)

Seq. No. 166209

Seq. ID LIB3177-099-P1-K1-E8

Method BLASTX
NCBI GI g115767
BLAST score 621
E value 6.0e-65
Match length 122
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372 emb CAA27541 (X03908) chlorophyll a/b binding



protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 166210

Seq. ID LIB3177-099-P1-K1-F1

Method BLASTX
NCBI GI g1702986
BLAST score 533
E value 1.0e-54
Match length 125
% identity 86

NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi

isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14

chi chain [Arabidopsis thaliana]

Seq. No. 166211

Seq. ID LIB3177-099-P1-K1-F10

Method BLASTN
NCBI GI g2351073
BLAST score 291
E value 1.0e-163
Match length 450
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 166212

Seq. ID LIB3177-099-P1-K1-F11

Method BLASTX
NCBI GI g2497886
BLAST score 300
E value 3.0e-27
Match length 54
% identity 100

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)

>gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis
thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis

thaliana]

Seq. No. 166213

Seq. ID LIB3177-099-P1-K1-F12

Method BLASTX
NCBI GI g2286069
BLAST score 547
E value 3.0e-56
Match length 118
% identity 88

NCBI Description (U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No. 166214

Seq. ID LIB3177-099-P1-K1-F2

Method BLASTX
NCBI GI g3953473
BLAST score 49
E value 3.0e-72
Match length 147
% identity 99

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]



```
Seq. No.
                  166215
Seq. ID
                  LIB3177-099-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2129533
BLAST score
                  710
E value
                  3.0e-75
Match length
                  146
% identity
                  96
NCBI Description
                  adenine nucleotide translocase - Arabidopsis thaliana
                  >gi_1051109_emb_CAA89201_ (Z49227) adenine nucleotide
                  translocase [Arabidopsis thaliana]
Seq. No.
                  166216
Seq. ID
                  LIB3177-099-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g267136
BLAST score
                  442
E value
                  6.0e-44
Match length
                  117
% identity
                  74
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED
                  TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)
                  >gi_217869_dbj_BAA02520_ (D13254) transmembrane channel
                  protein [Arabidopsis thaliana] >gi_4371283_gb_AAD18141
                   (AC006260) putative plasma membrane intrinsic protein 2C
                   [Arabidopsis thaliana] >gi_384324 prf 1905411A
                  transmembrane channel [Arabidopsis thaliana]
Seq. No.
                  166217
Seq. ID
                  LIB3177-099-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g4589440
BLAST score
                  431
E value
                  0.0e + 00
Match length
                  452
```

% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSD21, complete sequence

Seq. No. 166218

Seq. ID LIB3177-099-P1-K1-F9

Method BLASTX NCBI GI g4741962 BLAST score 328 E value 6.0e-39 Match length 125 57 % identity

NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No. 166219

Seq. ID LIB3177-099-P1-K1-G1

Method BLASTX NCBI GI g1769905 BLAST score 504 E value 4.0e-51 Match length 136



```
% identity
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                  166220
Seq. ID
                  LIB3177-099-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g99688
BLAST score
                  317
E value
                  2.0e-55
                  147
Match length
                  80
% identity
NCBI Description
                  translation elongation factor eEF-1 alpha chain (gene A4) -
                  Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                  166221
Seq. ID
                  LIB3177-099-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g4263712
BLAST score
                  453
E value
                  3.0e-45
Match length
                  121
                  76
% identity
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
                  166222
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3763935
BLAST score
                  46
                  3.0e-72
E value
Match length
                  136
% identity
                  99
NCBI Description (AC004450) putative myb-related transcription factor
                  [Arabidopsis thaliana]
Seq. No.
                  166223
Seq. ID
                  LIB3177-099-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  281
E value
                  5.0e-25
Match length
                  75
% identity
                  73
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  166224
Seq. ID
                  LIB3177-099-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1710780
BLAST score
                  384
E value
                  4.0e-37
Match length
                  106
% identity
                  72
```

22376

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433



(X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No. 166225

Seq. ID LIB3177-099-P1-K1-G4

Method BLASTX
NCBI GI g2493318
BLAST score 339
E value 8.0e-32
Match length 138
% identity 52

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963

(Z25471) blue copper protein [Pisum sativum]

>gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]

Seq. No. 166226

Seq. ID LIB3177-099-P1-K1-G6

Method BLASTX
NCBI GI 94204268
BLAST score 790
E value 1.0e-84
Match length 145
% identity 99

NCBI Description (AC005223) 62134 [Arabidopsis thaliana]

Seq. No. 166227

Seq. ID LIB3177-099-P1-K1-G7

Method BLASTX
NCBI GI g3201633
BLAST score 342
E value 8.0e-33
Match length 70

% identity 100

NCBI Description (AC004669) putative cell division protein [Arabidopsis

thaliana]

Seq. No. 166228

Seq. ID LIB3177-099-P1-K1-G8

Method BLASTN
NCBI GI g4469002
BLAST score 422
E value 0.0e+00
Match length 445
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 166229

Seq. ID LIB3177-099-P1-K1-G9

Method BLASTX
NCBI GI g3024434
BLAST score 464
E value 2.0e-46
Match length 113
% identity 84

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi 2564337 dbj BAA22951





(D88663) Tat binding protein 1 [Brassica rapa]

Seq. No. 166230 Seq. ID LIB3177-099-P1-K1-H10 BLASTX Method NCBI GI g2446981 BLAST score 758 E value 6.0e-81 Match length 147 % identity 99 NCBI Description (AB005560) AtGDI2 [Arabidopsis thaliana] >gi 2569936 emb CAA04727 (AJ001397) GDI2 [Arabidopsis thaliana]

Seq. No. 166231

Seq. ID LIB3177-099-P1-K1-H12

Method BLASTX
NCBI GI g1053047
BLAST score 582
E value 3.0e-60
Match length 116
% identity 100

NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)

histone H3 [Glycine max] >gi 1053051 (U38427) histone H3

[Glycine max]

Seq. No. 166232

Seq. ID LIB3177-099-P1-K1-H2

Method BLASTX
NCBI GI g4539316
BLAST score 392
E value 5.0e-38
Match length 81
% identity 100

NCBI Description (AL035679) putative fructose-bisphosphate aldolase

[Arabidopsis thaliana]

Seq. No. 166233

Seq. ID LIB3177-099-P1-K1-H3

Method BLASTN
NCBI GI g2618602
BLAST score 167
E value 7.0e-89
Match length 446
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 166234

Seq. ID LIB3177-099-P1-K1-H4

Method BLASTN
NCBI GI g4006885
BLAST score 318
E value 1.0e-179
Match length 411
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

% identity

83



fragment No

```
166235
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g541799
BLAST score
                  197
                  1.0e-15
E value
                  38
Match length
                  97
% identity
NCBI Description light-harvesting chlorophyll a/b-binding protein - ginkgo
                  >gi 349443 (L23107) light-harvesting chlorophyll a/b
                  binding protein of photosystem II [Ginkgo biloba]
Seq. No.
                  166236
Seq. ID
                  LIB3177-099-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g3550981
BLAST score
                  148
E value
                  2.0e-77
                  400
Match length
% identity
                  100
NCBI Description Arabidopsis thaliana mutM homologue gene, complete cds
Seq. No.
                  166237
Seq. ID
                  LIB3177-099-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  730
E value
                  1.0e-77
Match length
                  140
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  166238
Seq. ID
                  LIB3234-001-P1-K1-A10
                  BLASTN
Method
NCBI GI
                  q1313927
BLAST score
                  55
E value
                  5.0e-22
Match length
                  219
% identity
                  82
NCBI Description B.oleracea mRNA for IFA binding protein (sp10)
                  166239
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g2645198
BLAST score
                  45
                  5.0e-16
E value
Match length
                  162
```

sequence, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic



```
Seq. No.
                  166240
Seq. ID
                  LIB3234-001-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  g4204298
BLAST score
                  565
E value
                  3.0e-58
Match length
                  145
% identity
                  77
NCBI Description (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
                  166241
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3983125
BLAST score
                  665
E value
                  5.0e-70
Match length
                  145
% identity
                  88
NCBI Description (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  166242
Seq. ID
                  LIB3234-001-P1-K1-A3
                  BLASTN
Method
NCBI GI
                  g4510360
BLAST score
                  89
E value
                  2.0e-42
Match length
                  326
% identity
                  88
NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  166243
Seq. ID
                  LIB3234-001-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g135858
BLAST score
                  353
E value
                  2.0e-33
Match length
                  69
                  100
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
                  >gi_99760_pir S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi 16182 emb CAA45114 (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                  thaliana] >gi 166623 (M84343) tonoplast intrinsic protein
                  [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast
                  intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                  166244
Seq. ID
                  LIB3234-001-P1-K1-A5
Method
                  BLASTN
```

Method BLASTN
NCBI GI g4220628
BLAST score 457
E value 0.0e+00
Match length 461

Match length

% identity

99

40



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24C1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166245
Seq. ID
                  LIB3234-001-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g3172156
BLAST score
                  393
                  0.0e+00
E value
Match length
                  449
% identity
                  96
                  Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166246
Seq. ID
                  LIB3234-001-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  312
E value
                  1.0e-175
Match length
                  393
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  166247
Seq. ID
                  LIB3234-001-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  221
E value
                  8.0e-18
Match length
                  84
% identity
                  64
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  166248
Seq. ID
                  LIB3234-001-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  g2828180
BLAST score
                  190
E value
                  1.0e-102
Match length
                  264
% identity
                  93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166249
Seq. ID
                  LIB3234-001-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4506223
BLAST score
                  191
E value
                  2.0e-14
```



```
NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
                  >gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit
                  p40.5 [Homo sapiens]
Seq. No.
                  166250
Seq. ID
                  LIB3234-001-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3236248
BLAST score
                  535
E value
                  9.0e-55
Match length
                  140
% identity
                  77
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166251
                  LIB3234-001-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914002
BLAST score
                  701
E value
                  3.0e-74
Match length
                  154
% identity
                  91
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >qi 2935279
                  (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                  166252
Seq. ID
                  LIB3234-001-P1-K1-B6
                  BLASTX
Method
NCBI GI
                  g1709379
BLAST score
                  489
E value
                  2.0e-49
Match length
                  115
% identity
                  78
NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
                  >gi_881441 (U27653) NADH-plastoquinone oxidoreductase
                  [Lupinus luteus]
                  166253
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2459446
BLAST score
                  626
E value
                  2.0e-65
Match length
                  137
% identity
                  89
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
Seq. No.
                  166254
```

Seq. ID LIB3234-001-P1-K1-B9

Method BLASTN NCBI GI q4519195 BLAST score 434 E value 0.0e+00Match length 438 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:



MQC12, complete sequence

Seq. No. 166255 Seq. ID LIB323

Seq. ID LIB3234-001-P1-K1-C1

Method BLASTX
NCBI GI g3335171
BLAST score 674
E value 5.0e-71
Match length 151
% identity 84

NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No. 166256

Seq. ID LIB3234-001-P1-K1-C10

Method BLASTN
NCBI GI g3540210
BLAST score 344
E value 0.0e+00
Match length 428
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166257

Seq. ID LIB3234-001-P1-K1-C11

Method BLASTX
NCBI GI g3025445
BLAST score 164
E value 3.0e-11
Match length 123
% identity 25

NCBI Description (AC004528) R32184 1 [Homo sapiens]

Seq. No. 166258

Seq. ID LIB3234-001-P1-K1-C2

Method BLASTX
NCBI GI g3935149
BLAST score 408
E value 7.0e-40
Match length 144
% identity 56

NCBI Description (AC005106) T25N20.13 [Arabidopsis thaliana]

Seq. No. 166259

Seq. ID LIB3234-001-P1-K1-C3

Method BLASTX
NCBI GI g131286
BLAST score 552
E value 9.0e-57
Match length 133
% identity 80

NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN PRECURSOR (P6

PROTEIN) (CP43) >gi_2144937_pir__F2SP44 photosystem II chlorophyll a-binding protein psbC - spinach chloroplast >gi_12281_emb_CAA25864_ (X01724) 44 kd reaction-centre protein [Spinacia oleracea] >gi_343362 (M36833) 44 kD

chlorophyll a apoprotein [Spinacia oleracea]



```
Seq. No.
                  166260
Seq. ID
                  LIB3234-001-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q4589420
BLAST score
                  377
E value
                  0.0e + 00
Match length
                  413
% identity
                  92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K3G17, complete sequence
Seq. No.
                  166261
Seq. ID
                  LIB3234-001-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  217
E value
                  2.0e-17
Match length
                  99
% identity
                  42
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                  166262
                  LIB3234-001-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2194126
BLAST score
                  515
E value
                  2.0e-52
Match length
                  118
% identity
                  86
NCBI Description (AC002062) EST gb T43335 comes from this gene. [Arabidopsis
                  thaliana]
                  166263
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4467131
BLAST score
                  439
E value
                  0.0e+00
Match length
                  455
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                  (ESSA project)
Seq. No.
                  166264
Seq. ID
                  LIB3234-001-P1-K1-D1
                  BLASTX
Method
NCBI GI
                  g3461848
BLAST score
                  111
                  2.0e-19
E value
Match length
                  106
```

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

% identity

Seq. No.

Seq. ID LIB3234-001-P1-K1-D10

166265

58

Method BLASTX

E value

Match length

5.0e-22

71



```
q4204299
NCBI GI
BLAST score
                  646
E value
                  8.0e-68
Match length
                  143
% identity
                  88
NCBI Description (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  166266
Seq. ID
                  LIB3234-001-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2062164
BLAST score
                  333
E value
                  4.0e-31
Match length
                  125
% identity
                  27
NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
                  166267
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g421929
BLAST score
                  516
E value
                  1.0e-52
Match length
                  110
% identity
                  14
NCBI Description ubiquitin - tomato > gi 312160 emb CAA51679 (X73156)
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                  166268
Seq. ID
                  LIB3234-001-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2462744
BLAST score
                  237
E value
                  8.0e-20
Match length
                  149
                  34
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
                  166269
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2244792
BLAST score
                  237
                  8.0e-20
E value
Match length
                  66
                  70
% identity
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]
                  166270
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q4558586
BLAST score
                  55
```

E value

Match length

% identity

9.0e-65

118

100



% identity NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence, complete sequence 166271 Seq. No. LIB3234-001-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g4585990 BLAST score 124 E value 1.0e-06 Match length 139 % identity 6 NCBI Description (AC005287) Very similar to disease resistance proteins [Arabidopsis thaliana] 166272 Seq. No. Seq. ID LIB3234-001-P1-K1-D9 Method BLASTX NCBI GI g3297819 BLAST score 323 E value 7.0e-30 Match length 104 % identity 65 NCBI Description (AL031032) protein kinase-like protein [Arabidopsis thaliana] Seq. No. 166273 Seq. ID LIB3234-001-P1-K1-E1 Method BLASTN NCBI GI g4220643 BLAST score 226 E value 1.0e-124 230 Match length % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana] Seq. No. 166274 Seq. ID LIB3234-001-P1-K1-E10 Method BLASTX NCBI GI g1169598 BLAST score 155 E value 2.0e-81 Match length 149 % identity 100 NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12 desaturase [Arabidopsis thaliana] Seq. No. 166275 Seq. ID LIB3234-001-P1-K1-E11 Method BLASTX NCBI GI g3273743 BLAST score 620



```
(AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi 3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
Seq. No.
                  166276
Seq. ID
                  LIB3234-001-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g4115915
BLAST score
                  266
E value
                  3.0e-23
                  112
Match length
% identity
                  47
NCBI Description (AF118222) contains similarity to Helix pomatia br-1
                  protein (GB: X96994) [Arabidopsis thaliana]
Seq. No.
                  166277
                  LIB3234-001-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4063737
BLAST score
                  415
E value
                  0.0e + 00
Match length
                  423
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166278
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-E3
                  BLASTX
Method
NCBI GI
                  g4163997
BLAST score
                  747
E value
                  1.0e-79
Match length
                  138
                  99
% identity
NCBI Description (AF087483) alpha-xylosidase precursor [Arabidopsis
                  thaliana]
                  166279
Seq. No.
Seq. ID
                  LIB3234-001-P1-K1-E5
                  BLASTX
Method
NCBI GI
                  g3935158
BLAST score
                  401
E value
                  5.0e-39
Match length
                  100
% identity
NCBI Description (AC004557) F17L21.1 [Arabidopsis thaliana]
Seq. No.
                  166280
Seq. ID
                  LIB3234-001-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2129641
BLAST score
                  164
E value
                  2.0e-79
Match length
                  147
% identity
                  99
```

>gi 1107493 emb CAA63026 (X91960) major latex protein

NCBI Description major latex protein type 1 - Arabidopsis thaliana

Method

NCBI GI

BLASTX

q4557060



typel [Arabidopsis thaliana]

```
166281
Seq. No.
Seq. ID
                    LIB3234-001-P1-K1-E8
Method
                    BLASTX
NCBI GI
                    g2281082
BLAST score
                    324
E value
                    5.0e-30
                    80
Match length
% identity
                    80
NCBI Description (AC002333) polygalacturonase isolog, 3' partial
                    [Arabidopsis thaliana]
Seq. No.
                    166282
Seq. ID
                    LIB3234-001-P1-K1-E9
Method
                    BLASTX
NCBI GI
                    g1345973
BLAST score
                    337
E value
                    2.0e-35
Match length
                    94
                    80
% identity
NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                    >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                    omega-3 fatty acid desaturase [Arabidopsis thaliana]
                    >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                    microsomal omega-3 fatty acid desaturase [Arabidopsis
                    thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                    desaturase [Arabidopsis thaliana]
                    166283
Seq. No.
Seq. ID
                    LIB3234-001-P1-K1-F1
Method
                   BLASTX
NCBI GI
                    g4678299
BLAST score
                    711
E value
                    2.0e-75
Match length
                    140
% identity
                    99
NCBI Description (ALO49655) cysteine proteinase precursor-like protein
                    [Arabidopsis thaliana]
Seq. No.
                    166284
Seq. ID
                    LIB3234-001-P1-K1-F10
Method
                    BLASTN
NCBI GI
                    q4756963
BLAST score
                    100
E value
                    3.0e-49
Match length
                    140
% identity
                    93
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                    (ESSA project)
Seq. No.
                    166285
Seq. ID
                    LIB3234-001-P1-K1-F11
```



```
BLAST score
                   146
                   9.0e-46
E value
                   107
Match length
                   93
% identity
NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'
                   partial [Arabidopsis thaliana]
Seq. No.
                   166286
                   LIB3234-001-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245109
BLAST score
                   668
E value
                   2.0e-70
Match length
                   130
                   99
% identity
NCBI Description (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
                   thaliana]
Seq. No.
                   166287
Seq. ID
                   LIB3234-001-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   g3047100
BLAST score
                   392
E value
                   0.0e + 00
Match length
                   408
                   99
% identity
NCBI Description Arabidopsis thaliana BAC F6N23
Seq. No.
                   166288
Seq. ID
                   LIB3234-001-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   g3309259
BLAST score
                   215
E value
                   1.0e-117
Match length
                   398
% identity
                   87
NCBI Description Arabidopsis thaliana BAC F4H6, chromosome IV, complete
                   sequence
Seq. No.
                   166289
Seq. ID
                   LIB3234-001-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g1703108
BLAST score
                   520
E value
                   5.0e-53
                   97
Match length
% identity
                   98
NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
```

Seq. No. 166290

Seq. ID LIB3234-001-P1-K1-F8

Method BLASTX NCBI GI g131360



BLAST score 241 E value 3.0e-20 Match length 61 % identity 80

NCBI Description PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR

>gi_81727_pir__S02115 photosystem II protein psbK precursor

- white mustard chloroplast >gi_12209_emb_CAA31909_(X13558) K preprotein (AA -24 to 37) [Sinapis alba]

Seq. No. 166291

Seq. ID LIB3234-001-P1-K1-F9

Method BLASTX
NCBI GI g266693
BLAST score 593
E value 1.0e-61
Match length 141
% identity 84

NCBI Description OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis

thaliana >gl 16405 emb CAA44225 (X62353) oleosin [Arabidopsis thaliana] >gl 4455257 emb CAB36756.1 (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 166292

Seq. ID LIB3234-001-P1-K1-G1

Method BLASTN
NCBI GI 94757403
BLAST score 258
E value 1.0e-143
Match length 459
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJL12, complete sequence

Seq. No. 166293

Seq. ID LIB3234-001-P1-K1-G11

Method BLASTN
NCBI GI g4263813
BLAST score 344
E value 0.0e+00
Match length 360

NCBI Description Arabidopsis thaliana chromosome II BAC T13P21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166294

% identity

Seq. ID LIB3234-001-P1-K1-G12

41

Method BLASTX
NCBI GI 94538963
BLAST score 557
E value 2.0e-57
Match length 137
% identity 62

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 166295

BLAST score

Match length

E value

382

410

0.0e + 00



```
Seq. ID
                    LIB3234-001-P1-K1-G2
                    BLASTX
 Method
 NCBI GI
                    g2664214
 BLAST score
                    764
 E value
                    1.0e-81
 Match length
                    149
                    99
 % identity
 NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]
 Seq. No.
                    166296
 Seq. ID
                    LIB3234-001-P1-K1-G3
 Method
                    BLASTX
 NCBI GI
                    g399013
 BLAST score
                    642
 E value
                    3.0e-67
 Match length
                    126
 % identity
                    100
 NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                    >gi 99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                    thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]
                    >gi_445607_prf__1909354A adenylate translocator
                    [Arabidopsis thaliana]
                    166297
 Seq. No.
 Seg. ID
                    LIB3234-001-P1-K1-G4
 Method
                    BLASTX
 NCBI GI
                    g112682
 BLAST score
                    656
 E value
                    6.0e-69
Match length
                    149
 % identity
                    83
                   12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
 NCBI Description
                    cruciferin precursor (CRB) - Arabidopsis thaliana
                    >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                    thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                    storage protein [Arabidopsis thaliana]
Seq. No.
                    166298
 Seq. ID
                    LIB3234-001-P1-K1-G5
 Method
                    BLASTX
 NCBI GI
                    g3402696
 BLAST score
                    436
 E value
                    4.0e-43
 Match length
                    120
                    77
 % identity
 NCBI Description (AC004261) putative ferrodoxin-dependent glutamate
                    synthase, 3' partial [Arabidopsis thaliana]
 Seq. No.
                    166299
                    LIB3234-001-P1-K1-G6
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g4159705
```



```
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                   166300
Seq. ID
                  LIB3234-001-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g2656028
BLAST score
                  440
E value
                  0.0e + 00
Match length
                  456
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNF13
Seq. No.
                  166301
Seq. ID
                  LIB3234-001-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1931639
BLAST score
                  185
E value
                  1.0e-13
Match length
                  62
% identity
                  58
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                  166302
Seq. ID
                  LIB3234-001-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2244884
BLAST score
                  376
E value
                  4.0e-36
Match length
                  138
% identity
                  55
NCBI Description (Z97338) glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                  166303
Seq. ID
                  LIB3234-001-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  71
E value
                  3.0e-32
Match length
                  113
% identity
                  97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                  (ESSAII project)
Seq. No.
                  166304
Seq. ID
                  LIB3234-001-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4375831
BLAST score
                  625
```

E value 3.0e-65 Match length 152 % identity 79

NCBI Description (AJ006960) peroxidase [Arabidopsis thaliana]

Seq. No. 166305



```
Seq. ID
                    LIB3234-001-P1-K1-H4
Method
                   BLASTX
NCBI GI
                    g112737
BLAST score
                    380
E value
                    9.0e-37
Match length
                   110
% identity
                    73
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                    PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                    (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
Seq. No.
                   166306
Seq. ID
                   LIB3234-001-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1170503
BLAST score
                   584
E value
                   2.0e-60
Match length
                   113
% identity
                   100
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                   >gi_322503_pir JC1452 translation initiation factor
                   eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                    (X65052) eukaryotic translation in \overline{\text{i}} tiation factor 4A-\overline{\text{1}}
                    [Arabidopsis thaliana]
Seq. No.
                   166307
Seq. ID
                   LIB3234-001-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q231586
BLAST score
                   289
E value
                   6.0e-26
Match length
                   118
% identity
                   56
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi 82027_pir__S20504 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
Seq. No.
                   166308
Seq. ID
                   LIB3234-001-P1-K1-H8
Method
                   BLASTX
```

NCBI GI q4539293 BLAST score 481 E value 2.0e-48 Match length 151 % identity

NCBI Description (AL049480) putative membrane transporter [Arabidopsis

thalianal

Seq. No. 166309

Seq. ID LIB3234-001-P1-K1-H9

Method BLASTX



```
NCBI GI
                  q4678299
BLAST score
                  697
E value
                  9.0e-74
Match length
                  140
% identity
                  98
NCBI Description
                 (AL049655) cysteine proteinase precursor-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  166310
Seq. ID
                  LIB3234-003-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q2924651
BLAST score
                  37
E value
                  2.0e-11
Match length
                  312
% identity
                  95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166311
Seq. ID
                  LIB3234-003-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4415909
BLAST score
                  504
E value
                  3.0e-51
Match length
                  122
                  27
% identity
NCBI Description (AC006282) LEA protein AtECP63 [Arabidopsis thaliana]
Seq. No.
                  166312
Seq. ID
                  LIB3234-003-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q4415909
BLAST score
                  91
E value
                  6.0e-03
Match length
                  96
% identity
NCBI Description (AC006282) LEA protein AtECP63 [Arabidopsis thaliana]
Seq. No.
                  166313
Seq. ID
                  LIB3234-003-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2651299
BLAST score
                  370
                  1.0e-35
E value
Match length
                  119
% identity
                  64
NCBI Description
                  (AC002336) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  166314
Seq. ID
                  LIB3234-003-P1-K1-B4
Method
                  BLASTN
```

Method BLASTN
NCBI GI g4220627
BLAST score 111
E value 1.0e-55
Match length 257



% identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.

166315

Seq. ID

LIB3234-003-P1-K1-B5

Method NCBI GI BLASTX

BLAST score

g2494261

E value

182

2.0e-13

Match length % identity

35 100

precursor - soybean chloroplast >gi_18776_emb_CAA46864_

elongation factor Tu [Glycine max]

Seq. No.

166316

Seq. ID

LIB3234-003-P1-K1-B7

Method

BLASTN

NCBI GI

g2656026

BLAST score

334

E value

0.0e + 00

Match length

359

% identity

98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDF20

Seq. No.

166317

Seq. ID

LIB3234-003-P1-K1-C3

Method

BLASTN

NCBI GI

g4263694

BLAST score

44

E value

2.0e-15

Match length

165 85

% identity

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. Seq. ID

166318

Method

LIB3234-003-P1-K1-C4

NCBI GI

BLASTN

g2088638

BLAST score

280

E value

1.0e-156

Match length

280

% identity

100 NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

166319

Seq. ID

LIB3234-003-P1-K1-C5

Method NCBI GI BLASTN

BLAST score

g4199934

273

E value

1.0e-152



Match length 347 % identity 92

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 166320

Seq. ID LIB3234-003-P1-K1-C6

Method BLASTX
NCBI GI g115783
BLAST score 532
E value 1.0e-54
Match length 104
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 166321

Seq. ID LIB3234-003-P1-K1-C8

Method BLASTN
NCBI GI g12218
BLAST score 229
E value 1.0e-126
Match length 360
% identity 91

NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly

Seq. No. 166322

Seq. ID LIB3234-003-P1-K1-D11

Method BLASTX
NCBI GI g2499236
BLAST score 356
E value 6.0e-34
Match length 90
% identity 82

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST

>gi 1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis

thalianal

Seq. No. 166323

Seq. ID LIB3234-003-P1-K1-D12

Method BLASTX
NCBI GI g1084336
BLAST score 234
E value 1.0e-19
Match length 44
% identity 98

NCBI Description chlorophyll a/b-binding protein type II - Arabidopsis

thaliana >gi_541565 (U03395) PSI type II chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 166324

Seq. ID LIB3234-003-P1-K1-D3

Method BLASTN NCBI GI g3643588 BLAST score 70



E value 3.0e-31 Match length 133 % identity 88 NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 166325 Seq. ID LIB3234-003-P1-K1-D4 Method BLASTN NCBI GI q2842474 BLAST score 348 E value 0.0e + 00Match length 368 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project) 166326 Seq. No. Seq. ID LIB3234-003-P1-K1-D5 Method BLASTN NCBI GI g3063438 BLAST score 95 E value 6.0e-46 Match length 251 % identity 84 NCBI Description Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana] Seq. No. 166327 Seq. ID LIB3234-003-P1-K1-D6 Method BLASTN NCBI GI g2281648 BLAST score 203 E value 1.0e-110 Match length 207 100 % identity NCBI Description Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds Seq. No. 166328 Seq. ID LIB3234-003-P1-K1-D7 BLASTN Method NCBI GI g972918 BLAST score 160 9.0e-85 E value Match length 256 91 % identity

NCBI Description Arabidopsis thaliana IAA8 (IAA8) gene complete cds

Seq. No. 166329

Seq. ID LIB3234-003-P1-K1-D8

Method BLASTX
NCBI GI g132074
BLAST score 576
E value 1.0e-59
Match length 117
% identity 94



```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  166330
Seq. No.
Seq. ID
                  LIB3234-003-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4678285
BLAST score
                  195
E value
                  5.0e-15
Match length
                  113
                  42
% identity
NCBI Description (AL049660) putative protein [Arabidopsis thaliana]
                  166331
Seq. No.
Seq. ID
                  LIB3234-003-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  q4056476
                  79
BLAST score
E value
                  2.0e-36
Match length
                  259
% identity
                  83
NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166332
Seq. ID
                  LIB3234-003-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g140292
BLAST score
                  387
E value
                  1.0e-37
                  88
Match length
                  86
% identity
NCBI Description HYPOTHETICAL 21.5 KD PROTEIN (ORF 184)
                  >gi 82208 pir A05197 hypothetical protein 184 - common
                  tobacco chloroplast >gi_11843 emb CAA77363 (Z00044)
                  hypothetical protein [Nicotiana tabacum]
                  >gi 225211 prf 1211235AR ORF 184 [Nicotiana tabacum]
Seq. No.
                  166333
Seq. ID
                  LIB3234-003-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2288887
BLAST score
                  214
E value
                  3.0e-17
                  87
Match length
% identity
NCBI Description
                 (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
                  thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                  [Arabidopsis thaliana]
```

Seq. No. 166334

Seq. ID LIB3234-003-P1-K1-E4

Method BLASTX

% identity

94

```
NCBI GI
                  g4138179
BLAST score
                  439
E value
                  1.0e-43
Match length
                  99
                  86
% identity
                  (AJ223969) elongation factor 1 alpha subunit [Malus
NCBI Description
                  domestica]
Seq. No.
                  166335
Seq. ID
                  LIB3234-003-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g4001805
BLAST score
                  180
E value
                  3.0e-13
Match length
                  99
% identity
                  40
NCBI Description (AF041476) BAF53a [Mus musculus]
Seq. No.
                  166336
Seq. ID
                  LIB3234-003-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4001805
BLAST score
                  142
E value
                  9.0e-09
Match length
                  57
% identity
                  51
NCBI Description (AF041476) BAF53a [Mus musculus]
Seq. No.
                  166337
Seq. ID
                  LIB3234-003-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  149
                  9.0e-10
E value
Match length
                  74
% identity
                  45
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  166338
Seq. ID
                  LIB3234-003-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g4589446
BLAST score
                  44
E value
                  1.0e-15
Match length
                  192
% identity
                  81
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T12B11, complete sequence
Seq. No.
                  166339
Seq. ID
                  LIB3234-003-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g3176693
BLAST score
                  258
E value
                  1.0e-143
                  338
Match length
```

Seq. ID



```
NCBI Description Arabidopsis thaliana chromosome I BAC T27I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166340
                  LIB3234-003-P1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1109698
BLAST score
                  55
E value
                  3.0e-22
Match length
                  210
% identity
                  85
NCBI Description A.thaliana mRNA for gibberellin 20-oxidase (1425 bp)
Seq. No.
                  166341
                  LIB3234-003-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1109698
BLAST score
                  32
E value
                  1.0e-08
Match length
                  88
% identity
                  84
NCBI Description A.thaliana mRNA for gibberellin 20-oxidase (1425 bp)
Seq. No.
                  166342
Seq. ID
                  LIB3234-003-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3023217
BLAST score
                  357
                  5.0e - 34
E value
                  93
Match length
                  84
% identity
NCBI Description 14-3-3-LIKE PROTEIN GF14 NU >gi_1531631 (U60445) GF14 nu
                  [Arabidopsis thaliana]
Seq. No.
                  166343
Seq. ID
                  LIB3234-003-P1-K1-H2
                  BLASTN
Method
NCBI GI
                  g12218
BLAST score
                  212
                  1.0e-116
E value
                  320
Match length
                  91
% identity
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly
Seq. No.
                  166344
Seq. ID
                  LIB3234-003-P1-K1-H4
                  BLASTN
Method
NCBI GI
                  q3335170
BLAST score
                  199
                  1.0e-108
E value
Match length
                  367
                  88
% identity
NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,
                  complete cds
                  166345
Seq. No.
```

22400

LIB3234-004-P1-K1-A1

Method

NCBI GI

BLASTN q4580386



```
Method
                   BLASTX
NCBI GI
                   q419757
BLAST score
                   613
E value
                   6.0e-64
Match length
                   146
% identity
                   84
                  ketol-acid reductoisomerase (EC 1.1.1.86) precursor -
NCBI Description
                  Arabidopsis thaliana
Seq. No.
                   166346
Seq. ID
                   LIB3234-004-P1-K1-A10
Method
                  BLASTX
NCBI GI
                   q2702279
BLAST score
                   125
E value
                   1.0e-63
Match length
                   129
                   99
% identity
NCBI Description
                   (AC003033) putative phosphate transporter [Arabidopsis
                   \verb|thaliana| > \verb|gi_2780345_dbj_BAA24280_ (AB000093) inorganic| \\
                  phosphate transporter [Arabidopsis thaliana] >gi 2914691
                   (AC003974) putative phosphate transporter [Arabidopsis
                   thaliana]
                   166347
Seq. No.
Seq. ID
                   LIB3234-004-P1-K1-A11
Method
                  BLASTX
NCBI GI
                   q4539005
BLAST score
                   125
E value
                   2.0e-22
Match length
                  116
% identity
                   44
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  166348
Seq. ID
                  LIB3234-004-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  g2500378
BLAST score
                   445
E value
                   4.0e-44
                  89
Match length
                   93
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                  166349
Seq. ID
                  LIB3234-004-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1657268
BLAST score
                   610
E value
                   2.0e-63
Match length
                  165
% identity
                   68
NCBI Description (Y07701) aminopeptidase [Homo sapiens]
Seq. No.
                  166350
Seq. ID
                  LIB3234-004-P1-K1-A3
```



BLAST score 36 E value 5.0e-11 Match length 60 % identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T8018 genomic

sequence, complete sequence

Seq. No. 166351

Seq. ID LIB3234-004-P1-K1-A4

Method BLASTX
NCBI GI g1262171
BLAST score 689
E value 9.0e-73
Match length 138
% identity 99

NCBI Description (U21557) phosphoprotein phosphatase 2A, regulatory subunit

A [Arabidopsis thaliana]

Seq. No. 166352

Seq. ID LIB3234-004-P1-K1-A5

Method BLASTX
NCBI GI g2864614
BLAST score 188
E value 5.0e-14
Match length 140
% identity 66

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 166353

Seq. ID LIB3234-004-P1-K1-A6

Method BLASTN
NCBI GI g4006885
BLAST score 154
E value 5.0e-81
Match length 505
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 166354

Seq. ID LIB3234-004-P1-K1-A8

Method BLASTX
NCBI GI g1169598
BLAST score 414
E value 9.0e-41
Match length 90
% identity 84

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No. 166355

Seq. ID LIB3234-004-P1-K1-A9

Method BLASTN
NCBI GI g4580386
BLAST score 60

E value 6.0e-25



Match length 159 % identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T8018 genomic

sequence, complete sequence

Seq. No. 166356

Seq. ID LIB3234-004-P1-K1-B1

Method BLASTN
NCBI GI g3522932
BLAST score 212
E value 1.0e-115
Match length 516
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166357

Seq. ID LIB3234-004-P1-K1-B10

Method BLASTX
NCBI GI g127041
BLAST score 542
E value 1.0e-55
Match length 109
% identity 95

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_81647_pir__JN0131 methionine adenosyltransferase (EC
2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 166358

Seq. ID LIB3234-004-P1-K1-B12

Method BLASTX
NCBI GI g3421102
BLAST score 77
E value 4.0e-44
Match length 91
% identity 95

NCBI Description (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis

thaliana]

Seq. No. 166359

Seq. ID LIB3234-004-P1-K1-B3

Method BLASTN
NCBI GI g4539402
BLAST score 292
E value 1.0e-163
Match length 477
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13

(ESSA project)

Seq. No. 166360

Seq. ID LIB3234-004-P1-K1-B4

Method BLASTX NCBI GI g118926 BLAST score 242



E value 3.0e-45Match length 167 % identity 55

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR

> >gi_320600 pir E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 166361

Seq. ID LIB3234-004-P1-K1-B6

Method BLASTX NCBI GI q1345967 BLAST score 360 E value 3.0e - 34Match length 112 % identity 64

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(VERSION 2) >gi_322649_pir__A44227 omega-3 fatty acid desaturase (EC 1.14.99.-) - rape >gi_167148 (L01418)

linoleic acid desaturase [Brassica napus]

Seq. No. 166362

Seq. ID LIB3234-004-P1-K1-B7

Method BLASTX NCBI GI q1477480 BLAST score 164 E value 2.0e-27 Match length 88

% identity 78

NCBI Description (U40341) carbamoyl phosphate synthetase large chain

[Arabidopsis thaliana]

Seq. No. 166363

Seq. ID LIB3234-004-P1-K1-B8

Method BLASTN NCBI GI q4490734 BLAST score 279 E value 1.0e-155 Match length 451 98 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 166364

Seq. ID LIB3234-004-P1-K1-C1

Method BLASTX NCBI GI g3695396 BLAST score 305 E value 2.0e-35 Match length 97 % identity

NCBI Description (AF096372) contains similarity to Arabidopsis thaliana

retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]

Seq. No. 166365



```
Seq. ID
                  LIB3234-004-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1657268
BLAST score
                  621
E value
                  8.0e-65
Match length
                  164
% identity
                  70
NCBI Description (Y07701) aminopeptidase [Homo sapiens]
Seq. No.
                  166366
Seq. ID
                  LIB3234-004-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q4581146
BLAST score
                  615
E value
                  4.0e-64
Match length
                  136
% identity
                  90
NCBI Description
                  (AC006919) putative fructose-bisphosphate aldolase,
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  166367
Seq. ID
                  LIB3234-004-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4589437
BLAST score
                  153
E value
                  2.0e-80
Match length
                  440
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MPN9, complete sequence
Seq. No.
                  166368
Seq. ID
                  LIB3234-004-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q1169476
BLAST score
                  733
E value
                  6.0e-78
Match length
                  143
% identity
                  99
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                  166369
Seq. ID
                  LIB3234-004-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g3702724
BLAST score
                  81
                  1.0e-37
E value
Match length
                  421
% identity
                  86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K17N15, complete sequence [Arabidopsis thaliana]
```

Seq. No. 166370

Seq. ID LIB3234-004-P1-K1-C7

Method BLASTN



```
NCBI GI g3128142
BLAST score 396
E value 0.0e+00
Match length 479
% identity 99
NCBI Description Arabidop
MQN23, c
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No. 166371

Seq. ID LIB3234-004-P1-K1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 396
E value 5.0e-39
Match length 74
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 166372

Seq. ID LIB3234-004-P1-K1-D1

Method BLASTX
NCBI GI g3953473
BLAST score 702
E value 3.0e-74
Match length 145
% identity 96

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 166373

Seq. ID LIB3234-004-P1-K1-D10

Method BLASTX
NCBI GI g3273743
BLAST score 354
E value 3.0e-54
Match length 116
% identity 96

NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis

thaliana] $>gi_3786019$ (AC005499) unknown protein

[Arabidopsis thaliana]

Seq. No. 166374

Seq. ID LIB3234-004-P1-K1-D2

Method BLASTN
NCBI GI g4159706
BLAST score 50
E value 5.0e-19
Match length 114

% identity 87
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 166375

Seq. ID LIB3234-004-P1-K1-D4

Method BLASTX NCBI GI g2213597



```
BLAST score
                  112
E value
                  2.0e-35
Match length
                  85
                  92
% identity
NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]
Seq. No.
                  166376
Seq. ID
                  LIB3234-004-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  g4371278
BLAST score
                  307
E value
                  1.0e-172
Match length
                  431
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic
```

sequence, complete sequence [Arabidopsis thaliana] Seq. No. 166377 LIB3234-004-P1-K1-E10

Seq. ID Method BLASTN NCBI GI g2760165 BLAST score 66 E value 7.0e-29 Match length 185 % identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. Seq. ID LIB3234-004-P1-K1-E11 Method BLASTX NCBI GI g2245136 BLAST score 141 E value 1.0e-50 Match length 156 67 % identity

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 166379

Seq. ID LIB3234-004-P1-K1-E3

166378

Method BLASTN NCBI GI g3128166 BLAST score 36 1.0e-10 E value Match length 192 % identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166380

Seq. ID LIB3234-004-P1-K1-F1

Method BLASTX NCBI GI g3540208 BLAST score 220 E value 9.0e-18 Match length 124



```
% identity
                 (AC004260) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   166381
Seq. ID
                   LIB3234-004-P1-K1-F11
Method
                  BLASTX
NCBI GI
                   q2160133
BLAST score
                   138
E value
                   3.0e-25
Match length
                  143
% identity
                   50
                  (AC000375) Strong similarity to Arabidopsis
NCBI Description
                   gb X91953, F19K23.3, F19K23.15. ESTs
                   gb_T21984,gb_ATTS0219,gb ATTS0207,gb T21984 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  166382
Seq. ID
                  LIB3234-004-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  225
E value
                  2.0e-36
Match length
                  100
% identity
                  74
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  166383
Seq. ID
                  LIB3234-004-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  g3366536
BLAST score
                  461
E value
                  0.0e+00
Match length
                  477
% identity
                  99
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T25N2O,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166384
Seq. ID
                  LIB3234-004-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  g4079614
BLAST score
                  381
E value
                  0.0e+00
Match length
                  492
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166385
Seq. ID
                  LIB3234-004-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q4586098
BLAST score
                  262
E value
                  1.0e-145
```

Match length 306 % identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13



(ESSA project)

Seq. No. 166386 Seq. ID LIB3234-004-P1-K1-G6 Method BLASTN NCBI GI g4262221 BLAST score 105 E value 5.0e-52 Match length 289 % identity 88 NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 166387 Seq. ID LIB3234-004-P1-K1-H11 Method BLASTN NCBI GI g4678705 BLAST score 370 E value 0.0e+00Match length 461 % identity 95 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project) Seq. No. 166388 Seq. ID LIB3234-004-P1-K1-H2 Method BLASTX NCBI GI g416911 BLAST score 88 5.0e-11 E value Match length 90 41 % identity NCBI Description DIPHTERIA TOXIN RESISTANCE PROTEIN 2 >gi 419830 pir S34679 diphthamide synthesis protein DPH2 - yeast (Saccharomyces cerevisiae) >gi_296987 emb CAA49420 (X69765) diphtheria toxin resistance [Saccharomyces cerevisiae] >gi_395234_emb_CAA52247_ (X74151) orf1 [Saccharomyces
cerevisiae] >gi_486339_emb_CAA82035_ (Z28191) ORF YKL191w [Saccharomyces cerevisiae] >gi 765109 (L01424) diphthamide [Saccharomyces cerevisiae] 166389 Seq. No. Seq. ID LIB3234-004-P1-K1-H4 Method BLASTX NCBI GI g2129659 BLAST score 213 E value 5.0e-17 Match length 146 % identity 36 NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No. 166390

Seq. ID LIB3234-004-P1-K1-H5

Method BLASTN NCBI GI g2689438 BLAST score 45



E value 2.0e-16 Match length 183 % identity 86

NCBI Description Arabidopsis thaliana BAC F2401 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No. 166391

Seq. ID LIB3234-006-P1-K1-A10

Method BLASTX
NCBI GI g66179
BLAST score 532
E value 2.0e-54
Match length 119
% identity 82

NCBI Description NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -

common tobacco chloroplast >gi_225255_prf__1211235CP NADH

dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. No. 166392

Seq. ID LIB3234-006-P1-K1-A11

Method BLASTN
NCBI GI g4159712
BLAST score 114
E value 2.0e-57
Match length 230
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 166393

Seq. ID LIB3234-006-P1-K1-A2

Method BLASTX
NCBI GI g3063449
BLAST score 451
E value 3.0e-45
Match length 98
% identity 92

NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]

Seq. No. 166394

Seq. ID LIB3234-006-P1-K1-A4

Method BLASTN
NCBI GI g4539378
BLAST score 230
E value 1.0e-126
Match length 384
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 166395

Seq. ID LIB3234-006-P1-K1-A5

Method BLASTX
NCBI GI g131336
BLAST score 330
E value 8.0e-31
Match length 72



```
% identity
NCBI Description
                    PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
                    photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
>gi_225225_prf__1211235BG photosystem II 10kD
                    phosphoprotein [Nicotiana tabacum]
Seq. No.
                    166396
Seq. ID
                    LIB3234-006-P1-K1-A6
Method
                    BLASTX
NCBI GI
                    q4056502
BLAST score
                    586
E value
                    7.0e-61
Match length
                    126
% identity
                    95
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                    166397
Seq. ID
                    LIB3234-006-P1-K1-A7
Method
                    BLASTX
NCBI GI
                    g3063449
BLAST score
                    582
E value
                    2.0e-60
Match length
                    124
% identity
                    94
NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]
Seq. No.
                    166398
Seq. ID
                    LIB3234-006-P1-K1-A8
Method
                    BLASTN
NCBI GI
                    q3063438
BLAST score
                    105
E value
                    2.0e-52
Match length
                    140
                    97
% identity
NCBI Description Complete sequence of Arabidopsis F22013, complete sequence
                    [Arabidopsis thaliana]
Seq. No.
                    166399
Seq. ID
                    LIB3234-006-P1-K1-A9
Method
                    BLASTX
NCBI GI
                    g1695717
BLAST score
                    492
E value
                    7.0e-50
Match length
                   123
% identity
NCBI Description
                  (D89341) luminal binding protein [Arabidopsis thaliana]
Seq. No.
                   166400
                   LIB3234-006-P1-K1-B1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4006815
BLAST score
                    67
```

3.0e-29 Match length 141

% identity 86

E value



```
NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166401
                  LIB3234-006-P1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g511598
BLAST score
                  122
E value
                  4.0e-62
Match length
                  301
% identity
                  64
NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,
                  complete cds
                  166402
Seq. No.
Seq. ID
                  LIB3234-006-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g625977
BLAST score
                  424
E value
                  7.0e-42
Match length
                  94
                  85
% identity
NCBI Description p40 protein homolog - Arabidopsis thaliana >qi 402904
                  (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  166403
Seq. ID
                  LIB3234-006-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g4091806
BLAST score
                  95
E value
                  2.0e-03
Match length
                  86
% identity
                  27
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                  166404
Seq. ID
                  LIB3234-006-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4490734
BLAST score
                  36
E value
                  4.0e-11
Match length
                  206
% identity
                  80
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                  project)
Seq. No.
                  166405
Seq. ID
                  LIB3234-006-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4263771
```

Method BLASTX
NCBI GI 9426377
BLAST score 227
E value 9.0e-19
Match length 64
% identity 66

NCBI Description (AC006218) putative nonspecific lipid-transfer protein

precursor [Arabidopsis thaliana]



>gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
nonspecific lipid-transfer protein precursor [Arabidopsis
thaliana]

Seq. No. 166406

Seq. ID LIB3234-006-P1-K1-B5

Method BLASTN
NCBI GI g3510336
BLAST score 207
E value 1.0e-113
Match length 388
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 166407

Seq. ID LIB3234-006-P1-K1-B6

Method BLASTX
NCBI GI g2160164
BLAST score 209
E value 1.0e-16
Match length 125
% identity 48

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 166408

Seq. ID LIB3234-006-P1-K1-B7

Method BLASTN
NCBI GI g4159701
BLAST score 152
E value 6.0e-80
Match length 330
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence

Seq. No. 166409

Seq. ID LIB3234-006-P1-K1-B8

Method BLASTX
NCBI GI 9730645
BLAST score 396
E value 1.0e-38
Match length 93
% identity 87

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seg. No. 166410

Seq. ID LIB3234-006-P1-K1-C10

Method BLASTX NCBI GI g2129659



BLAST score 358 4.0e-34 E value 118 Match length 60 % identity oleosin, isoform 21K - Arabidopsis thaliana >gi 725260 NCBI Description (L40954) oleosin [Arabidopsis thaliana] 166411 Seq. No. Seq. ID LIB3234-006-P1-K1-C11 BLASTX Method NCBI GI q1109600 BLAST score 657 3.0e-69 E value Match length 123 % identity 100 (D16628) ATsEH [Arabidopsis thaliana] >gi 2760840 NCBI Description (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana] 166412 Seq. No. Seq. ID LIB3234-006-P1-K1-C12 Method BLASTN NCBI GI q2618600 BLAST score 265 E value 1.0e-147 Match length 382 % identity 92 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana] 166413 Seq. No. LIB3234-006-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g2160186 BLAST score 332 E value 4.0e-31 77 Match length 87 % identity NCBI Description (AC000132) Identical to A. thaliana HEMA2 (gb_U27118). [Arabidopsis thaliana] Seq. No. 166414 Seq. ID LIB3234-006-P1-K1-C4 Method BLASTN NCBI GI g511598 BLAST score 342 E value 0.0e+00Match length 358 32 % identity NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,

complete cds

166415 Seq. No.

Seq. ID LIB3234-006-P1-K1-C5

Method BLASTX NCBI GI q1628583 BLAST score 212 4.0e-17 E value



Match length 47 % identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 166416

Seq. ID LIB3234-006-P1-K1-C6

Method BLASTN
NCBI GI g3241927
BLAST score 211
E value 1.0e-115
Match length 381
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 166417

Seq. ID LIB3234-006-P1-K1-C8

Method BLASTX
NCBI GI g1346263
BLAST score 400
E value 5.0e-39
Match length 82
% identity 98

NCBI Description GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)

>gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor
- Arabidopsis thaliana >gi_1049057 (U27118) glutamyl-tRNA

reductase [Arabidopsis thaliana]

Seq. No. 166418

Seq. ID LIB3234-006-P1-K1-D1

Method BLASTN
NCBI GI g2842474
BLAST score 161
E value 1.0e-85
Match length 180
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 166419

Seq. ID LIB3234-006-P1-K1-D10

Method BLASTN
NCBI GI g2656025
BLAST score 149
E value 3.0e-78
Match length 201

% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCD7

Seq. No. 166420

Seq. ID LIB3234-006-P1-K1-D12

Method BLASTX NCBI GI g4773906 BLAST score 423



```
1.0e-41
E value
Match length
                   92
% identity
                   89
                   (AF074021) putative symbiosis-related protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166421
Seq. ID
                   LIB3234-006-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   q4580381
BLAST score
                   181
E value
                   2.0e-97
Match length
                   305
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T11P11 genomic
                   sequence, complete sequence
Seq. No.
                   166422
Seq. ID
                   LIB3234-006-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q2924729
BLAST score
                   40
E value
                   4.0e-13
Match length
                   72
% identity
                   89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNA5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166423
Seq. ID
                   LIB3234-006-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2330885
BLAST score
                   205
                   3.0e-16
E value
Match length
                   123
                   39
% identity
NCBI Description (AJ000486) methionine gamma-lyase [Trichomonas vaginalis]
Seq. No.
                   166424
Seq. ID
                   LIB3234-006-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   g4756963
BLAST score
                   318
E value
                   1.0e-179
Match length
                   338
                   99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   166425
Seq. ID
                   LIB3234-006-P1-K1-E10
```

Method BLASTX NCBI GI g1172498 BLAST score 655 E value 6.0e-69 Match length 126 74 % identity



```
PHYTOCHROME E >gi_1076376_pir__S46313 phytochrome E - Arabidopsis thaliana >gi_452817_emb_CAA54075_ (X76610)
NCBI Description
                   phytochrome E [Arabidopsis thaliana]
                   166426
Seq. No.
                   LIB3234-006-P1-K1-E2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2213606
BLAST score
                   372
E value
                   0.0e+00
Match length
                   380
                   99
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,
                   complete sequence [Arabidopsis thaliana]
                   166427
Seq. No.
Seq. ID
                   LIB3234-006-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   g2673901
BLAST score
                   337
E value
                   0.0e + 00
Match length
                   353
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   166428
Seq. No.
                   LIB3234-006-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3808062
BLAST score
                   155
                   3.0e-10
E value
Match length
                   64
% identity
                   45
NCBI Description (AB019195) PV100 [Cucurbita maxima]
                   166429
Seq. No.
Seq. ID
                   LIB3234-006-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g4510397
BLAST score
                   662
E value
                   9.0e-70
                   126
Match length
                   99
% identity
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                   166430
Seq. ID
                   LIB3234-006-P1-K1-F1
Method
                   BLASTN
                   g3449326
```

NCBI GI 34 BLAST score E value 1.0e-09 54 Match length 91 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M22, complete sequence [Arabidopsis thaliana]

% identity

100 NCBI Description petB2 gene [Pisum sativum]



```
Seq. No.
                  166431
Seq. ID
                  LIB3234-006-P1-K1-F10
Method
                  BLASTX
                  g2894574
NCBI GI
BLAST score
                  623
E value
                  3.0e-65
                  127
Match length
% identity
                  97
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                  >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
                  166432
Seq. No.
Seq. ID
                  LIB3234-006-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3169175
BLAST score
                  153
E value
                  5.0e-10
Match length
                  41
% identity
                  66
NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
Seq. No.
                  166433
Seq. ID
                  LIB3234-006-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2129658
BLAST score
                  319
E value
                  1.0e-29
Match length
                  116
                  56
% identity
NCBI Description oleosin type 2 - Arabidopsis thaliana
                  >gi_1107497_emb_CAA63022 (X91956) oleosin type2
                  [Arabidopsis thaliana]
Seq. No.
                  166434
Seq. ID
                  LIB3234-006-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q4325282
BLAST score
                  290
E value
                   4.0e-26
                  56
Match length
                  93
% identity
NCBI Description
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                  >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                  166435
Seq. No.
Seq. ID
                  LIB3234-006-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g226996
BLAST score
                  330
E value
                  7.0e-31
Match length
                  61
```



```
Seq. No.
                  166436
Seq. ID
                  LIB3234-006-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  629
E value
                  7.0e-66
Match length
                  125
% identity
                  98
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  166437
Seq. ID
                  LIB3234-006-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g4150874
BLAST score
                  145
E value
                  1.0e-09
Match length
                  69
                  39
% identity
NCBI Description (AJ011848) ndhD gene product [Hordeum vulgare]
Seq. No.
                  166438
Seq. ID
                  LIB3234-006-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  q4589439
BLAST score
                  144
E value
                  3.0e-75
Match length
                  304
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQM1, complete sequence
Seq. No.
                  166439
Seq. ID
                  LIB3234-006-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g12279
BLAST score
                  34
E value
                  1.0e-09
Match length
                  42
                  95
% identity
NCBI Description
                  Spinach chloroplast genes for the D2 and 44 kd reaction
                  centre, chlorophyll a-binding protein and for tRNA-Ser
                  (UGA)
Seq. No.
                  166440
Seq. ID
                  LIB3234-006-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q4455342
BLAST score
                  360
E value
                  2.0e-34
Match length
                  122
% identity
NCBI Description
                  (AL035522) O-methyltransferase-like protein [Arabidopsis
                  thaliana]
```

166441

LIB3234-006-P1-K1-H1

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g3935149
BLAST score
                  627
E value
                  1.0e-65
                  127
Match length
% identity
                  98
NCBI Description (AC005106) T25N20.13 [Arabidopsis thaliana]
Seq. No.
                  166442
Seq. ID
                  LIB3234-006-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4587532
BLAST score
                  333
E value
                  4.0e-31
                  113
Match length
                  57
% identity
NCBI Description
                 (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                  gb AC004238. This gene
                  166443
Seq. No.
Seq. ID
                  LIB3234-006-P1-K1-H11
Method
                  BLASTN
                  g2924651
NCBI GI
BLAST score
                  131
                  2.0e-67
E value
Match length
                  329
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
                  166444
Seq. No.
Seq. ID
                  LIB3234-006-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4406775
BLAST score
                  190
E value
                  2.0e-14
Match length
                  106
% identity
                  35
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166445
Seq. ID
                  LIB3234-006-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q1109699
BLAST score
                  530
E value
                  3.0e-54
Match length
                  101
% identity
                  100
NCBI Description (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
                  166446
Seq. No.
```

Seq. ID LIB3234-006-P1-K1-H3

Method BLASTX
NCBI GI g112682
BLAST score 591
E value 2.0e-61



Match length 118 % identity 95

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 166447

Seq. ID LIB3234-006-P1-K1-H4

Method BLASTN
NCBI GI g2827538
BLAST score 370
E value 0.0e+00
Match length 390
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17

(ESSAII project)

Seq. No. 166448

Seq. ID LIB3234-006-P1-K1-H5

Method BLASTN
NCBI GI g408482
BLAST score 44
E value 2.0e-15
Match length 195
% identity 90

NCBI Description Arabidopsis thaliana chloroplast omega-r fatty acid

desaturase gene, complete cds

Seq. No. 166449

Seq. ID LIB3234-006-P1-K1-H7

Method BLASTN
NCBI GI g4733953
BLAST score 226
E value 1.0e-124
Match length 304
% identity 95

NCBI Description Arabidopsis thaliana chromosome I BAC F13011 genomic

sequence, complete sequence

Seq. No. 166450

Seq. ID LIB3234-006-P1-K1-H8

Method BLASTX
NCBI GI g1076632
BLAST score 544
E value 6.0e-56
Match length 126
% identity 81

NCBI Description protein kinase - common tobacco >gi_506534_emb_CAA50374_

(X71057) protein kinase [Nicotiana tabacum]

Seq. No. 166451

Seq. ID LIB3234-006-P1-K1-H9

Method BLASTN NCBI GI g2160689 BLAST score 312



```
1.0e-175
E value
Match length
                  320
                  99
% identity
NCBI Description Arabidopsis thaliana B' regulatory subunit of PP2A
                  (AtB'alpha) mRNA, complete cds
Seq. No.
                  166452
Seq. ID
                  LIB3234-008-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q633890
BLAST score
                  241
E value
                  9.0e-21
                  75
Match length
% identity
                  65
NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  166453
Seq. ID
                  LIB3234-008-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g3600045
BLAST score
                  121
E value
                  2.0e-61
Match length
                  370
% identity
                  94
NCBI Description Arabidopsis thaliana BAC F2P3
Seq. No.
                  166454
                  LIB3234-008-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860247
BLAST score
                  558
E value
                  1.0e-57
Match length
                  107
% identity
                  96
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166455
Seq. ID
                  LIB3234-008-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q1419388
BLAST score
                  340
E value
                  5.0e-32
Match length
                  75
% identity
                  84
NCBI Description (X98925) stromal ascorbate peroxidase [Arabidopsis
                  thaliana]
Seq. No.
                  166456
Seq. ID
                  LIB3234-008-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g116527
BLAST score
                  460
```

E value 4.0e-46Match length 97 % identity 88

NCBI Description PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)



>gi_1143166 (U32397) ClpP protease [Nicotiana tabacum]
>gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease
proteolytic subuni [Nicotiana tabacum]

Seq. No. 166457 Seq. ID LIB3234-008-P1-K1-A5

Method BLASTX
NCBI GI g2245006
BLAST score 218
E value 1.0e-17
Match length 87
% identity 49

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 166458

Seq. ID LIB3234-008-P1-K1-A6

Method BLASTX
NCBI GI g2577957
BLAST score 448
E value 1.0e-44
Match length 122
% identity 73

NCBI Description (AJ002473) ABI3 protein [Arabidopsis thaliana]

Seq. No. 166459

Seq. ID LIB3234-008-P1-K1-A7

Method BLASTX
NCBI GI g1345973
BLAST score 425
E value 5.0e-42
Match length 96
% identity 81

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 166460

Seq. ID LIB3234-008-P1-K1-A8

Method BLASTX
NCBI GI g3002603
BLAST score 238
E value 2.0e-30
Match length 86
% identity 79

NCBI Description (AF033679) histone H3 [Bellamya heudi guangdungensis]

Seq. No. 166461

Seq. ID LIB3234-008-P1-K1-A9

Method BLASTN
NCBI GI g3176695
BLAST score 315



1.0e-177 E value Match length 331 % identity 52

NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic

sequence contains phyA marker, complete sequence

[Arabidopsis thaliana]

Seq. No. 166462

Seq. ID LIB3234-008-P1-K1-B10

Method BLASTN NCBI GI q3047100 BLAST score 325 E value 0.0e + 00Match length 359 97 % identity

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 166463

Seq. ID LIB3234-008-P1-K1-B12

Method BLASTN NCBI GI g3241916 BLAST score 346 E value 0.0e + 00Match length 374 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15N18, complete sequence [Arabidopsis thaliana]

Seq. No. Seq. ID 166464

LIB3234-008-P1-K1-B4

Method BLASTX NCBI GI g112682 BLAST score 641 E value 2.0e-67 Match length 122 % identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 166465

Seq. ID LIB3234-008-P1-K1-B5 Method

BLASTN

NCBI GI g4006815 87 BLAST score E value 3.0e-41Match length 250 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic

sequence, complete sequence [Arabidopsis thaliana]

~Seq. No. 166466

Seq. ID LIB3234-008-P1-K1-B6

Method BLASTN NCBI GI g2252848



BLAST score E value 1.0e-09 Match length 165 85 % identity NCBI Description Arabidopsis thaliana BAC TM018A10 Seq. No. 166467 Seq. ID LIB3234-008-P1-K1-B9 Method BLASTN NCBI GI g2244870 BLAST score 364 E value 0.0e+00Match length 376 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No 166468 Seq. No. Seq. ID LIB3234-008-P1-K1-C1 Method BLASTX NCBI GI g2959734 BLAST score 345 E value 1.0e-32 Match length 88 % identity 78 NCBI Description (Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana] Seq. No. 166469 Seq. ID LIB3234-008-P1-K1-C12 Method BLASTN NCBI GI g12216 BLAST score 240 E value 1.0e-132 Match length 316 94 % identity NCBI Description Sinapis alba chloroplast rps16 gene Seq. No. 166470 Seq. ID LIB3234-008-P1-K1-C2 Method BLASTN NCBI GI g4699904 BLAST score 320 E value 1.0e-180 Match length 374 90 % identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,

complete sequence

Seq. No. 166471

Seq. ID LIB3234-008-P1-K1-C3

Method BLASTN NCBI GI g4581161 BLAST score 75 E value 4.0e-34

Match length 242 % identity 23



NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No. 166472

LIB3234-008-P1-K1-C4 Seq. ID

Method BLASTN NCBI GI g4510360 BLAST score 352 E value 0.0e+00Match length 368 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 166473

Seq. ID LIB3234-008-P1-K1-C5

Method BLASTX NCBI GI g1107501 BLAST score 386 E value 2.0e-37 Match length 99 80 % identity

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No. 166474

Seq. ID LIB3234-008-P1-K1-C7

Method BLASTX NCBI GI g112740 BLAST score 236 E value 8.0e-20 Match length 112 % identity 50

NCBI Description NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)

>gi 81691 pir A25997 napin precursor (napA) - rape

>gi 167153 (J02586) prepronapin [Brassica napus] >gi_167155

(J02798) napin [Brassica napus]

Seq. No. 166475

Seq. ID LIB3234-008-P1-K1-C9

Method BLASTX NCBI GI g4204299 BLAST score 629 E value 6.0e-66 Match length 124 % identity 96

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

166476 Seq. No.

Seq. ID LIB3234-008-P1-K1-D1

Method BLASTX NCBI GI q1107501 BLAST score 371

E value 1.0e-35



Match length 111 % identity 68

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs
gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 166477

Seq. ID LIB3234-008-P1-K1-D10

Method BLASTN
NCBI GI 94519195
BLAST score 339
E value 0.0e+00
Match length 355
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MQC12, complete sequence

Seq. No. 166478

Seq. ID LIB3234-008-P1-K1-D11

Method BLASTX
NCBI GI g112682
BLAST score 590
E value 2.0e-61
Match length 117
% identity 96

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 166479

Seq. ID LIB3234-008-P1-K1-D2

Method BLASTX
NCBI GI g3808062
BLAST score 155
E value 3.0e-10
Match length 64
% identity 45

NCBI Description (AB019195) PV100 [Cucurbita maxima]

Seq. No. 166480

Seq. ID LIB3234-008-P1-K1-D3

Method BLASTX
NCBI GI g2459417
BLAST score 626
E value 1.0e-65
Match length 125
% identity 98

NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19

[Arabidopsis thaliana]

Seq. No. 166481

Seq. ID LIB3234-008-P1-K1-D4

Method BLASTX NCBI GI g3068713



```
BLAST score
E value
                  6.0e-24
Match length
                  113
% identity
                  60
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  166482
Seq. ID
                  LIB3234-008-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g3510337
                  74
BLAST score
E value
                  2.0e-33
                  234
Match length
% identity
                  83
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166483
Seq. ID
                  LIB3234-008-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2342727
BLAST score
                  357
E value
                  5.0e-34
                  92
Match length
% identity
                  75
NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  166484
Seq. ID
                  LIB3234-008-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g2264306
BLAST score
                  366
E value
                  0.0e+00
Match length
                  374
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166485
                  LIB3234-008-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q207905
BLAST score
                  171
E value
                  3.0e-12
Match length
                  122
% identity
                  34
NCBI Description (M18027) alpha globulin B [Artificial gene]
Seq. No.
                  166486
                  LIB3234-008-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266693
BLAST score
                  367
E value
                  2.0e-35
Match length
                  96
```

22428

NCBI Description OLEOSIN >gi 282875 pir S22538 oleosin - Arabidopsis

79

% identity



thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 166487

Seq. ID LIB3234-008-P1-K1-E11

Method BLASTX
NCBI GI g480450
BLAST score 329
E value 9.0e-31
Match length 80
% identity 86

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >qi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 166488

Seq. ID LIB3234-008-P1-K1-E12

Method BLASTX
NCBI GI g477280
BLAST score 169
E value 6.0e-12
Match length 59
% identity 58

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K

protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

534 aa]

Seq. No. 166489

Seq. ID LIB3234-008-P1-K1-E4

Method BLASTX
NCBI GI g2129659
BLAST score 289
E value 4.0e-26
Match length 92
% identity 63

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 166490

Seq. ID LIB3234-008-P1-K1-E5

Method BLASTN
NCBI GI g4263694
BLAST score 365
E value 0.0e+00
Match length 369
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166491

Seq. ID LIB3234-008-P1-K1-E6

Method BLASTX NCBI GI g2191176 BLAST score 486



```
E value
                  4.0e-49
Match length
                  107
% identity
                  90
NCBI Description (AF007270) Similar to SRF-type transcription factor
                  [Arabidopsis thaliana]
Seq. No.
                  166492
                  LIB3234-008-P1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757390
BLAST score
                  357
E value
                  0.0e+00
Match length
                  377
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F24B18, complete sequence
Seq. No.
                  166493
Seq. ID
                  LIB3234-008-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1176658
BLAST score
                  242
E value
                  2.0e-20
Match length
                  101
                  47
% identity
NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                  >gi_726363 (U23168) No definition line found
                  [Caenorhabditis elegans]
Seq. No.
                  166494
                  LIB3234-008-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g544415
BLAST score
                  292
E value
                  2.0e-26
Match length
                  109
% identity
                  54
NCBI Description
                 GLYCEROL-3-PHOSPHATE DEHYDROGENASE MITOCHONDRIAL PRECURSOR
                  (GPD-M) (GPDH-M) >gi 627996 pir A54051
                  glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) precursor
                  - rat >gi_493022 (U08027) glycerolphosphate dehydrogenase
                  [Rattus norvegicus] >gi_603583 emb CAA55329 (X78593)
                  glycerol-3-phosphate dehydrogenase [Rattus norvegicus]
Seq. No.
                  166495
Seq. ID
                  LIB3234-008-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g419757
BLAST score
                  491
E value
                  9.0e-50
Match length
                  119
% identity
                  83
```

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) precursor -

Arabidopsis thaliana

Seq. No. 166496

Seq. ID LIB3234-008-P1-K1-F11



Method BLASTX
NCBI GI g3915961
BLAST score 273
E value 1.0e-24
Match length 57
% identity 95

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)

>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 166497

Seq. ID LIB3234-008-P1-K1-F12

Method BLASTX
NCBI GI g3063706
BLAST score 342
E value 3.0e-32
Match length 78
% identity 82

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 166498

Seq. ID LIB3234-008-P1-K1-F4

Method BLASTX
NCBI GI g2499964
BLAST score 690
E value 4.0e-73
Match length 123
% identity 99

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2

>gi_669096_emb_CAA58958 (X84153) photosystem I subunit

[Antirrhinum majus]

Seq. No. 166499

Seq. ID LIB3234-008-P1-K1-F6

Method BLASTX
NCBI GI g1916613
BLAST score 462
E value 2.0e-46
Match length 96
% identity 100

NCBI Description (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]

Seq. No. 166500

Seq. ID LIB3234-008-P1-K1-F8

Method BLASTX
NCBI GI g4539421
BLAST score 368
E value 3.0e-35
Match length 97
% identity 72

NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 166501

Seq. ID LIB3234-008-P1-K1-F9

Method BLASTX NCBI GI g421836



BLAST score 454 E value 2.0e-45Match length 92 100 % identity

NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi 553040 (M96855) GF14 [Arabidopsis thaliana]

166502 Seq. No.

Seq. ID LIB3234-008-P1-K1-G1

BLASTX Method NCBI GI q544424 BLAST score 423 E value 9.0e-42Match length 89 93 % identity

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 166503

Seq. ID LIB3234-008-P1-K1-G10

Method BLASTN NCBI GI g4733953 BLAST score 311 E value 1.0e-175 Match length 369 % identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F13011 genomic

sequence, complete sequence

Seq. No. 166504

Seq. ID LIB3234-008-P1-K1-G11

Method BLASTX NCBI GI q3925239 BLAST score 407 E value 7.0e-40Match length 105 % identity 76

NCBI Description (AF037037) 6-phosphogluconate dehydrogenase isoenzyme A

[Zea mays]

Seq. No. 166505

LIB3234-008-P1-K1-G12 Seq. ID

Method BLASTX NCBI GI g2605714 BLAST score 447 E value 1.0e-44 Match length 110 % identity 81

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 166506



```
LIB3234-008-P1-K1-G2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g135858
                    276
BLAST score
E value
                    2.0e-24
Match length
                    56
% identity
                    98
NCBI Description
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
                    >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                    [Arabidopsis Thaliana] >gi_445128_prf__1908432A tonoplast
                    intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                    166507
Seq. ID
                    LIB3234-008-P1-K1-G3
Method
                    BLASTX
NCBI GI
                    g3023848
BLAST score
                    531
E value
                    2.0e-54
Match length
                    105
% identity
                    56
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                    PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                    >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis
                    thaliana]
Seq. No.
                    166508
                    LIB3234-008-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                    q3063706
BLAST score
                    345
E value
                    1.0e-32
Match length
                    79
% identity
                    81
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                    166509
Seq. ID
                   LIB3234-008-P1-K1-G5
Method
                   BLASTN
NCBI GI
                    g2924653
BLAST score
                    98
E value
                    4.0e-48
                    134
Match length
% identity
                    93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166510
Seq. ID
                    LIB3234-008-P1-K1-G6
Method
                    BLASTX
```

Method BLASTX
NCBI GI g2505874
BLAST score 194
E value 6.0e-15
Match length 57
% identity 74

NCBI Description

thaliana]



```
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.
                                                 166511
Seq. ID
                                                LIB3234-008-P1-K1-G7
Method
                                                BLASTN
NCBI GI
                                                 g3080406
BLAST score
                                                 59
E value
                                                 5.0e-25
                                                 99
Match length
                                                 90
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12
                                                 (ESSA project)
Seq. No.
                                                 166512
Seq. ID
                                                LIB3234-008-P1-K1-G8
Method
                                                BLASTX
NCBI GI
                                                g2781394
BLAST score
                                                386
E value
                                                1.0e-37
Match length
                                                82
                                                 99
% identity
NCBI Description (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
Seq. No.
                                                166513
Seq. ID
                                                LIB3234-008-P1-K1-H11
Method
                                                BLASTN
NCBI GI
                                                g2656025
BLAST score
                                                342
E value
                                                 0.0e+00
Match length
                                                370
% identity
                                                 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                                                MCD7
Seq. No.
                                                166514
Seq. ID
                                                LIB3234-008-P1-K1-H12
Method
                                                BLASTX
NCBI GI
                                                g2832777
BLAST score
                                                272
                                                 5.0e-24
E value
Match length
                                                123
% identity
                                                 50
NCBI Description
                                               (AL021086) /prediction=(method:; /prediction=(method:;
                                                 /match=(desc:; /
                                                EST embl_AA735498_AA735498 comes from the 5' UTR
                                                 [Drosophila melanogaster]
Seq. No.
                                                166515
Seq. ID
                                                LIB3234-008-P1-K1-H3
Method
                                                BLASTX
NCBI GI
                                                g2979541
BLAST score
                                                661
E value
                                                1.0e-69
Match length
                                                124
% identity
                                                97
```

22434

(AC003680) hypothetical protein, 5' partial [Arabidopsis

BLAST score

% identity

E value Match length 202 7.0e-16

113

42



```
Seq. No.
                   166516
Seq. ID
                   LIB3234-008-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g118926
BLAST score
                   251
E value
                   1.0e-21
Match length
                   96
% identity
                   54
NCBI Description
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
                   >gi_320600_pir__E45509 desiccation-related protein (clone
                   PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                   dessication-related protein [Craterostigma plantagineum]
                   >gi_227781_prf__1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
Seq. No.
                   166517
Seq. ID
                  LIB3234-008-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   g625977
BLAST score
                   555
E value
                   3.0e-57
Match length
                   108
% identity
                   100
NCBI Description p40 protein homolog - Arabidopsis thaliana >gi 402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thalianal
Seq. No.
Seq. ID
                   166518
                  LIB3234-008-P1-K1-H6
Method
                  BLASTN
NCBI GI
                   q4006815
BLAST score
                  92
E value
                   4.0e-44
Match length
                  186
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166519
Seq. ID
                  LIB3234-008-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2618688
BLAST score
                  191
E value
                  2.0e-26
Match length
                  76
% identity
NCBI Description (AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.
                  166520
Seq. ID
                  LIB3234-008-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1592677
```

Seq. No.

166526



```
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                  166521
                  LIB3234-008-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3985949
BLAST score
                  286
E value
                  1.0e-160
Match length
                  358
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166522
                  LIB3234-009-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757392
BLAST score
                  323
E value
                  0.0e+00
Match length
                  374
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
Seq. No.
                  166523
Seq. ID
                  LIB3234-009-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q2961390
BLAST score
                  559
E value
                  1.0e-57
Match length
                  103
% identity
                  100
NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  166524
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-A3
                  {\tt BLASTX}
Method
NCBI GI
                  g3123279
BLAST score
                  309
E value
                  2.0e-28
                  72
Match length
                  83
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S26 >gi 2651298 (AC002336) putative
                  ribosomal protein S26 [Arabidopsis thaliana]
                  166525
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  106
                  1.0e-56
E value
Match length
                  119
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
```



LIB3234-009-P1-K1-A9 Seq. ID

Method BLASTX NCBI GI a585165 BLAST score 304 1.0e-27 E value 78 Match length 76 % identity

GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM NCBI Description

(G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato

>gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No. 166527

Seq. ID LIB3234-009-P1-K1-B3

Method BLASTX NCBI GI q1628583 79 BLAST score 2.0e-61 E value Match length 123

% identity 92 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 166528

LIB3234-009-P1-K1-B4 Seq. ID

Method BLASTX NCBI GI q2388571 BLAST score 472 E value 1.0e-47 Match length 93 98 % identity

NCBI Description (AC000098) Strong similarity to Arabidopsis peroxidase

ATPEROX7A (gb X98321). [Arabidopsis thaliana] >gi 2738254

(U97684) peroxidase precursor [Arabidopsis thaliana]

166529 Seq. No.

Seq. ID LIB3234-009-P1-K1-B5

Method BLASTX NCBI GI g231586 BLAST score 589 E value 3.0e-61 Match length 126 % identity 90

ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

> >gi 82027 pir S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

166530 Seq. No.

Seq. ID LIB3234-009-P1-K1-B7

Method BLASTX NCBI GI g3775987 BLAST score 557 2.0e-57 E value



```
Match length
                  120
% identity
NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  166531
Seq. ID
                  LIB3234-009-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q3763916
BLAST score
                  291
E value
                  2.0e-26
Match length
                  88
% identity
                  60
NCBI Description
                  (AC004450) unknown protein [Arabidopsis thaliana]
                  >gi_4531439_gb_AAD22124.1 AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  166532
Seq. ID
                  LIB3234-009-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q3461850
BLAST score
                  329
E value
                  1.0e-30
Match length
                  92
% identity
                  78
NCBI Description (AC005315) putative ligand-gated ionic channel [Arabidopsis
                  thaliana]
                  166533
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2239083
BLAST score
                  287
E value
                  8.0e-26
Match length
                  118
% identity
NCBI Description
                  (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
Seq. No.
                  166534
Seq. ID
                  LIB3234-009-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1076442
BLAST score
                  611
E value
                  8.0e-64
                  119
Match length
% identity
                  90
NCBI Description
                 beta-glucosidase (EC 3.2.1.21) - rape
```

>gi_757740_emb_CAA57913_ (X82577) beta-glucosidase

[Brassica napus]

Seq. No. 166535

Seq. ID LIB3234-009-P1-K1-C2

Method BLASTX NCBI GI g3063472 BLAST score 514

% identity

83



```
E value
                   2.0e-52
Match length
                  99
                   97
% identity
NCBI Description (AC003981) F22013.34 [Arabidopsis thaliana]
Seq. No.
                  166536
                  LIB3234-009-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2760167
BLAST score
                  34
E value
                  2.0e-10
Match length
                  50
                  92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCO15, complete sequence [Arabidopsis thaliana]
                  166537
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  239
E value
                  4.0e-20
Match length
                  60
% identity
                  72
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis
                  thaliana]
Seq. No.
                  166538
Seq. ID
                  LIB3234-009-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3687221
BLAST score
                  57
E value
                  2.0e-23
Match length
                  206
% identity
                  94
NCBI Description Arabidopsis thaliana chromosome II BAC F6F22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166539
Seq. ID
                  LIB3234-009-P1-K1-C9
                  BLASTN
Method
NCBI GI
                  g4210331
BLAST score
                  195
E value
                  1.0e-106
Match length
                  259
                  94
% identity
NCBI Description Arabidopsis thaliana mRNA for 2-oxoglutarate dehydrogenase
                  E2 subunit
                  166540
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  g4757662
BLAST score
                  76
E value
                  1.0e-34
Match length
                  252
```



```
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
                  chromosome I, complete sequence
Seq. No.
                  166541
Seq. ID
                  LIB3234-009-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g2264315
BLAST score
                  286
E value
                  1.0e-160
Match length
                  358
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRN17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166542
Seq. ID
                  LIB3234-009-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1731324
BLAST score
                  164
E value
                  7.0e-13
Match length
                  57
% identity
                  74
NCBI Description HYPOTHETICAL PROTEIN >gi_166306 (M23451) steroid receptor
                  [Achlya ambisexualis]
Seq. No.
                  166543
Seq. ID
                  LIB3234-009-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4587584
BLAST score
                  358
E value
                  3.0e-34
Match length
                  109
% identity
                  71
NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166544
Seq. ID
                  LIB3234-009-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g82228
BLAST score
                  247
E value
                  4.0e-21
                  78
Match length
% identity
                  69
NCBI Description hypothetical protein 77 - common tobacco chloroplast
                  >gi_225199_prf__1211235AD ORF 77 [Nicotiana tabacum]
Seq. No.
                  166545
Seq. ID
                  LIB3234-009-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  q2252823
BLAST score
                  174
```

E value 2.0e-93 Match length 178 % identity 99

NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 166546



```
LIB3234-009-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266410
BLAST score
                  348
E value
                  5.0e-33
Match length
                  120
                  60
% identity
                  CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi_82507_pir__$13934
NCBI Description
                  protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog -
                  rice >gi_20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related
                  protein kinase [Oryza sativa]
Seq. No.
                  166547
                  LIB3234-009-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3687221
                  280
BLAST score
                  1.0e-156
E value
                  384
Match length
                  94
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F6F22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166548
Seq. No.
                  LIB3234-009-P1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2160132
BLAST score
                  100
E value
                  6.0e-49
Match length
                  164
                  90
% identity
NCBI Description
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166549
Seq. ID
                  LIB3234-009-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  q1448916
BLAST score
                  155
E value
                  7.0e-82
                  283
Match length
% identity
                  89
NCBI Description Arabidopsis thaliana threonine synthase mRNA, 3' end of cds
Seq. No.
                  166550
Seq. ID
                  LIB3234-009-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  190
```

E value 1.0e-102 384 Match length % identity 97

NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 166551

LIB3234-009-P1-K1-E2 Seq. ID

Method BLASTX



```
NCBI GI
                   q1931647
BLAST score
                   352
E value
                   2.0e-33
                   78
Match length
% identity
NCBI Description
                  (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
Seq. No.
                   166552
Seq. ID
                   LIB3234-009-P1-K1-E3
Method
                  BLASTX
NCBI GI
                   q1418323
BLAST score
                   438
E value
                   2.0e-43
Match length
                   122
% identity
                   68
NCBI Description
                  (X98671) zinc finger protein [Arabidopsis thaliana]
                   >gi_1418333_emb_CAA67228_ (X98670) zinc finger protein
                   [Arabidopsis thaliana]
Seq. No.
                   166553
Seq. ID
                  LIB3234-009-P1-K1-E4
Method
                  BLASTN
NCBI GI
                   q4469002
BLAST score
                  255
E value
                   1.0e-141
Match length
                  382
% identity
                   92
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                   (ESSA project)
Seq. No.
                   166554
Seq. ID
                  LIB3234-009-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  q4512656
BLAST score
                  155
E value
                  9.0e-82
Match length
                  293
% identity
                  85
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  166555
Seq. ID
                  LIB3234-009-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g16473
BLAST score
                  159
                  4.0e-84
E value
                  711
Match length
                  17
% identity
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
```

Seq. No. 166556

Seq. ID LIB3234-009-P1-K1-E8

Method BLASTX NCBI GI g112682 BLAST score 272



E value 1.0e-24
Match length 58
% identity 93

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 166557

Seq. ID LIB3234-009-P1-K1-F1

Method BLASTX
NCBI GI g1345973
BLAST score 406
E value 9.0e-40
Match length 93
% identity 81

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 166558

Seq. ID LIB3234-009-P1-K1-F11

Method BLASTX
NCBI GI g2648032
BLAST score 292
E value 2.0e-26
Match length 128
% identity 45

NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 166559

Seq. ID LIB3234-009-P1-K1-F12

Method BLASTN
NCBI GI g4159709
BLAST score 203
E value 1.0e-110
Match length 312
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLN21, complete sequence

Seq. No. 166560

Seq. ID LIB3234-009-P1-K1-F2

Method BLASTX
NCBI GI g2245019
BLAST score 630
E value 5.0e-66
Match length 123
% identity 98

NCBI Description (Z97341) proteinase homolog [Arabidopsis thaliana]

Match length

% identity

216

100



```
Seq. No.
                    166561
Seq. ID
                    LIB3234-009-P1-K1-F3
Method
                    BLASTN
NCBI GI
                    g3449331
BLAST score
                    370
E value
                    0.0e+00
Match length
                    374
% identity
                    27
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166562
Seq. ID
                    LIB3234-009-P1-K1-F4
Method
                    BLASTX
NCBI GI
                    g1616787
BLAST score
                    600
E value
                    2.0e-62
Match length
                    117
% identity
                    97
NCBI Description (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
Seq. No.
                    166563
Seq. ID
                    LIB3234-009-P1-K1-F5
Method
                    BLASTX
NCBI GI
                    q4454028
BLAST score
                    264
E value
                    4.0e-23
                    55
Match length
% identity
                    91
NCBI Description
                   (AL035394) tyrosine transaminase like protein [Arabidopsis
                    thaliana]
                    166564
Seq. No.
Seq. ID
                    LIB3234-009-P1-K1-F6
Method
                    BLASTX
NCBI GI
                    g119194
BLAST score
                    349
E value
                    5.0e - 33
Match length
                    123
% identity
                    59
NCBI Description
                    ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                    >gi 81607 pir S09152 translation elongation factor Tu
                    precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A
                    elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                    166565
Seq. ID
                    LIB3234-009-P1-K1-F9
Method
                    BLASTN
NCBI GI
                    g3449312
BLAST score
                    114
E value
                    2.0e-57
```

22444

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



K16L22, complete sequence [Arabidopsis thaliana]

Seq. No. 166566 Seq. ID LIB3234-009-P1-K1-G10 Method BLASTN NCBI GI g4512656 BLAST score 147 E value 5.0e-77 Match length 303 % identity 89 NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence Seq. No. 166567 LIB3234-009-P1-K1-G11 Seq. ID Method BLASTN NCBI GI g4220640 BLAST score 349 E value 0.0e + 00Match length 373 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana] Seq. No. 166568 LIB3234-009-P1-K1-G12 Seq. ID Method BLASTN NCBI GI q3366536 BLAST score 137 E value 3.0e-71Match length 193 % identity 95 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana] Seq. No. 166569 Seq. ID LIB3234-009-P1-K1-G2 Method BLASTN NCBI GI q4159712 BLAST score 105 E value 6.0e-52Match length 353 78 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence 166570 Seq. No. Seq. ID LIB3234-009-P1-K1-G3 Method BLASTX NCBI GI g267073 BLAST score 561 E value 6.0e-58 102 Match length % identity 100

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700)

beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)



beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 166571 Seq. ID LIB3234-009-P1-K1-G4 Method BLASTX NCBI GI g2160158 BLAST score 676 E value 2.0e-71 Match length 126 99 % identity NCBI Description (ACO00132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana] Seq. No. 166572 Seq. ID LIB3234-009-P1-K1-G6 Method BLASTX NCBI GI g3738257 BLAST score 149 E value 5.0e-10 50 Match length % identity 66 NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra] Seq. No. 166573 Seq. ID LIB3234-009-P1-K1-G8 Method BLASTX NCBI GI g2062167 BLAST score 234 E value 1.0e-19 Match length 87 51 % identity NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana] Seq. No. 166574 Seq. ID LIB3234-009-P1-K1-G9 Method BLASTX NCBI GI g207905 BLAST score 141 E value 1.0e-08 Match length 64 % identity 41 NCBI Description (M18027) alpha globulin B [Artificial gene] Seq. No. 166575 Seq. ID LIB3234-009-P1-K1-H1 Method BLASTX NCBI GI g1616787 BLAST score 515 E value 1.0e-52 Match length 114 % identity NCBI Description (U71122) pyruvate decarboxylase [Arabidopsis thaliana]

Seq. No. 166576



```
Seq. ID
                   LIB3234-009-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   q4159705
BLAST score
                   183
E value
                   9.0e-99
Match length
                   207
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                   166577
Seq. ID
                  LIB3234-009-P1-K1-H12
Method
                  BLASTX
NCBI GI
                   g2465923
BLAST score
                  258
                   2.0e-22
E value
Match length
                   74
% identity
                   65
NCBI Description
                  (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                  166578
Seq. ID
                  LIB3234-009-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  q3885325
BLAST score
                  284
                  1.0e-159
E value
Match length
                   372
                   94
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T20P8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166579
Seq. ID
                  LIB3234-009-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g131360
BLAST score
                  241
E value
                  2.0e-20
Match length
                  61
% identity
NCBI Description
                  PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                  >gi_81727_pir__S02115 photosystem II protein psbK precursor
                   - white mustard chloroplast >gi_12209_emb CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.
                  166580
Seq. ID
                  LIB3234-009-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  526
E value
                  7.0e-54
Match length
                  100
% identity
                  100
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
```

Seq. No. 166581

[Arabidopsis thaliana]



Seq. ID LIB3234-010-P1-K1-A10 Method BLASTX NCBI GI q2262167 BLAST score 514 E value 2.0e-52 Match length 98 100 % identity NCBI Description (AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana] Seq. No. 166582 LIB3234-010-P1-K1-A12 Seq. ID Method BLASTN NCBI GI g4510323 BLAST score 348 0.0e + 00E value Match length 360 99 % identity NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence 166583 Seq. No. Seq. ID LIB3234-010-P1-K1-A3 Method BLASTN g3402747 NCBI GI BLAST score 351 0.0e + 00E value Match length 351 100 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project) Seq. No. 166584 Seq. ID LIB3234-010-P1-K1-A6 Method BLASTN NCBI GI q3540210 BLAST score 314 E value 1.0e-176 Match length 346 % identity 98 NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 166585 Seq. ID LIB3234-010-P1-K1-A8 Method BLASTX NCBI GI g3785989 BLAST score 413 E value 1.0e-40 Match length 80 % identity 100

Seq. No. 166586

Seq. ID LIB3234-010-P1-K1-A9

Method BLASTN NCBI GI g3985950

22448

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]



BLAST score 131 E value 1.0e-67 Match length 251 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI10, complete sequence [Arabidopsis thaliana]

Seq. No. 166587

Seq. ID LIB3234-010-P1-K1-B1

Method BLASTX
NCBI GI g2914700
BLAST score 431
E value 1.0e-42
Match length 86
% identity 99

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

Seq. No. 166588

Seq. ID LIB3234-010-P1-K1-B10

Method BLASTN
NCBI GI g4159712
BLAST score 185
E value 1.0e-99
Match length 289
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 166589

Seq. ID LIB3234-010-P1-K1-B11

Method BLASTN
NCBI GI 94467131
BLAST score 192
E value 1.0e-104
Match length 315
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13

(ESSA project)

Seq. No. 166590

Seq. ID LIB3234-010-P1-K1-B12

Method BLASTX
NCBI GI g4582436
BLAST score 482
E value 1.0e-48
Match length 115
% identity 79

NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 166591

Seq. ID LIB3234-010-P1-K1-B3

Method BLASTX
NCBI GI g4204298
BLAST score 378
E value 1.0e-36
Match length 90

% identity

NCBI Description



```
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
                  166592
Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  q2760170
BLAST score
                  363
E value
                  0.0e+00
Match length
                  367
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIO24, complete sequence [Arabidopsis thaliana]
                  166593
Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  347
                  0.0e+00
E value
Match length
                  367
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166594
                  LIB3234-010-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1864017
BLAST score
                  554
E value
                  4.0e-57
Match length
                  105
% identity
                  100
NCBI Description
                 (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  166595
Seq. ID
                  LIB3234-010-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g1872522
BLAST score
                  119
E value
                  3.0e-60
Match length
                  119
                  100
% identity
                  Arabidopsis thaliana zinc-finger protein Lsd1 (LSD1) gene,
NCBI Description
                  complete cds
                  166596
Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3335171
BLAST score
                  557
E value
                  2.0e-57
Match length
                  121
```

22450

(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]



Seq. No. 166597

Seq. ID LIB3234-010-P1-K1-C2

Method BLASTX
NCBI GI g1173345
BLAST score 450
E value 6.0e-45
Match length 118
% identity 78

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa]

[Arabidopsis thaliana]

Seq. No. 166598

Seq. ID LIB3234-010-P1-K1-C3

Method BLASTX
NCBI GI g3915961
BLAST score 606
E value 3.0e-63
Match length 122
% identity 95

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)

>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 166599

Seq. ID LIB3234-010-P1-K1-C6

Method BLASTX
NCBI GI g3913418
BLAST score 610
E value 1.0e-63
Match length 118
% identity 98

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi 1531763 emb CAA69073 (Y07765)

S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No. 166600

Seq. ID LIB3234-010-P1-K1-C7

Method BLASTN
NCBI GI g4220643
BLAST score 319
E value 1.0e-179
Match length 323

Match length 323 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 166601

Seq. ID LIB3234-010-P1-K1-C8

Method BLASTX NCBI GI g4704766 BLAST score 391



```
E value
                   5.0e-38
Match length
                  107
% identity
                   45
NCBI Description
                   (AF131223) protein disulfide isomerase homolog; PDI
                   [Datisca glomerata]
Seq. No.
                  166602
Seq. ID
                  LIB3234-010-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  q3402671
BLAST score
                  329
E value
                  0.0e + 00
Match length
                  336
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166603
Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  q3766106
BLAST score
                  365
E value
                  0.0e + 00
Match length
                  373
% identity
                  99
NCBI Description Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166604
Seq. ID
                  LIB3234-010-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2583111
BLAST score
                  621
E value
                  5.0e-65
Match length
                  117
% identity
                  100
NCBI Description (AC002387) putative dihydrodipicolinate synthase
                   [Arabidopsis thaliana]
Seq. No.
                  166605
Seq. ID
                  LIB3234-010-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  257
E value
                  1.0e-142
Match length
                  281
                  98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
```

166606 Seq. No. Seq. ID LIB3234-010-P1-K1-D5 Method BLASTX NCBI GI g4099349

BLAST score 590 E value 2.0e-61 Match length 120



% identity NCBI Description (U86394) ATP synthase beta subunit [Papaver orientale] 166607 Seq. No. LIB3234-010-P1-K1-D6 Seq. ID Method BLASTX g3335169 NCBI GI BLAST score 599 E value 2.0e-62 Match length 116 98 % identity NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] 166608 Seq. No. LIB3234-010-P1-K1-D7 Seq. ID BLASTN Method NCBI GI g4199934 BLAST score 321 E value 0.0e+00Match length 325 100 % identity Genomic sequence for Arabidopsis thaliana BAC T3P18, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 166609 LIB3234-010-P1-K1-D8 Seq. ID Method BLASTX NCBI GI g2499605 BLAST score 599 2.0e-62 E value Match length 123 93 % identity MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (MAP KINASE 1) NCBI Description (ATMPK1) >gi_533280_dbj_BAA03535_ (D14713) ATMPK1 [Arabidopsis thaliana] 166610 Seq. No. Seq. ID LIB3234-010-P1-K1-D9 Method BLASTX NCBI GI g2597824 BLAST score 547 E value 3.0e-56 Match length 123 % identity NCBI Description (AJ002532) endo-polygalacturonase [Arabidopsis thaliana] >gi 4090973 (AF037367) endo-polygalacturonase [Arabidopsis thaliana] Seq. No. 166611

Seq. ID LIB3234-010-P1-K1-E10

Method BLASTX NCBI GI g4586044 BLAST score 275 E value 2.0e-24 Match length 110

NCBI Description



```
% identity
NCBI Description
                  (AC007020) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  166612
Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  q3046856
                  288
BLAST score
E value
                  1.0e-161
Match length
                  351
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXI22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166613
Seq. ID
                  LIB3234-010-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g3047060
BLAST score
                  34
E value
                  1.0e-09
Match length
                  66
                  88
% identity
NCBI Description Arabidopsis thaliana BAC F7N22
Seq. No.
                  166614
Seq. ID
                  LIB3234-010-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g1279629
BLAST score
                  341
E value
                  0.0e+00
Match length
                  376
% identity
                  98
NCBI Description O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA
                  genes
Seq. No.
                  166615
Seq. ID
                  LIB3234-010-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g4519195
BLAST score
                  72
                  3.0e-32
E value
Match length
                  138
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  166616
Seq. ID
                  LIB3234-010-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  333
E value
                  3.0e-31
Match length
                  75
% identity
                  88
```

22454

40S ribosomal protein S2 [Arabidopsis thaliana]

40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative



Seq. No. 166617 Seq. ID

LIB3234-010-P1-K1-E7

Method BLASTN NCBI GI g3510339 BLAST score 368 E value 0.0e+00Match length 368 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 166618

Seq. ID LIB3234-010-P1-K1-E8

Method BLASTN NCBI GI g1279629 BLAST score 325 E value 0.0e+00Match length 360 % identity 98

O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA NCBI Description

genes

Seq. No. 166619

Seq. ID LIB3234-010-P1-K1-E9

Method BLASTX NCBI GI q464986 BLAST score 480 E value 2.0e-48 Match length 89 % identity 98

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana

>gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis Thaliana]

>gi_4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 166620

Seq. ID LIB3234-010-P1-K1-F1

Method BLASTX NCBI GI g2583108 BLAST score 597 E value 3.0e-62 Match length 120 % identity

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 166621

Seq. ID LIB3234-010-P1-K1-F11

Method BLASTX NCBI GI g2497540



BLAST score 408
E value 3.0e-40
Match length 96
% identity 88

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No. 166622

Seq. ID LIB3234-010-P1-K1-F12

Method BLASTX
NCBI GI g3980412
BLAST score 123
E value 6.0e-07
Match length 78
% identity 7

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 166623

Seq. ID LIB3234-010-P1-K1-F2

Method BLASTN
NCBI GI g4309719
BLAST score 332
E value 0.0e+00
Match length 365
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166624

Seq. ID LIB3234-010-P1-K1-F4

Method BLASTX
NCBI GI g2583125
BLAST score 511
E value 4.0e-52

Match length 94 % identity 100

NCBI Description (AC002387) putative transketolase precursor [Arabidopsis

thaliana]

Seq. No. 166625

Seq. ID LIB3234-010-P1-K1-F5

Method BLASTX
NCBI GI g2583125
BLAST score 450
E value 4.0e-45
Match length 96
% identity 86

NCBI Description (AC002387) putative transketolase precursor [Arabidopsis

thaliana]

Seq. No. 166626

Seq. ID LIB3234-010-P1-K1-G10

Method BLASTX
NCBI GI g1864017
BLAST score 477

E value 4.0e-48 Match length 91 100



```
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
                   166627
Seq. No.
                  LIB3234-010-P1-K1-G12
Seq. ID
Method
                  BLASTX
                   g2832620
NCBI GI
BLAST score
                   392
                   3.0e - 38
E value
Match length
                   108
% identity
                   69
NCBI Description
                 (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166628
                  LIB3234-010-P1-K1-G2
Seq. ID
Method
                  BLASTN
                   q4199934
NCBI GI
                   46
BLAST score
E value
                   1.0e-16
Match length
                   110
                   85
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
                   166629
"Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-G3
Method
                  BLASTX
NCBI GI
                   g4467139
BLAST score
                   157
E value
                   1.0e-10
Match length
                   43
% identity
                   77
                  (AL035540) putative protein phosphatase-2c [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166630
Seq. ID
                   LIB3234-010-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q112741
BLAST score
                   644
E value
                   1.0e-67
Match length
                   117
% identity
                   100
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   166631
Seq. ID
                   LIB3234-010-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   g3024871
BLAST score
                   193
E value
```

22457

2.0e-18

107

Match length

Match length

% identity

105 99

NCBI Description (AC006550) F1003.7 [Arabidopsis thaliana]



```
% identity
                  50
NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                  >gi 1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
                  sp.]
                  166632
Seq. No.
                  LIB3234-010-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g137579
BLAST score
                  180
                  3.0e-13
E value
Match length
                  108
% identity
                  37
NCBI Description PROVICILIN (TYPE A) >gi 72292 pir FWPMVA vicilin type A
                  precursor - garden pea (fragment)
                  166633
Seq. No.
                  LIB3234-010-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586053
BLAST score
                  230
E value
                  3.0e-19
                  117
Match length
% identity
                  47
NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana]
Seq. No.
                  166634
                  LIB3234-010-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3540196
BLAST score
                  178
                  1.0e-13
E value
Match length
                  59
                  63
% identity
NCBI Description (AC004260) Putative amp-binding protein [Arabidopsis
                  thalianal
Seq. No.
                  166635
Seq. ID
                  LIB3234-010-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  g1070376
BLAST score
                  67
E value
                  3.0e-29
Match length
                  141
                  91
% identity
NCBI Description P.deltoides chloroplast psbT and psbH genes
Seq. No.
                  166636
Seq. ID
                  LIB3234-010-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4587567
BLAST score
                  552
E value
                  6.0e - 57
```



Seq. No. 166637

Seq. ID LIB3234-010-P1-K1-H8

Method BLASTX
NCBI GI g3850928
BLAST score 388
E value 1.0e-37
Match length 85
% identity 87

NCBI Description (AF060404) ATP synthase beta subunit [Adenanthos obovatus]

Seq. No. 166638

Seq. ID LIB3234-010-P1-K1-H9

Method BLASTX
NCBI GI g2959781
BLAST score 604
E value 5.0e-63
Match length 119
% identity 99

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 166639

Seq. ID LIB3234-011-P1-K1-A11

Method BLASTX
NCBI GI g4679028
BLAST score 268
E value 1.0e-23
Match length 115
% identity 48

NCBI Description (AF077207) HSPC021 [Homo sapiens]

Seq. No. 166640

Seq. ID LIB3234-011-P1-K1-A2

Method BLASTN
NCBI GI g4539309
BLAST score 136
E value 1.0e-70
Match length 188
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22

(ESSA project)

Seq. No. 166641

Seq. ID LIB3234-011-P1-K1-A4

Method BLASTX
NCBI GI 94056457
BLAST score 590
E value 2.0e-61
Match length 116
% identity 100

NCBI Description (AC005990) ESTs gb_234051 and gb_F13722 come from this

gene. [Arabidopsis thaliana]

Seq. No. 166642

Seq. ID LIB3234-011-P1-K1-A5

Method BLASTN NCBI GI g2914688 BLAST score 176



```
E value
                  2.0e-94
Match length
                  353
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166643
                  LIB3234-011-P1-K1-A8
Seg. ID
                  BLASTX
Method
NCBI GI
                  g132074
                  441
BLAST score
                  4.0e-44
E value
                  87
Match length
                  94
% identity
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1

ribulose-bisphosphate carboxylase (\overline{EC} 4. $\overline{1.1.39}$) small chain

Al precursor - Arabidopsis thaliana

% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

166645 Seq. No. Seq. ID LIB3234-011-P1-K1-B10 Method BLASTN NCBI GI g2656028 BLAST score 161 2.0e-85 E value Match length 353 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

 Seq. No.
 166646

 Seq. ID
 LIB3234-011-P1-K1-B11

 Method
 BLASTN

 NCBI GI
 q4558656

NCBI GI g455865
BLAST score 181
E value 2.0e-97
Match length 285
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T10F5 genomic

sequence, complete sequence

Seq. No. 166647

Seq. ID LIB3234-011-P1-K1-B12

MethodBLASTXNCBI GIg21911BLAST score196



```
E value
                    3.0e-15
Match length
                    79
                    46
% identity
NCBI Description
                   (X62625) vicilin [Theobroma cacao]
                   166648
Seq. No.
                   LIB3234-011-P1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                    q544424
BLAST score
                    60
                    8.0e-37
E value
Match length
                   85
                    98
% identity
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                    protein [Arabidopsis thaliana]
                   >gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                    166649
Seq. No.
                   LIB3234-011-P1-K1-B8
Seq. ID
Method
                   BLASTX
                   g166570
NCBI GI
                    174
BLAST score
E value
                    1.0e-12
Match length
                    31
                    100
% identity
NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                    166650
                    LIB3234-011-P1-K1-C1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3851636
BLAST score
                    382
E value
                    5.0e-37
Match length
                    99
                    71
% identity
NCBI Description
                   (AF098519) unknown [Avicennia marina] >qi 4128206
                    (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                    166651
                    LIB3234-011-P1-K1-C10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q464988
BLAST score
                    175
E value
                    1.0e-12
Match length
                    36
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 (UBIQUITIN-PROTEIN
NCBI Description
                    LIGASE 11) (UBIQUITIN CARRIER PROTEIN 11)
                    >gi_421856_pir__S32673 ubiquitin--protein ligase (EC
6.3.2.19) UBC11 - Arabidopsis thaliana (fragment)
                    >gi 297880 emb CAA78716 (Z14992) ubiquitin conjugating
                    enzyme [Arabidopsis thaliana] >gi 349215 (L00641) ubiquitin
```

22461

conjugating enzyme [Arabidopsis thaliana]

Seq. No.

166657



```
Seq. No.
                   166652
Seq. ID
                   LIB3234-011-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3269286
BLAST score
                   435
E value
                   3.0e-43
Match length
                   107
% identity
                   88
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   166653
Seq. No.
Seq. ID
                   LIB3234-011-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q3688175
BLAST score
                   281
E value
                   3.0e-25
Match length
                   91
% identity
                   63
NCBI Description (AL031804) gamma-VPE (vacuolar processing enzyme)
                    [Arabidopsis thaliana]
Seq. No.
                   166654
Seq. ID
                   LIB3234-011-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g1710581
BLAST score
                   483
E value
                   8.0e-49
Match length
                   100
% identity
                   94
NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_
                   (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.
                   166655
Seq. ID
                   LIB3234-011-P1-K1-C4
                   BLASTN
Method
NCBI GI
                   g2494110
BLAST score
                   309
E value
                   1.0e-173
                   309
Match length
% identity
                   100
NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166656
Seq. ID
                   LIB3234-011-P1-K1-C5
                   BLASTN
Method
NCBI GI
                   q4199934
BLAST score
                   291
E value
                   1.0e-163
Match length
                   306
% identity
                   99
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
```

22462

complete sequence [Arabidopsis thaliana]



```
LIB3234-011-P1-K1-C6
Seq. ID
Method
                  BLASTN
                  g2494110
NCBI GI
BLAST score
                  276
E value
                  1.0e-154
Match length
                  308
                  97 ~
% identity
NCBI Description
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
                  166658
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-C9
Method
                  BLASTX
                  g4567199
NCBI GI
BLAST score
                  535
E value
                  6.0e-55
Match length
                  112
                  92
% identity
                 (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166659
                  LIB3234-011-P1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4544365
BLAST score
                  44
E value
                  1.0e-15
Match length
                   300
% identity
                   91
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F26H6 genomic
                   sequence, complete sequence
                   166660
Seq. No.
                  LIB3234-011-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4510392
BLAST score
                   99
E value
                  2.0e-48
Match length
                  103
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic
                  sequence, complete sequence
Seq. No.
                   166661
Seq. ID
                  LIB3234-011-P1-K1-D2
Method
                  BLASTX
NCBI GI
                   g687844
BLAST score
                   101
E value
                   5.0e-04
```

78 Match length % identity

(U21320) contains TPR domain-like repeats [Caenorhabditis NCBI Description

elegans]

166662 Seq. No.

Seq. ID LIB3234-011-P1-K1-D3

Method BLASTN NCBI GI g3859658



BLAST score 327 E value 0.0e+00 Match length 339 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 166663

Seq. ID LIB3234-011-P1-K1-D4

Method BLASTN
NCBI GI g3256065
BLAST score 272
E value 1.0e-151
Match length 292
% identity 98

NCBI Description Arabidopsis thaliana mRNA for chloroplast NAD-dependent

malate dehydrogenase

Seq. No. 166664

Seq. ID LIB3234-011-P1-K1-D5

Method BLASTN
NCBI GI g2114077
BLAST score 188
E value 1.0e-101
Match length 321
% identity 92

NCBI Description Arabidopsis thaliana DNA for larger subunit of Rubisco,

beta subunit of coupling factor one, partial cds

Seq. No. 166665

Seq. ID LIB3234-011-P1-K1-D6

Method BLASTN
NCBI GI g3256065
BLAST score 277
E value 1.0e-154

Match length 293 % identity 99

NCBI Description Arabidopsis thaliana mRNA for chloroplast NAD-dependent

malate dehydrogenase

Seq. No. 166666

Seq. ID LIB3234-011-P1-K1-D7

Method BLASTN
NCBI GI g2351068
BLAST score 231
E value 1.0e-127
Match length 347
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRH10, complete sequence [Arabidopsis thaliana]

Seq. No. 166667

Seq. ID LIB3234-011-P1-K1-D8

Method BLASTN
NCBI GI g2924257
BLAST score 50
E value 4.0e-19



```
Match length
                  113
                  86
% identity
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  166668
                  LIB3234-011-P1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869069
BLAST score
                  189
                  1.0e-102
E value
Match length
                  351
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
                  166669
Seq. No.
                  LIB3234-011-P1-K1-E10
Seq. ID
Method
                  BLASTN
                  q2583106
NCBI GI
BLAST score
                  282
                   1.0e-157
E value
                   347
Match length
                   99
% identity
```

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166670 LIB3234-011-P1-K1-E11 Seq. ID Method BLASTN NCBI GI q2656031 BLAST score 302 E value 1.0e-169

Match length 347 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC20

Seq. No. 166671

LIB3234-011-P1-K1-E12 Seq. ID

Method BLASTX NCBI GI g3522946 BLAST score 423 E value 8.0e-42 92 Match length % identity 88

NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 166672

LIB3234-011-P1-K1-E2 Seq. ID

Method BLASTX NCBI GI q4263791 BLAST score 298 E value 4.0e-27 116 Match length 53 % identity

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No.

Seq. ID

166678

LIB3234-011-P1-K1-F11



```
166673
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  480 .
E value
                  2.0e-48
Match length
                  105
                  95
% identity
NCBI Description
                  (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
Seq. No.
                  166674
                  LIB3234-011-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4512646
                  301
BLAST score
E value
                  1.0e-169
Match length
                  348
                  37
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F23N11 genomic
                  sequence, complete sequence
                  166675
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-E9
Method
                  BLASTN
                  g3985952
NCBI GI
BLAST score
                   260
                  1.0e-144
E value
                   346
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MRC8, complete sequence [Arabidopsis thaliana]
                   166676
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-F1
Method
                  BLASTX
NCBI GI
                   q4741960
BLAST score
                   363
E value
                   9.0e-35
Match length
                   93
% identity
                   77
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                   166677
Seq. ID
                   LIB3234-011-P1-K1-F10
Method
                  BLASTX
NCBI GI
                   g4586249
BLAST score
                   325
E value
                   2.0e-30
Match length
                  103
                   59
% identity
                  (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                   thaliana]
```

NCBI GI

E value

BLAST score

q2160144

164 2.0e-11



```
Method
                  BLASTN
NCBI GI
                  g2264306
BLAST score
                  331
                  0.0e+00
E value
Match length
                  343
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166679
                  LIB3234-011-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4585977
BLAST score
                  194
E value
                  6.0e-15
Match length
                  59
% identity
                  61
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  166680
Seq. ID
                  LIB3234-011-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  g2252823
BLAST score
                  273
E~value
                  1.0e-152
Match length
                  346
% identity
                  98
NCBI Description Arabidopsis thaliana BAC IG005I10
Seq. No.
                  166681
                  LIB3234-011-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4337186
BLAST score
                  196
E value
                  1.0e-106
Match length
                  241
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T28I24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166682
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g2160144
BLAST score
                  151
                  6.0e-10
E value
Match length
                  63
                  43
% identity
NCBI Description (AC000375) Strong similarity to Arabidopsis oligopeptide
                  transporter (gb X77503). [Arabidopsis thaliana]
                  166683
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-F6
Method
                  BLASTX
```



```
Match length
                   63
% identity
                   44
                  (AC000375) Strong similarity to Arabidopsis oligopeptide
NCBI Description
                   transporter (gb X77503). [Arabidopsis thaliana]
Seq. No.
                  166684
                  LIB3234-011-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3935151
BLAST score
                   535
E value
                   6.0e-55
Match length
                  100
% identity
                   99
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
                   166685
Seq. No.
                  LIB3234-011-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512666
BLAST score
                   587
E value
                   5.0e-61
Match length
                   115
                   92
% identity
                  (AC006931) putative mei2 protein [Arabidopsis thaliana]
NCBI Description
                   166686
Seq. No.
Seq. ID
                   LIB3234-011-P1-K1-G1
                   BLASTN
Method
NCBI GI
                   q2815404
                   252
BLAST score
E value
                   1.0e-140
Match length
                   300
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166687
Seq. ID
                   LIB3234-011-P1-K1-G10
Method
                   BLASTN
                                                            4.
NCBI GI
                   q4220641
BLAST score
                   318
E value
                   1.0e-179
Match length
                   346
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUL3, complete sequence [Arabidopsis thaliana]
                   166688
Seq. No.
                   LIB3234-011-P1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1362162
```

Method BLASTX
NCBI GI g1362162
BLAST score 262
E value 6.0e-23
Match length 66
% identity 74

NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]



166689

BLASTN

LIB3234-011-P1-K1-G12

Seq. No.

Seq. ID Method

```
NCBI GI
                  g2196463
BLAST score
                  341
E value
                  0.0e+00
Match length
                  357
                  99
% identity
NCBI Description Arabidopsis thaliana chloroplast trnC, rpoB & rpoC1 genes
                  166690
Seq. No.
                  LIB3234-011-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3327957
                  161
BLAST score
E value
                  4.0e-11
Match length
                  51
                  55
% identity
                  (AF060490) TLS-associated protein TASR-2 [Mus musculus]
NCBI Description
                  >gi_3327976 (AF067730) TLS-associated protein TASR-2 [Homo
                  sapiens]
                  166691
Seq. No.
                  LIB3234-011-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1592677
BLAST score
                  189
                  2.0e-14
E value
Match length
                  38
                  97
% identity
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                  166692
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  475
E value
                  6.0e - 48
Match length
                  96
% identity
                  99
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  166693
Seq. ID
                  LIB3234-011-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q3941528
BLAST score
                  647
E value
                  4.0e-68
Match length
                  116
% identity
                  99
NCBI Description
                  (AF062918) putative transcription factor [Arabidopsis
                  thaliana]
                  166694
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G6
Method
                  BLASTX
```



```
NCBI GI
                  q2341034
BLAST score
                  464
                  1.0e-46
E value
Match length
                  94
                  99
% identity
                 (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
                  166695
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q4510338
                  178
BLAST score
                  2.0e-95
E value
                  314
Match length
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC F2H17 genomic
NCBI Description
                  sequence, complete sequence
                  166696
Seq. No.
                  LIB3234-011-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  g2921158
NCBI GI
BLAST score
                  533
E value
                  1.0e-54
Match length
                  112
                  97
% identity
NCBI Description (AF022909) ClpC [Arabidopsis thaliana]
                  166697
Seq. No.
                  LIB3234-011-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2864607
BLAST score
                  317
E value
                   1.0e-178
Match length
                  341
% identity
                   98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
Seq. No.
                   166698
Seq. ID
                  LIB3234-011-P1-K1-H5
Method
                  BLASTN
NCBI GI
                   g2618683
BLAST score
                  317
E value
                   1.0e-178
Match length
                   345
% identity
                   98
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

166699 Seq. No.

Seq. ID LIB3234-011-P1-K1-H9

Method BLASTX NCBI GI g2605714 BLAST score 103 E value 2.0e-40 Match length 113



% identity 81

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 166700

Seq. ID LIB3234-012-P1-K1-A1

Method BLASTX
NCBI GI g2252844
BLAST score 354
E value 1.0e-33
Match length 78
% identity 83

NCBI Description (AF013293) belongs to the cytochrome p450 family

[Arabidopsis thaliana]

Seq. No. 166701

Seq. ID LIB3234-012-P1-K1-A10

Method BLASTX
NCBI GI g1345973
BLAST score 52
E value 9.0e-21
Match length 91
% identity 62

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis
thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 166702

Seq. ID LIB3234-012-P1-K1-A11

Method BLASTN
NCBI GI 94006885
BLAST score 312
E value 1.0e-175

E value 1.0e-3 Match length 324 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 166703

Seq. ID LIB3234-012-P1-K1-A2

Method BLASTN
NCBI GI g4309719
BLAST score 24
E value 1.0e-03
Match length 331
% identity 79

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166704

Seq. ID LIB3234-012-P1-K1-A4



```
Method
                     BLASTX
NCBI GI
                     q3763916
BLAST score
                     146
                      2.0e-09
E value
Match length
                     50
                      52
% identity
                     (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                     >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown
                     protein [Arabidopsis thaliana]
                     166705
Seq. No.
                     LIB3234-012-P1-K1-A5
Seq. ID
Method
                     BLASTN
                     g4417264
NCBI GI
BLAST score
                     111
E value
                     1.0e-55
Match length
                      302
                      72
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7D8 genomic
                     sequence, complete sequence [Arabidopsis thaliana]
                     166706
Seq. No.
                     LIB3234-012-P1-K1-A6
Seq. ID
Method
                     BLASTX
NCBI GI
                      q1914683
BLAST score
                      240
E value
                      2.0e-20
Match length
                      65
                      72
% identity
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
                      166707
Seq. No.
Seq. ID
                     LIB3234-012-P1-K1-A7
Method
                     BLASTX
NCBI GI
                      q1345973
BLAST score
                      440
E value
                      8.0e-44
Match length
                      94
% identity
                     OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
NCBI Description
                      omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                      microsomal omega-3 fatty acid desaturase [Arabidopsis
                      thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                      desaturase [Arabidopsis thaliana]
                      166708
Seq. No.
Seq. ID
                     LIB3234-012-P1-K1-A8
Method
                     BLASTN
```

NCBI GI g4159712
BLAST score 284
E value 1.0e-159
Match length 333
% identity 98



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No. 166709
```

Seq. ID LIB3234-012-P1-K1-A9 Method BLASTX
NCBI GI g1345973
BLAST score 629
E value 6.0e-66
Match length 114
% identity 100

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)

microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

```
Seq. No. 166710
```

Seq. ID LIB3234-012-P1-K1-B1

Method BLASTN
NCBI GI g3046856
BLAST score 338
E value 0.0e+00
Match length 350
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 166711

Seq. ID LIB3234-012-P1-K1-B11

Method BLASTX
NCBI GI g4512673
BLAST score 344
E value 1.0e-32
Match length 67
% identity 100

NCBI Description (AC006931) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 166712

Seq. ID LIB3234-012-P1-K1-B12

Method BLASTN
NCBI GI g2864607
BLAST score 39
E value 2.0e-13

Match length 67 % identity 67

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 166713

Seq. ID LIB3234-012-P1-K1-B4

Method BLASTN



```
NCBI GI
                  g4512656
BLAST score
                   301
E value
                   1.0e-169
                  343
Match length
% identity
                   89
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  166714
Seq. ID
                  LIB3234-012-P1-K1-B5
Method
                  BLASTN
NCBI GI
                   q4220637
BLAST score
                   318
E value
                   1.0e-179
Match length
                   342
% identity
                   89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166715
Seq. ID
                  LIB3234-012-P1-K1-B8
Method
                  BLASTN
NCBI GI
                   q4335711
BLAST score
                   339
E value
                   0.0e + 00
                   347
Match length
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166716
Seq. ID
                   LIB3234-012-P1-K1-B9
Method
                  BLASTN
NCBI GI
                   g4589421
                  99
BLAST score
E value
                   2.0e-48
Match length
                   140
                   92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K5K13, complete sequence
Seq. No.
                   166717
Seq. ID
                   LIB3234-012-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g4325340
BLAST score
                   282
E value
                   1.0e-157
Match length
                   350
                   95
% identity
NCBI Description Arabidopsis thaliana BAC T1J1
                   166718
Seq. No.
```

Seq. ID LIB3234-012-P1-K1-C11

Method BLASTX
NCBI GI g2129759
BLAST score 179
E value 4.0e-13



```
Match length
                  42
                  86
% identity
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
NCBI Description
                  >gi 1143392 emb CAA90941 (Z54214) uridine diphosphate
                  glucose epimerase [Arabidopsis thaliana]
                  166719
Seq. No.
                  LIB3234-012-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                  340
                  4.0e-32
E value
Match length
                  98
                  72
% identity
                  (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  166720
Seq. No.
                  LIB3234-012-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q343996
BLAST score
                  41
                  5.0e-14
E value
                  122
Match length
% identity
                  88
NCBI Description Pea chloroplast psbM gene for photosystem II polypeptide M
                  166721
Seq. No.
                  LIB3234-012-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21911
BLAST score
                  187
                  4.0e-14
E value
Match length
                  77
% identity
                  44
NCBI Description (X62625) vicilin [Theobroma cacao]
                  166722
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  48
E value
                  6.0e-18
Match length
                  72
% identity
                  92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
                  166723
Seq. No.
                  LIB3234-012-P1-K1-D1
Seq. ID
                  BLASTN
                  g3449326
```

Method NCBI GI BLAST score 34 E value 1.0e-09 Match length 54 91 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

Seq. No.

166729



```
K19M22, complete sequence [Arabidopsis thaliana]
```

Seq. No. 166724 LIB3234-012-P1-K1-D10 Seq. ID Method BLASTX NCBI GI q2996096 598 BLAST score 2.0e-62 E value Match length 113 100 % identity NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa] Seq. No. 166725 LIB3234-012-P1-K1-D12 Seq. ID Method BLASTN NCBI GI g511598 BLAST score 313 1.0e-176 E value Match length 341 33 % identity NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds Seq. No. 166726 Seq. ID LIB3234-012-P1-K1-D2 Method BLASTN NCBI GI g3046853 59 BLAST score 1.0e-24 E value 136 Match length 85 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRA19, complete sequence [Arabidopsis thaliana] 166727 Seq. No. Seq. ID LIB3234-012-P1-K1-D3 Method BLASTN NCBI GI q3046853 BLAST score 40 3.0e-13E value Match length 127 % identity 90 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana] Seq. No. 166728 Seq. ID LIB3234-012-P1-K1-D4 Method BLASTX NCBI GI q4582436 BLAST score 66 E value 9.0e-50 Match length 112 % identity NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]



```
LIB3234-012-P1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4263791
BLAST score
                   491
E value
                   8.0e-50
Match length
                   93
                   99
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   166730
Seq. No.
                   LIB3234-012-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q541847
BLAST score
                   608
E value
                   2.0e-63
                   114
Match length
                   100
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
                   166731
Seq. No.
                   LIB3234-012-P1-K1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220628
BLAST score
                   218
E value
                   1.0e-119
Match length
                   313
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24C1, complete sequence [Arabidopsis thaliana]
                   166732
Seq. No.
                   LIB3234-012-P1-K1-E2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2244747
BLAST score
                   338
E value
                   0.0e + 00
Match length
                   346
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   166733
                   LIB3234-012-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351837
BLAST score
                   522
                   2.0e-53
E value
Match length
                   110
                   91
% identity
NCBI Description ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
                   BETA >gi 2144155 pir S66564 acetyl CoA carboxylase type II
                   beta-carboxyltransferase chain - rape chloroplast
                   >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase
carboxyltransferase (beta subunit) [Brassica napus]
```

[Brassica napus]

>gi 1589046 prf 2210244G Ac-CoA carboxylase:SUBUNIT=beta



39

NCBI Description vicilin gene B [Saguinus oedipus]

% identity

```
166734
Seq. No.
                  LIB3234-012-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g2281085
NCBI GI
BLAST score
                  375
E value
                  3.0e-36
                  113
Match length
                  59
% identity
NCBI Description
                  (AC002333) CTR1 protein kinase isolog [Arabidopsis
                  thaliana]
                  166735
Seq. No.
                  LIB3234-012-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g4165132
NCBI GI
                  549
BLAST score
                  1.0e-56
E value
                  115
Match length
                  84
% identity
                 (AF098292) endo-beta-1,4-D-glucanase [Lycopersicon
NCBI Description
                  esculentum]
                  166736
Seq. No.
                  LIB3234-012-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345944
BLAST score
                  517
                  7.0e-53
E value
                  113
Match length
                  88
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR
NCBI Description
                   (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) >gi 598075
                   (L31891) 3-ketoacyl-acyl carrier protein synthase III (KAS
                   III) [Arabidopsis thaliana]
Seq. No.
                   166737
Seq. ID
                  LIB3234-012-P1-K1-E8
Method
                  BLASTN
NCBI GI
                   q4582411
BLAST score
                  250
E value
                   1.0e-138
Match length
                   345
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
                  complete sequence
Seq. No.
                   166738
Seq. ID
                   LIB3234-012-P1-K1-F1
Method
                  BLASTX
NCBI GI
                   g226120
BLAST score
                   239
E value
                   3.0e-20
                  115
Match length
```



```
Seq. No.
                  166739
                  LIB3234-012-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1946354
BLAST score
                  342
                  0.0e+00
E value
                  342
Match length
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                  sequence, complete sequence
```

 Seq. No.
 166740

 Seq. ID
 LIB3234-012-P1-K1-F11

 Method
 BLASTN

 NCBI GI
 g3292807

NCBI GI g329280
BLAST score 174
E value 4.0e-93
Match length 334
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No. 166741 LIB3234-012-P1-K1-F12 Seq. ID BLASTN Method NCBI GI g2618683 BLAST score 327 0.0e+00E value 331 Match length % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166742

Seq. ID LIB3234-012-P1-K1-F2

Method BLASTX
NCBI GI g2315135
BLAST score 214
E value 2.0e-17
Match length 49
% identity 88

NCBI Description (AB003522) beta subunit of coupling factor one [Arabidopsis

thaliana]

Seq. No. 166743

Seq. ID LIB3234-012-P1-K1-F3

Method BLASTX
NCBI GI g1172704
BLAST score 562
E value 4.0e-58
Match length 105
% identity 100

NCBI Description PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)

>gi_633940 (L39082) transport protein [Arabidopsis

thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine

transport protein PTR2-B [Arabidopsis thaliana]



```
166744
Seq. No.
                  LIB3234-012-P1-K1-F4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1707006
                  90
BLAST score
                  1.0e-43
E value
                  90
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166745
                  LIB3234-012-P1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589425
                  168
BLAST score
E value
                  1.0e-89
                  342
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBA10, complete sequence
                  166746
Seq. No.
                  LIB3234-012-P1-K1-F8
Seq. ID
Method
                  BLASTN
                  g4079614
NCBI GI
                   77
BLAST score
                   7.0e-36
E value
Match length
                  85
                   99
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   166747
Seq. No.
Seq. ID
                   LIB3234-012-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g3935151
BLAST score
                   615
E value
                   2.0e-64
Match length
                   113
% identity
                   100
NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                   166748
                   LIB3234-012-P1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2570223
BLAST score
                   78
                   7.0e-36
E value
                   258
Match length
                   84
% identity
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB3234-012-P1-K1-G2

Method BLASTX



NCBI GI g1079280 BLAST score 437 E value 2.0e-43 Match length 113 % identity 77

NCBI Description chaperonin containing TCP-1 complex gamma chain - African clawed frog >gi_793886_emb_CAA59350_ (X84990) Cctg [Xenopus

laevis]

Seq. No. 166750

Seq. ID LIB3234-012-P1-K1-G3

Method BLASTX
NCBI GI g2494125
BLAST score 375
E value 2.0e-36
Match length 91
% identity 86

NCBI Description (AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb_D70895). [Arabidopsis thaliana]

Seq. No. 166751

Seq. ID LIB3234-012-P1-K1-G4

Method BLASTX
NCBI GI g3107931
BLAST score 536
E value 4.0e-55
Match length 115
% identity 91

NCBI Description (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No. 166752

Seq. ID LIB3234-012-P1-K1-G5

Method BLASTX
NCBI GI g3107931
BLAST score 486
E value 3.0e-49
Match length 114
% identity 84

NCBI Description (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No. 166753

Seq. ID LIB3234-012-P1-K1-G7

Method BLASTX
NCBI GI g4204298
BLAST score 483
E value 7.0e-49
Match length 111
% identity 85

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 166754

Seq. ID LIB3234-012-P1-K1-G8

Method BLASTN
NCBI GI g3641835
BLAST score 302
E value 1.0e-169

E value

Match length

% identity

1.0e-114

309

94



Match length 339 % identity 97 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project) Seq. No. 166755 Seq. ID LIB3234-012-P1-K1-G9 Method BLASTX NCBI GI q3269286 BLAST score 395 E value 1.0e-38 Match length 98 % identity NCBI Description (AL030978) putative protein [Arabidopsis thaliana] 166756 Seq. No. Seq. ID LIB3234-012-P1-K1-H1 Method BLASTX NCBI GI g3688191 BLAST score 341 E value 3.0e-32 Match length 94 % identity 71 NCBI Description (AJ010090) MAP3K alpha protein kinase [Arabidopsis * thaliana] Seq. No. 166757 Seq. ID LIB3234-012-P1-K1-H11 Method BLASTN NCBI GI g14352 BLAST score 215 E value 1.0e-117 Match length 343 % identity 91 NCBI Description N.plumbaginifolia chloroplast 16SrDNA, trnV and trnI genes for 16S ribosomal RNA, transfer RNA-Val and transfer RNA-Ile (5'exon) Seq. No. 166758 Seq. ID LIB3234-012-P1-K1-H12 Method BLASTN NCBI GI g3869075 BLAST score 345 E value 0.0e+00Match length 345 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana] 166759 Seq. No. Seq. ID LIB3234-012-P1-K1-H2 Method BLASTN NCBI GI g3402695 BLAST score 210



```
NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166760
                  LIB3234-012-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  626
E value
                   1.0e-65
Match length
                  120
% identity
                   100
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  166761
Seq. ID
                  LIB3234-012-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2894574
BLAST score
                  524
E value
                  1.0e-53
Match length
                  99
                   100
% identity
NCBI Description
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
                  >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                  166762
Seq. ID
                  LIB3234-012-P1-K1-H8
Method `
                  BLASTN
NCBI GI
                  g3108024
BLAST score
                  325
E value
                  0.0e + 00
Match length
                  333
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T1F15 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166763
Seq. ID
                  LIB3234-012-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g3108024
BLAST score
                  171
                  2.0e-91
E value
Match length
                  263
% identity
                  91
NCBI Description Arabidopsis thaliana chromosome 1 BAC T1F15 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166764
Seq. ID
                  LIB3234-013-P1-K1-A1
                  BLASTX
                  g4204299
```

Method NCBI GI BLAST score 534 E value 1.0e-54Match length 109 % identity 93

NCBI Description (AC003027) lcl_prt_seq No definition line found



[Arabidopsis thaliana]

```
Seq. No.
                   166765
Seq. ID
                   LIB3234-013-P1-K1-A11
Method
                   BLASTN
NCBI GI
                   q2760167
BLAST score
                   159
                   2.0e-84
E value
Match length
                   167
% identity
                   34
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
                   166766
Seq. No.
Seq. ID
                   LIB3234-013-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q134025
BLAST score
                   403
E value
                   2.0e-39
Match length
                   96
                   82
% identity
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi 70913 pir R3NT8
                   ribosomal protein S8 - common tobacco chloroplast
                   >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8
[Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal
                   protein S8 [Nicotiana tabacum]
Seq. No.
                   166767
Seq. ID
                   LIB3234-013-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g3661595
BLAST score
                   300
E value
                   2.0e-27
Match length
                   54
% identity
                   100
NCBI Description
                   (AF091844) aminoalcoholphosphotransferase [Arabidopsis
                   thaliana]
Seq. No.
                   166768
Seq. ID
                   LIB3234-013-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   g4741797
BLAST score
                   148
E value
                   1.0e-77
Match length
                   302
% identity
                   97
NCBI Description Arabidopsis thaliana repeat region IID2-8 sequence
Seq. No.
                   166769
Seq. ID
                   LIB3234-013-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g99697
BLAST score
                   667
E value
                   2.0e-70
Match length
                   122
% identity
                   98
```

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone



lambdaAtgsr2) - Arabidopsis thaliana

Seq. No. 166770 Seq. ID

LIB3234-013-P1-K1-A7

Method BLASTX NCBI GI g4204299 BLAST score 611 8.0e-64 E value Match length 122 98 % identity

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 166771

LIB3234-013-P1-K1-A8 Seq. ID

Method BLASTX NCBI GI q2104949 BLAST score 388 E value 1.0e-37 Match length 95 % identity 80

NCBI Description (U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No. 166772

Seq. ID LIB3234-013-P1-K1-B1

Method BLASTN NCBI GI q4678315 BLAST score 317 E value 1.0e-178 Match length 361 % identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15

(ESSA project)

Seq. No. 166773

Seq. ID LIB3234-013-P1-K1-B12

Method BLASTX NCBI GI g4490330 BLAST score 328 E value 4.0e-31 Match length 67 % identity 90

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis

thaliana]

Seq. No. 166774

Seq. ID LIB3234-013-P1-K1-B3

Method BLASTX NCBI GI q132939 BLAST score 522 E value 2.0e-53 Match length 107 % identity 92

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 81657 pir JQ0771 ribosomal

protein L3 (ARP1) - Arabidopsis thaliana >gi 166858 (M32654) ribosomal protein [Arabidopsis thaliana]



166775 Seq. No.

Seq. ID LIB3234-013-P1-K1-B5

Method BLASTX NCBI GI q2244750 BLAST score 514 2.0e-52E value Match length 114 % identity

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

166776 Seq. No.

Seq. ID LIB3234-013-P1-K1-B6

Method BLASTX NCBI GI a129871 BLAST score 179 4.0e-13 E value Match length 36 % identity 100

NCBI Description CYTOCHROME B6-F COMPLEX SUBUNIT 5 >gi_65644_pir__WMRZ4

cytochrome b6-f complex 4.2K protein - rice chloroplast >gi_100947_pir__A32159 plastoquinol--plastocyanin reductase

(EC 1.10.99.1) chain V - maize chloroplast

>gi_2147243_pir__S68166 cytochrome b6-f complex chain 5 -

beet chloroplast >gi_12006_emb_CAA33967_ (X15901)

cytochrome b /f complex subunit 5 [Oryza sativa] >gi 342588 (J04502) cytochrome b6-f complex subunit 5 (petE) [Zea

mays] >gi_533296_dbj_BAA07216_ (D38019) cytochrome b6/f complex subunit 5 [Beta vulgaris] >gi_533302_dbj_BAA07222_ (D38020) cytochrome b6/f complex subunit 5 [Beta trigyna] >gi_533304_dbj_BAA07223_ (D38021) cytochrome b6/f complex subunit 5 [Beta webbiana] >gi_860888_emb_CAA60964_ (X87636)

cytochrome b6-f complex subunit 5 [Beta vulgaris]

>gi_860894_emb_CAA60969 (X87637) petG [Beta vulgaris]
>gi_902240_emb_CAA60304 (X86563) cytochrome b /f complex
subunit 5 [Zea mays] >gi_2612818_emb_CAA75627 (Y15429) cytochrome b6/f-complex subunit V [Populus deltoides] >gi_2924268_emb_CAA77420_ (Z00044) cytochrome b/f complex

subunit V [Nicotiana tabacum] >gi 226628 prf 1603356BB cytochrome b/f complex 5 [Oryza sativa]

Seq. No. 166777

Seq. ID LIB3234-013-P1-K1-B7

Method BLASTX NCBI GI q2076623 BLAST score 162 E value 4.0e-11 Match length 110 34 % identity

NCBI Description (Z95151) PtrB [Mycobacterium leprae]

Seq. No. 166778

Seq. ID LIB3234-013-P1-K1-B8

Method BLASTN NCBI GI g3193305 BLAST score 357

E value

Match length

% identity

2.0e-19

74

58



```
E value
                   0.0e + 00
Match length
                   361
% identity
                   100
NCBI Description
                  Arabidopsis thaliana BAC F3D13
                   166779
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-C1
Method
                  BLASTN
NCBI GI
                   q2264303
BLAST score
                   38
E value
                   6.0e-12
Match length
                   66
                   89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBB18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166780
Seq. ID
                  LIB3234-013-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g4584841
BLAST score
                  157
E value
                   6.0e-83
                   372
Match length
% identity
                   47
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T23E23,
                   complete sequence
Seq. No.
                   166781
Seq. ID
                  LIB3234-013-P1-K1-C11
Method
                  BLASTN
NCBI GI
                   g3241917
BLAST score
                   363
E value
                   0.0e+00
Match length
                   367
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166782
Seq. ID
                  LIB3234-013-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g3241917
BLAST score
                  246
E value
                   1.0e-136
Match length
                  330
% identity
                   94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166783
Seq. ID
                  LIB3234-013-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4679028
BLAST score
                  233
```

% identity



```
NCBI Description (AF077207) HSPC021 [Homo sapiens]
                  166784
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3046851
BLAST score
                  319
E value
                  1.0e-179
Match length
                  368
                  99
% identity
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166785
                  LIB3234-013-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g2275202
NCBI GI
BLAST score
                  309
E value
                  2.0e-28
Match length
                  59
                  100
% identity
NCBI Description
                  (AC002337) acyl-CoA synthetase isolog [Arabidopsis
                  thaliana]
Seq. No.
                  166786
                  LIB3234-013-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2970654
                  437
BLAST score
E value
                  2.0e-43
Match length
                  120
% identity
                  71
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                  unguiculata]
Seq. No.
                  166787
Seq. ID
                  LIB3234-013-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2130051
BLAST score
                  348
E value
                   5.0e-33
Match length
                  96
% identity
                   68
NCBI Description
                  xylose isomerase (EC 5.3.1.5) - barley
                  >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase
                   [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                  isomerase [Hordeum vulgare]
Seq. No.
                  166788
Seq. ID
                  LIB3234-013-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g82051
BLAST score
                  294
E value
                  1.0e-26
Match length
                  111
```

22488

NCBI Description lipid body-associated membrane protein - carrot



>gi_259453_bbs_117620 (S47635) lipid body membrane
protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
180 aa] [Daucus carota]

Seq. No. 166789

Seq. ID LIB3234-013-P1-K1-D3

Method BLASTX
NCBI GI g1170939
BLAST score 372
E value 8.0e-36
Match length 74
% identity 95

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi 1084408 pir S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 166790

Seq. ID LIB3234-013-P1-K1-D4

Method BLASTN
NCBI GI g4519184
BLAST score 207
E value 1.0e-113

E value 1.0e-11 Match length 252 % identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K16F13, complete sequence

Seq. No. 166791

Seq. ID LIB3234-013-P1-K1-D5

Method BLASTN
NCBI GI g3242700
BLAST score 39
E value 1.0e-12
Match length 107
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F26B6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166792

Seq. ID LIB3234-013-P1-K1-D7

Method BLASTX
NCBI GI g2244800
BLAST score 348
E value 5.0e-33
Match length 86
% identity 78

NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No. 166793

Seq. ID LIB3234-013-P1-K1-D8

Method BLASTX
NCBI GI g2244800
BLAST score 519
E value 5.0e-53



```
Match length
                   104
% identity
NCBI Description
                  (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.
                  166794
Seq. ID
                  LIB3234-013-P1-K1-E1
                  BLASTX
Method
                  g541847
NCBI GI
BLAST score
                   262
E value
                   3.0e-23
Match length
                   54
                   93
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                  166795
Seq. ID
                  LIB3234-013-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  582
E value
                  2.0e-60
Match length
                  121
% identity
                   91
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937 emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  166796
                  LIB3234-013-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1402904
BLAST score
                  548
E value
                  2.0e-56
Match length
                  104
% identity
                  100
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                  166797
Seq. ID
                  LIB3234-013-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2459432
BLAST score
                  247
E value
                  3.0e-21
Match length
                  49
% identity
                  88
                  (AC002332) CONSTANS-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166798
Seq. ID
                  LIB3234-013-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  g4757662
BLAST score
                  145
E value
                  8.0e-76
Match length
                  370
% identity
                  99
```

22490

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

Match length

113



chromosome I, complete sequence

Seq. No. 166799 Seq. ID LIB3234-013-P1-K1-E6 Method BLASTN NCBI GI q4220645 BLAST score 199 1.0e-108 E value Match length 354 % identity 97 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MYA6, complete sequence [Arabidopsis thaliana] 166800 Seq. No. LIB3234-013-P1-K1-E7 Seq. ID Method BLASTX g115778 NCBI GI BLAST score 141 E value 5.0e-31 Match length 90 % identity 78 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_282896_pir S22511 chlorophyll a/b-binding protein (cab-1) - white mustard >gi_21138_emb_CAA34459 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi_21140_emb_CAA33903 (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba] Seq. No. 166801 LIB3234-013-P1-K1-E8 Seq. ID Method BLASTN NCBI GI q2618603 BLAST score 225 E value 1.0e-123 Match length 345 % identity 97 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSL3, complete sequence [Arabidopsis thaliana] Seq. No. 166802 Seq. ID LIB3234-013-P1-K1-E9 Method BLASTN NCBI GI g3449334 BLAST score 333 E value 0.0e+00Match length 358 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana] Seq. No. 166803 Seq. ID LIB3234-013-P1-K1-F1 Method BLASTX NCBI GI g2252844 BLAST score 594 E value 8.0e-62



```
% identity
                   100
NCBI Description
                  (AF013293) belongs to the cytochrome p450 family
                   [Arabidopsis thaliana]
Seq. No.
                  166804
                  LIB3234-013-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  277
E value
                  1.0e-154
Match length
                  349
% identity
                  92
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166805
                  LIB3234-013-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                  623
E value
                  3.0e-65
Match length
                  120
                  100
% identity
NCBI Description
                  (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  166806
                  LIB3234-013-P1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  277
E value
                  1.0e-154
Match length
                  347
% identity
                  92
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166807
Seq. ID
                  LIB3234-013-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  399
E value
                  6.0e - 39
Match length
                  81
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  166808
Seq. ID
                  LIB3234-013-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  309
```

2.0e-28 E value Match length 95 % identity 64

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260



(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 166809

Seq. ID LIB3234-013-P1-K1-F6

Method BLASTX
NCBI GI g4165488
BLAST score 583
E value 2.0e-60
Match length 107
% identity 100

NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 166810

Seq. ID LIB3234-013-P1-K1-F7

Method BLASTN
NCBI GI g1490552
BLAST score 87
E value 3.0e-41
Match length 218
% identity 86

NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase

(SAMdc) mRNA, complete cds

Seq. No. 166811

Seq. ID LIB3234-013-P1-K1-F8

Method BLASTN
NCBI GI g4581161
BLAST score 50
E value 5.0e-19
Match length 134
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 166812

Seq. ID LIB3234-013-P1-K1-F9

Method BLASTN
NCBI GI g3869069
BLAST score 274
E value 1.0e-153
Match length 359
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 166813

Seq. ID LIB3234-013-P1-K1-G10

Method BLASTN
NCBI GI 94587986
BLAST score 201
E value 1.0e-109
Match length 328
% identity 98

NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete

sequence

Seq. No. 166814



```
LIB3234-013-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707657
BLAST score
                  218
                  1.0e-17
E value
                  88
Match length
                  57
% identity
                  (Z71640) DnaJ homologue [Pisum sativum]
NCBI Description
Seq. No.
                  166815
Seq. ID
                  LIB3234-013-P1-K1-G2
Method
                  BLASTN
NCBI GI
                   q2894591
BLAST score
                   366
E value
                   0.0e + 00
Match length
                  366
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                   (ESSAII project)
                   166816
Seq. No.
                  LIB3234-013-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1531762
                  195
BLAST score
E value
                   5.0e-15
Match length
                   51
                   75
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   166817
Seq. No.
Seq. ID
                   LIB3234-013-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g4580454
BLAST score
                   353
E value
                   0.0e + 00
Match length
                   370
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic
                   sequence, complete sequence
Seq. No.
                   166818
Seq. ID
                   LIB3234-013-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   150
E value
                   9.0e-10
                   76
Match length
                   59
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
```

Seq. No. 166819

storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

166824

LIB3234-013-P1-K1-H2



```
LIB3234-013-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q881615
BLAST score
                   558
E value
                   1.0e-57
Match length
                  118
                   92
% identity
NCBI Description
                   (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                  >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
Seq. No.
                   166820
                  LIB3234-013-P1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3789706
BLAST score
                   38
E value
                   6.0e-12
Match length
                  106
                   59
% identity
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  166821
Seq. No.
                  LIB3234-013-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4406752
BLAST score
                   266
E value
                   1.0e-148
                   340
Match length
                   49
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F19B11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   166822
Seq. No.
                   LIB3234-013-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2541876
BLAST score
                   181
E value
                   2.0e-13
Match length
                   58
                   52
% identity
NCBI Description
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
                   [Nicotiana tabacum]
Seq. No.
                   166823
Seq. ID
                   LIB3234-013-P1-K1-H12
Method
                   BLASTN
NCBI GI
                   g166913
BLAST score
                   192
                   1.0e-104
E value
Match length
                   221
% identity
                   100
                  Arabidopsis thaliana alpha-2 tubulin (TUA2) gene, exon and
NCBI Description
                   5' end
```



```
Method
                  BLASTN
NCBI GI
                  g4455321
BLAST score
                  369
E value
                  0.0e+00
Match length
                  369
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                  (ESSAII project)
Seq. No.
                  166825
Seq. ID
                  LIB3234-013-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g2760165
BLAST score
                  300
E value
                  1.0e-168
Match length
                  365
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166826
Seq. ID
                  LIB3234-013-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4432845
BLAST score
                  149
E value
                  1.0e-09
Match length
                  63
                  57
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166827
Seq. ID
                  LIB3234-015-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g131378
BLAST score
                  210
E value
                  9.0e-17
Match length
                  43
% identity
                  98
NCBI Description
                  PHOTOSYSTEM II REACTION CENTRE N PROTEIN
                  >gi_2924272_emb_CAA77424 (Z00044) PSII N-protein
                  [Nicotiana tabacum]
Seq. No.
                  166828
Seq. ID
                  LIB3234-015-P1-K1-A11
Method
                  BLASTN
                  q2114077
                  114
                  2.0e-57
                  238
```

NCBI GI BLAST score E value Match length % identity 89

NCBI Description Arabidopsis thaliana DNA for larger subunit of Rubisco,

beta subunit of coupling factor one, partial cds

Seq. No. 166829

Seq. ID LIB3234-015-P1-K1-A12

Method BLASTX NCBI GI g4582446



```
BLAST score
                  210
                  8.0e-17
E value
Match length
                  87
% identity
                  55
                 (AC007071) putative RING finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166830
Seq. ID
                  LIB3234-015-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  q4558521
BLAST score
                  284
E value
                  1.0e-158
Match length
                  332
% identity
                  99
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
Seq. No.
                  166831
Seq. ID
                  LIB3234-015-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g2213606
BLAST score
                  351
E value
                  0.0e + 00
Match length
                  367
                  99
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
                  166832
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-A7
                  BLASTN
Method
                  g1490552
NCBI GI
                  266
BLAST score
E value
                  1.0e-148
                  296
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase
                  (SAMdc) mRNA, complete cds
Seq. No.
                  166833
Seq. ID
                  LIB3234-015-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q1903034
BLAST score
                  250
E value
                  2.0e-21
Match length
                  106
                  46
% identity
NCBI Description (X94625) amp-binding protein [Brassica napus]
                  166834
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-B3
Method
                  BLASTN
```

NCBI GI q3482964 BLAST score 319 E value 1.0e-179 351

Match length



```
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
                   (ESSAII project)
Seq. No.
                  166835
                  LIB3234-015-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3482964
BLAST score
                  193
E value
                  1.0e-104
Match length
                  310
% identity
                  92
NCBI Description Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
                  (ESSAII project)
Seq. No.
                  166836
Seq. ID
                  LIB3234-015-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2245070
BLAST score
                  166
E value
                  1.0e-11
Match length
                  102
                  32
% identity
NCBI Description
                 (Z97342) hypothetical protein [Arabidopsis thaliana]
                  166837
Seq. No.
                  LIB3234-015-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377815
                  562
BLAST score
E value
                  4.0e-58
Match length
                  123
                  91
% identity
NCBI Description
                  (AF076275) similar to protein kinases (Pfam: pkinase.hmm,
                  score: 255.71) [Arabidopsis thaliana]
Seq. No.
                  166838
                  LIB3234-015-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q395203
BLAST score
                  52
                  7.0e-21
E value
Match length
                  68
% identity
                  69
NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's
Seq. No.
                  166839
Seq. ID
                  LIB3234-015-P1-K1-B8
Method
                  BLASTX
                  g225280
NCBI GI
BLAST score
                  357
E value
                  5.0e - 34
Match length
                  71
                  97
% identity
NCBI Description rpoC-like ORF 548 [Nicotiana tabacum]
```

Seq. No. 166840



```
Seq. ID
                    LIB3234-015-P1-K1-B9
 Method
                    BLASTN
 NCBI GI
                    g4220635
  BLAST score
                    161
                    2.0e-85
 E value
 Match length
                    327
  % identity
                    97
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                    MDB19, complete sequence [Arabidopsis thaliana]
                    166841
  Seq. No.
                    LIB3234-015-P1-K1-C1
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2879800
 BLAST score
                    259
 E value
                    2.0e-22
 Match length
                    123
  % identity
                    41
                    (AL021813) phenylalanyl-trna synthetase alpha chain
 NCBI Description
                    [Schizosaccharomyces pombe]
Seq. No.
                    166842
 Seq. ID
                    LIB3234-015-P1-K1-C10
 Method
                    BLASTX
 NCBI GI
                    g4586249
 BLAST score
                    339
                    7.0e-32
 E value
 Match length
                    102
  % identity
                    63
                    (AL049640) putative pollen surface protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    166843
                    LIB3234-015-P1-K1-C4
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2342673
 BLAST score
                    359
 E value
                    0.0e + 00
                    367
 Match length
  % identity
                    99
                    Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
 NCBI Description
                    1, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    166844
                    LIB3234-015-P1-K1-C7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4582468
 BLAST score
                    549
 E value
                    2.0e-56
 Match length
                    112
  % identity
 NCBI Description
                    (AC007071) putative 40S ribosomal protein; contains
                    C-terminal domain [Arabidopsis thaliana]
```

Seq. No. 166845

Seq. ID LIB3234-015-P1-K1-C8

Method BLASTN

```
NCBI GI
                   g4140256
BLAST score
                   358
E value
                   0.0e + 00
Match length
                   374
                   79
% identity
NCBI Description Arabidopsis thaliana mRNA for LEA-like protein
Seq. No.
                   166846
                   LIB3234-015-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3808062
BLAST score
                   159
E value
                   8.0e-11
Match length
                   66
% identity
                   45
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                   166847
                   LIB3234-015-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   656
E value
                   4.0e-69
Match length
                   124
% identity
                   100
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   166848
                   LIB3234-015-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982437
BLAST score
                   453
E value
                  .3.0e-45
Match length
                . 123
% identity
                   68
NCBI Description
                  (AL022224) terpene cyclase like protein [Arabidopsis
                   thaliana]
                   166849
Seq. No.
Seq. ID
                   LIB3234-015-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g2982437
BLAST score
                   355
E value
                   8.0e-34
Match length
                   102
% identity
                   65
NCBI Description
                   (AL022224) terpene cyclase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   166850
Seq. ID
                   LIB3234-015-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g4757414
BLAST score
                   356
E value
                   0.0e + 00
Match length
                   372
```



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
                  166851
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-D2
Method
                  BLASTX
                  g1708464
NCBI GI
BLAST score
                  225
                  1.0e-18
E value
                  62
Match length
                  66
% identity
                  PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)
NCBI Description
                  (2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_
                  (Z69795) unknown [Schizosaccharomyces pombe]
                  166852
Seq. No.
                  LIB3234-015-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  486
                  4.0e-49
E value
                  112
Match length
                  85
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  166853
                  LIB3234-015-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  q3980417
NCBI GI
BLAST score
                  656
                  4.0e-69
E value
                  123
Match length
% identity
NCBI Description
                 (AC004561) pumilio-like protein [Arabidopsis thaliana]
                  166854
Seq. No.
                  LIB3234-015-P1-K1-D5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2564049
BLAST score
                  63
                  7.0e-27
E value
Match length
                  131
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
                  166855
```

Seq. No. LIB3234-015-P1-K1-D6 Seq. ID

BLASTX Method g3149952 NCBI GI

259 BLAST score 2.0e-22 E value



Match length 44 % identity 100

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 166856

Seq. ID LIB3234-015-P1-K1-D7

Method BLASTN
NCBI GI g2618604
BLAST score 264
E value 1.0e-147
Match length 362
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 166857

Seq. ID LIB3234-015-P1-K1-D8

Method BLASTX
NCBI GI g2160137
BLAST score 211
E value 7.0e-17
Match length 93
% identity 56

NCBI Description (AC000375) Similar to Arabidopsis light repressible

receptor protein kinase (gb_X97774). [Arabidopsis thaliana]

Seq. No. 166858

Seq. ID LIB3234-015-P1-K1-E11

Method BLASTX
NCBI GI g2462931
BLAST score 634
E value 2.0e-66
Match length 122
% identity 97

NCBI Description (Z83833) UDP-glucose:sterol glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 166859

Seq. ID LIB3234-015-P1-K1-E12

Method BLASTX
NCBI GI g266839
BLAST score 271
E value 6.0e-24
Match length 57
% identity 98

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir__S29240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha

chain - Arabidopsis thaliana >gi_16445_emb_CAA47298_ (X66825) proteosome alpha subunit [Arabidopsis thaliana]

>gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
proteasome:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 166860

Seq. ID LIB3234-015-P1-K1-E3

Method BLASTX



```
NCBI GI
                  g4204298
BLAST score
                  517
                  9.0e-53
E value
Match length
                  118
% identity
                  85
                   (AC003027) lcl_prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  166861
Seq. No.
                  LIB3234-015-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4261517
BLAST score
                  194
                  6.0e-15
E value
Match length
                  77
                  58
% identity
                  (AF117334) cysteine proteinase inhibitor [Ipomoea batatas]
NCBI Description
                  166862
Seq. No.
                  LIB3234-015-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3985934
BLAST score
                   329
                   0.0e+00
E value
Match length
                   367
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
                  166863
Seq. No.
                  LIB3234-015-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g585744
NCBI GI
                   138
BLAST score
                   7.0e-09
E value
                   29
Match length
% identity
                   97
NCBI Description PHOTOSYSTEM II REACTION CENTRE T PROTEIN
                   166864
Seq. No.
                   LIB3234-015-P1-K1-F1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2275194
BLAST score
                   47
                   2.0e-17
E value
Match length
                   103
```

166865 Seq. No.

% identity

NCBI Description

LIB3234-015-P1-K1-F11 Seq. ID

86

Method BLASTX NCBI GI g3451071 BLAST score 488 2.0e-49 E value Match length 104

22503

Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 166866

Seq. ID LIB3234-015-P1-K1-F12

Method BLASTX
NCBI GI g3763925
BLAST score 231
E value 3.0e-19
Match length 44
% identity 100

NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No. 166867

Seq. ID LIB3234-015-P1-K1-F2

Method BLASTN
NCBI GI g4468801
BLAST score 293
E value 1.0e-164
Match length 367
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17

(ESSA project)

Seq. No. 166868

Seq. ID LIB3234-015-P1-K1-F4

Method BLASTX
NCBI GI g1864017
BLAST score 548
E value 2.0e-56
Match length 104
% identity 100

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 166869

Seq. ID LIB3234-015-P1-K1-F5

Method BLASTN
NCBI GI g2264321
BLAST score 223
E value 1.0e-122
Match length 372
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 166870

Seq. ID LIB3234-015-P1-K1-F6

Method BLASTX
NCBI GI g1107501
BLAST score 462
E value 2.0e-46
Match length 112
% identity 84

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

Match length

% identity

45 91



this gene. [Arabidopsis thaliana]

```
Seq. No.
                   166871
                  LIB3234-015-P1-K1-G1
Seq. ID
Method
                  BLASTN
                   g2760165
NCBI GI
                   82
BLAST score
                   3.0e-38
E value
                   360
Match length
                   84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166872
                  LIB3234-015-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3873174
BLAST score
                   317
                   1.0e-178
E value
                   353
Match length
                   97
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   166873
                   LIB3234-015-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131336
BLAST score
                   339
                   6.0e-32
E value
Match length
                   73
% identity
                   93
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
NCBI Description
                   photosystem II phosphoprotein psbH - common tobacco
                   chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
                   >gi_225225_prf__1211235BG photosystem II 10kD
                   phosphoprotein [Nicotiana tabacum]
Seq. No.
                   166874
Seq. ID
                   LIB3234-015-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q3702331
BLAST score
                   390
E value
                   6.0e-38
Match length
                   118
% identity
NCBI Description
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166875
Seq. ID
                   LIB3234-015-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1669668
BLAST score
                   215
E value
                   1.0e-17
```



```
(X97131) EF1-alpha [Forsythia x intermedia]
NCBI Description
                   166876
Seq. No.
                   LIB3234-015-P1-K1-G7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4531433
                   332
BLAST score
                   0.0e+00
E value
                   364
Match length
                   98
% identity
                   Arabidopsis thaliana chromosome II P1 MFL8 genomic
NCBI Description
                   sequence, complete sequence
                   166877
Seq. No.
                   LIB3234-015-P1-K1-G8
Seq. ID
Method
                   BLASTN
                   g2262155
NCBI GI
BLAST score
                   366
                   0.0e + 00
E value
                   370
Match length
                   100
% identity
NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from
                   chromosome IV, complete sequence [Arabidopsis thaliana]
                   166878
Seq. No.
                   LIB3234-015-P1-K1-G9
Seq. ID
                   BLASTX
Method
                   g125576
NCBI GI
                   401
BLAST score
                   3.0e - 39
E value
                   96
Match length
                   84
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana
                   >gi_16441_emb_CAA41155 (X58149) Ribulose-5-phosphate
                   kinase [Arabidopsis thaliana]
Seq. No.
                   166879
                   LIB3234-015-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3395432
                   513
BLAST score
                   3.0e-52
E value
                   100
Match length
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   166880
                   LIB3234-015-P1-K1-H11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3334860
BLAST score
                   66
E value
                   1.0e-28
                   220
Match length
                   92
% identity
NCBI Description Solanum tuberosum chloroplast tRNA-Asn, tRNA-Arg genes
```



Seq. No. 166881 LIB3234-015-P1-K1-H12 Seq. ID Method BLASTX NCBI GI g3033386 BLAST score 242 1.0e-20 E value 82 Match length 66 % identity (AC004238) RING3-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 166882 LIB3234-015-P1-K1-H3 Seq. ID Method BLASTX NCBI GI q2827699 BLAST score 409 4.0e-40 E value 96 Match length 83 % identity (AL021684) predicted protein [Arabidopsis thaliana] NCBI Description Seq. No. 166883 LIB3234-015-P1-K1-H4 Seq. ID Method BLASTX NCBI GI g4335749 533 BLAST score E value 1.0e-54 Match length 103 99 % identity NCBI Description (AC006284) unknown protein [Arabidopsis thaliana] Seq. No. 166884 LIB3234-015-P1-K1-H5 Seq. ID Method BLASTX NCBI GI g1350783 BLAST score 324 E value 2.0e-30 Match length 76 86 % identity NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi 282883 pir S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana] Seq. No. 166885 Seq. ID LIB3234-015-P1-K1-H6 Method BLASTX

Method BLASTX
NCBI GI g3033386
BLAST score 391
E value 5.0e-38
Match length 124
% identity 68

NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No. 166886



Seq. ID LIB3234-015-P1-K1-H7 Method BLASTN NCBI GI q12279 89 BLAST score 2.0e-42 E value Match length 165 % identity 94 Spinach chloroplast genes for the D2 and 44 kd reaction NCBI Description centre, chlorophyll a-binding protein and for tRNA-Ser (UGA) Seq. No. 166887 LIB3234-015-P1-K1-H8 Seq. ID Method BLASTX NCBI GI q1345973 BLAST score 421 2.0e-41 E value Match length 95 % identity 81 NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana] Seq. No. 166888 LIB3234-015-P1-K1-H9 Seq. ID Method BLASTX g2781354 NCBI GI 254 BLAST score 5.0e-22 E value 49 Match length 100 % identity NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana] 166889 Seq. No. LIB3234-016-P1-K1-A10 Seq. ID Method BLASTX NCBI GI q3096910 BLAST score 535 6.0e-55 E value 114 Match length 88 % identity NCBI Description (AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana] Seq. No. 166890 LIB3234-016-P1-K1-A11 Seq. ID

Method BLASTN

NCBI GI g4510338 BLAST score 339 0.0e + 00E value Match length 343



% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No. 166891

Seq. ID LIB3234-016-P1-K1-A12

Method BLASTN
NCBI GI g3046852
BLAST score 196
E value 1.0e-106
Match length 336
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No. 166892

Seq. ID LIB3234-016-P1-K1-A2

Method BLASTN
NCBI GI g2864607
BLAST score 350
E value 0.0e+00
Match length 357
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 166893

Seq. ID LIB3234-016-P1-K1-A3

Method BLASTX
NCBI GI g1864017
BLAST score 502
E value 5.0e-51
Match length 95
% identity 100

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 166894

Seq. ID LIB3234-016-P1-K1-A4

Method BLASTX
NCBI GI g1669668
BLAST score 370
E value 1.0e-35
Match length 80
% identity 91

NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]

Seq. No. 166895

Seq. ID LIB3234-016-P1-K1-A5

Method BLASTX
NCBI GI 94455342
BLAST score 143
E value 6.0e-09
Match length 29
% identity 100

NCBI Description (AL035522) O-methyltransferase-like protein [Arabidopsis

thaliana]



```
166896
Seq. No.
Seq. ID
                  LIB3234-016-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  q4455339
BLAST score
                  242
                  1.0e-134
E value
Match length
                  331
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
NCBI Description
                  (ESSAII project)
Seq. No.
                  166897
                  LIB3234-016-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3249107
BLAST score
                  434
                  4.0e-43
E value
Match length
                  90
                  91
% identity
NCBI Description
                  (AC003114) Contains similarity to phloem-specific lectin
                  PP2 gb Z17331 from Cucubita maxima. [Arabidopsis thaliana]
Seq. No.
                  166898
                  LIB3234-016-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  247
E value
                  4.0e-21
                  85
Match length
% identity
                  58
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  166899
                  LIB3234-016-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99688
BLAST score
                  603
E value
                  6.0e-63
Match length
                  116
                  99
% identity
NCBI Description
                  translation elongation factor eEF-1 alpha chain (gene A4) -
                  Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                  166900
                  LIB3234-016-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  166
                  2.0e-88
E value
Match length
                  355
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
```

Seq. No. 166901

Seq. ID LIB3234-016-P1-K1-B10

Method BLASTX



```
g4056485
NCBI GI
                  133
BLAST score
                  8.0e-08
E value
Match length
                  89
                  10
% identity
NCBI Description
                  (AC005896) hypothetical protein [Arabidopsis thaliana]
                  166902
Seq. No.
                  LIB3234-016-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2894574
                  513
BLAST score
                  2.0e-52
E value
Match length
                  97
                  100
% identity
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
                  166903
Seq. No.
                  LIB3234-016-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g4585966
NCBI GI
BLAST score
                  553
                  5.0e-57
E value
Match length
                  114
                  94
% identity
NCBI Description
                  (AC005287) Putative dihyrdolipoamide acetyltransferase
                  [Arabidopsis thaliana]
                  166904
Seq. No.
                  LIB3234-016-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g3337361
NCBI GI
BLAST score
                  668
E value
                  2.0e-70
Match length
                  117
% identity
                  99
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  166905
Seq. No.
Seq. ID
                  LIB3234-016-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3935151
                  547
BLAST score
                  2.0e-56
E value
Match length
                  103
% identity
                   99
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
                   166906
```

Seq. No.

Seq. ID LIB3234-016-P1-K1-B6

Method BLASTN NCBI GI g4006815 BLAST score 262 E value 1.0e-145 Match length 295

% identity NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 166907 LIB3234-016-P1-K1-B8 Seq. ID Method BLASTX g1619602 NCBI GI BLAST score 388 E value 1.0e-37 Match length 112 % identity 39 NCBI Description (Y08726) MtN3 [Medicago truncatula] Seq. No. 166908 Seq. ID LIB3234-016-P1-K1-B9

Seq. ID LIB3234-016-P1-K1-B9
Method BLASTX
NCBI GI g3582328
BLAST score 256
E value 3.0e-22

BLAST score 256
E value 3.0e-2
Match length 111
% identity 12

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 166909

Seq. ID LIB3234-016-P1-K1-C1

Method BLASTX
NCBI GI g1711513
BLAST score 408
E value 5.0e-40
Match length 85
% identity 99

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54)

>gi_515681 (U12127) signal recognition particle 54 kDa

subunit [Arabidopsis thaliana]

Seq. No. 166910

Seq. ID LIB3234-016-P1-K1-C11

Method BLASTX
NCBI GI g11837
BLAST score 223
E value 2.0e-18
Match length 70
% identity 61

NCBI Description (Z00044) NADH dehydrogenase 27kD subunit [Nicotiana

tabacum] >gi_225205 prf 1211235AK bhpB gene [Nicotiana

tabacum]

Seq. No. 166911

Seq. ID LIB3234-016-P1-K1-C3

Method BLASTX
NCBI GI g2583125
BLAST score 524
E value 1.0e-53
Match length 118
% identity 85

NCBI Description (AC002387) putative transketolase precursor [Arabidopsis

Match length

% identity

92

98



thaliana]

```
166912
Seq. No.
                  LIB3234-016-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  q2583125
NCBI GI
                  425
BLAST score
                  5.0e-42
E value
                  114
Match length
                  75
% identity
NCBI Description
                  (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
                  166913
Seq. No.
                  LIB3234-016-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4773885
BLAST score
                  523
                  2.0e-53
E value
                  99
Match length
                  98
% identity
NCBI Description
                  (AF076243) putative aspartic protease [Arabidopsis
                  thaliana]
                  166914
Seq. No.
                  LIB3234-016-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g1170503
NCBI GI
                  561
BLAST score
                  5.0e-58
E value
                  113
Match length
                  98
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                  >gi_322503_pir__JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
                  166915
Seq. No.
                  LIB3234-016-P1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4567300
BLAST score
                  219
                  1.0e-120
E value
Match length
                  352
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic
                  sequence, complete sequence
Seq. No.
                   166916
Seq. ID
                  LIB3234-016-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q119143
BLAST score
                   470
E value
                  3.0e-47
```

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-lalpha-Al [Arabidopsis thaliana] >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana] Seq. No. 166917 LIB3234-016-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g1864017 549 BLAST score E value 1.0e-56 Match length 105 99 % identity NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum] 166918

Seq. No.

LIB3234-016-P1-K1-D8 Seq. ID

Method BLASTX g4263704 NCBI GI BLAST score 221 E value 4.0e-18 Match length 76 54 % identity

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

166919 Seq. No.

Seq. ID LIB3234-016-P1-K1-D9

Method BLASTN NCBI GI q3402671 BLAST score 341 E value 0.0e + 00Match length 345 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166920

Seq. ID LIB3234-016-P1-K1-E10

Method BLASTX NCBI GI g4581146 BLAST score 441 E value 6.0e-44Match length 98 91 % identity

NCBI Description (AC006919) putative fructose-bisphosphate aldolase,

cytoplasmic [Arabidopsis thaliana]

166921 Seq. No.

Seq. ID LIB3234-016-P1-K1-E11

Method BLASTN



NCBI GI g4220643 BLAST score 310 1.0e-174 E value Match length 342 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana] 166922 Seq. No. LIB3234-016-P1-K1-E12 Seq. ID Method BLASTN NCBI GI g4159712 BLAST score 334 E value 0.0e+00338 Match length 100 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence Seq. No. 166923 LIB3234-016-P1-K1-E5 Seq. ID Method BLASTX NCBI GI g3395435 407 BLAST score 6.0e-40E value Match length 98 89 % identity NCBI Description (AC004683) myosin heavy chain-like protein [Arabidopsis thaliana] 166924 Seq. No. LIB3234-016-P1-K1-E7 Seq. ID Method BLASTX NCBI GI g166570 174 BLAST score E value 1.0e-12 Match length 31 % identity 100 (L04173) glycine rich protein [Arabidopsis thaliana] NCBI Description 166925 Seq. No. Seq. ID LIB3234-016-P1-K1-E8 Method BLASTX NCBI GI g2738248 BLAST score 514 E value 2.0e-52 Match length 98 % identity

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 166926

LIB3234-016-P1-K1-E9 Seq. ID

BLASTX Method NCBI GI g2880051 BLAST score 233 E value 2.0e-19



```
Match length
                   56
                   80
% identity
NCBI Description
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  166927
                  LIB3234-016-P1-K1-F1
Seq. ID
Method
                  BLASTN
                  g4589435
NCBI GI
BLAST score
                  316
E value
                  1.0e-178
Match length
                  348
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOE17, complete sequence
Seq. No.
                  166928
                  LIB3234-016-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  609
E value
                  1.0e-63
Match length
                  115
                  100
% identity
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  166929
Seq. ID
                  LIB3234-016-P1-K1-F11
Method
                  BLASTX
                  g633890
NCBI GI
                  370
BLAST score
E value
                  1.0e-35
Match length
                  115
% identity
                  66
NCBI Description
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  166930
Seq. ID
                  LIB3234-016-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q2618601
BLAST score
                  164
E value
                  3.0e-87
Match length
                  343
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166931
Seq. ID
                  LIB3234-016-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1929056
```

BLAST score 417 E value 4.0e-41 Match length 116 73 % identity

NCBI Description (Y12090) putative 3,4-dihydroxy-2-butanone kinase

[Lycopersicon esculentum]



```
Seq. No.
                    166932
Seq. ID
                    LIB3234-016-P1-K1-F7
Method
                    BLASTN
NCBI GI
                    g2642152
BLAST score
                    264
E value
                    1.0e-147
Match length
                    349
% identity
                    100
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T517 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166933
Seq. ID
                    LIB3234-016-P1-K1-F8
Method
                    BLASTX
NCBI GI
                    g135858
BLAST score
                    204
E value
                    4.0e-16
Match length
                    41
                    100
% identity
                    TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                    >gi_99760 pir S22201 tonoplast intrinsic protein alpha -
                    Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                    [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                    intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                    166934
Seq. ID
                    LIB3234-016-P1-K1-F9
Method
                    BLASTN
NCBI GI
                    g4589410
BLAST score
                    340
E value
                    0.0e + 00
Match length
                    344
% identity
                    100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    F2015, complete sequence
Seq. No.
                    166935
Seq. ID
                    LIB3234-016-P1-K1-G11
Method
                    BLASTN
NCBI GI
                    g2351069
BLAST score
                    235
E value
                    1.0e-129
                    349
Match length
% identity
                    100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166936
```

Seq. ID LIB3234-016-P1-K1-G12 Method BLASTX

NCBI GI q4454032 BLAST score 592 E value 1.0e-61 Match length 114



```
% identity
NCBI Description
                  (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                   166937
Seq. ID
                   LIB3234-016-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3334123
BLAST score
                   377
E value
                   2.0e-36
Match length
                   97
% identity
                   82
                   ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
                   (AC002334) mitochondrial F1-ATPase, gamma subunit
                   [Arabidopsis thaliana]
Seq. No.
                   166938
Seq. ID
                   LIB3234-016-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g3157930
BLAST score
                   548
E value
                   2.0e-56
Match length
                   103
% identity
                   99
NCBI Description
                   (AC002131) Strong similarity to
                   amino-cyclopropane-carboxylic acid oxidase qb L27664 from
                   Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   166939
Seq. ID
                   LIB3234-016-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1363488
BLAST score
                   524
E value
                   1.0e-53
Match length
                   103
                   99
% identity
NCBI Description
                   IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
                   IAA8 [Arabidopsis thaliana] >gi 4314364 gb AAD15575
                   (AC006340) auxin-induced IAA8 protein [Arabidopsis
                   thaliana]
Seq. No.
                   166940
Seq. ID
                   LIB3234-016-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   g4589969
BLAST score
                   325
E value
                   0.0e+00
```

Match length 346 98 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F1P15 genomic

sequence, complete sequence

Seq. No. 166941

Seq. ID LIB3234-016-P1-K1-G8

Method BLASTX



NCBI GI g3915847
BLAST score 314
E value 5.0e-29
Match length 71
% identity 87
NCBI Description 40S RIBO
40S ribos

NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 166942

Seq. ID LIB3234-016-P1-K1-G9

Method BLASTX
NCBI GI g1550740
BLAST score 461
E value 3.0e-46
Match length 88
% identity 100

NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No. 166943

Seq. ID LIB3234-016-P1-K1-H10

Method BLASTN
NCBI GI 94006885
BLAST score 232
E value 1.0e-128
Match length 346
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 166944

Seq. ID LIB3234-016-P1-K1-H2

Method BLASTX
NCBI GI g2944446
BLAST score 336
E value 1.0e-31
Match length 105
% identity 57

NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus

communis]

Seq. No. 166945

Seq. ID LIB3234-016-P1-K1-H3

Method BLASTX
NCBI GI g2944446
BLAST score 272
E value 4.0e-24
Match length 92
% identity 52

NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus

communis]

Seq. No. 166946

Seq. ID LIB3234-016-P1-K1-H4

Method BLASTX NCBI GI g1531762 BLAST score 155 E value 2.0e-10



Match length 44 % identity 70

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 166947

Seq. ID LIB3234-016-P1-K1-H6

Method BLASTX
NCBI GI 9881615
BLAST score 513
E value 2.0e-52
Match length 108
% identity 93

NCBI Description (U29142) fatty acid elongase 1 [Arabidopsis thaliana]

>gi_3096921 emb CAA18831.1 (AL023094) fatty acid elongase

1 [Arabidopsis thaliana]

Seq. No. 166948

Seq. ID LIB3234-016-P1-K1-H7

Method BLASTX
NCBI GI g3122724
BLAST score 351
E value 2.0e-33
Match length 69
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal

protein L38 isolog [Arabidopsis thaliana]

Seq. No. 166949

Seq. ID LIB3234-016-P1-K1-H8

Method BLASTN
NCBI GI g3449331
BLAST score 346
E value 0.0e+00
Match length 346
% identity 29

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

Seq. No. 166950

Seq. ID LIB3234-016-P1-K1-H9

Method BLASTN
NCBI GI 94733952
BLAST score 176
E value 2.0e-94
Match length 349
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No. 166951

Seq. ID LIB3234-017-P1-K1-A1

Method BLASTX
NCBI GI g3935151
BLAST score 505
E value 2.0e-51
Match length 101



49

% identity

NCBI Description

```
% identity
                  92
NCBI Description
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
                  166952
Seq. No.
                  LIB3234-017-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1531758
BLAST score
                  275
E value
                  2.0e-24
Match length
                  67
                  79
% identity
NCBI Description
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
                  unknown protein [Arabidopsis thaliana]
                  166953
Seq. No.
                  LIB3234-017-P1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  162
E value
                  6.0e-86
Match length
                  366
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDC11, complete sequence
Seq. No.
                  166954
Seq. ID
                  LIB3234-017-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  127
E value
                  5.0e-65
Match length
                  353
% identity
                  92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDC11, complete sequence
Seq. No.
                  166955
Seq. ID
                  LIB3234-017-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q602076
BLAST score
                  493
E value
                  5.0e-50
Match length
                  102
% identity
                  22
NCBI Description
                  (X77456) pentameric polyubiquitin [Nicotiana tabacum]
Seq. No.
                  166956
Seq. ID
                  LIB3234-017-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g3449331
BLAST score
                  109
E value
                  2.0e-54
Match length
                  263
```

22521

MNC17, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

NCBI GI

E value

BLAST score

q4757414

0.0e + 00

343



```
166957
Seq. No.
                   LIB3234-017-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4056502
                   552
BLAST score
                   6.0e-57
E value
                   117
Match length
                   91
% identity
NCBI Description
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                   166958
                   LIB3234-017-P1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g113595
BLAST score
                   416
                   6.0e-41
E value
Match length
                   118
% identity
                   65
                   ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
NCBI Description
                   >gi_100562_pir__S15024 aldose reductase-related protein -
                   barley >gi_18891_emb_CAA40747_ (X57526) aldose
                   reductase-related protein [Hordeum vulgare]
                   166959
Seq. No.
Seq. ID
                   LIB3234-017-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2801442
BLAST score
                   561
E value
                   6.0e-58
                   111
Match length
% identity
                   89
                   (AF028338) ubiquitin-conjugating enzyme 15 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166960
Seq. ID
                   LIB3234-017-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g4503755
BLAST score
                   163
E value
                   3.0e-11
Match length
                   97
                   45
% identity
NCBI Description
                   flavin containing monooxygenase 1
                   >gi_399505_sp_Q01740 FMO1 HUMAN DIMETHYLANILINE
                   MONOOXYGENASE (N-OXIDE FORMING) 1 (FETAL HEPATIC
                   FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE
                   OXIDASE 1) >gi_105847_pir__A40876 dimethylaniline monooxygenase (N-oxide-forming) (EC 1.14.13.8), hepatic 1 -
                   human >gi 182671 (M64082) flavin-containing monooxygenase
                   [Homo sapiens]
Seq. No.
                   166961
Seq. ID
                   LIB3234-017-P1-K1-B11
Method
                   BLASTN
```



Match length 351 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 166962

Seq. ID LIB3234-017-P1-K1-B12

Method BLASTX
NCBI GI g3169287
BLAST score 596
E value 4.0e-62
Match length 117
% identity 100

NCBI Description (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium

hirsutum]

Seq. No. 166963

Seq. ID LIB3234-017-P1-K1-B2

Method BLASTX
NCBI GI g1345973
BLAST score 400
E value 4.0e-39
Match length 92
% identity 80

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 166964

Seq. ID LIB3234-017-P1-K1-B3

Method BLASTN
NCBI GI g4531433
BLAST score 359
E value 0.0e+00
Match length 367
% identity 99

NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic

sequence, complete sequence

Seq. No. 166965

Seq. ID LIB3234-017-P1-K1-B4

Method BLASTX
NCBI GI g3075399
BLAST score 207
E value 2.0e-16
Match length 83
% identity 49

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 166966

Seq. ID LIB3234-017-P1-K1-B5



```
Method
                  BLASTX
NCBI GI
                  q2809246
BLAST score
                  200
E value
                  1.0e-15
Match length
                  120
% identity
                  38
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                  166967
                  LIB3234-017-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g1931655
NCBI GI
BLAST score
                  351
                  2.0e-33
E value
Match length
                  70
% identity
                  100
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]
Seq. No.
                  166968
Seq. ID
                  LIB3234-017-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  614
E value
                  3.0e-64
Match length
                  118
% identity
                  96
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  166969
Seq. ID
                  LIB3234-017-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q3924597
BLAST score
                  335
E value
                  2.0e-31
Match length
                  122
% identity
                  61
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  166970
Seq. ID
                  LIB3234-017-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4325340
BLAST score
                  339
```

E value 0.0e + 00Match length 363 98 % identity

NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 166971

Seq. ID LIB3234-017-P1-K1-C9

Method BLASTX



NCBI GI g1616787 BLAST score 503 4.0e-51 E value Match length 94 100 % identity

NCBI Description (U71122) pyruvate decarboxylase [Arabidopsis thaliana]

166972 Seq. No.

LIB3234-017-P1-K1-D11 Seq. ID

BLASTN Method NCBI GI g2924257 BLAST score 35 E value 3.0e-10 55 Match length % identity 91

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 166973

LIB3234-017-P1-K1-D12 Seq. ID

Method BLASTN NCBI GI g2864607 BLAST score 216 1.0e-118 E value 299 Match length

99 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 166974

LIB3234-017-P1-K1-D2 Seq. ID

Method BLASTN NCBI GI g3510337 BLAST score 235 E value 1.0e-129 Match length 353 97 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E20, complete sequence [Arabidopsis thaliana]

166975 Seq. No.

Seq. ID LIB3234-017-P1-K1-D3

Method BLASTX NCBI GI q2498329 BLAST score 137 E value 9.0e-16 Match length 86 % identity 53

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571

pattern-formation protein GNOM - Arabidopsis thaliana

>gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 166976



LIB3234-017-P1-K1-D4 Seq. ID Method BLASTX

NCBI GI g1592677 BLAST score 183 E value 1.0e-13 38 Match length 95 % identity

(X91912) LEA76 homologue type2 [Arabidopsis thaliana] NCBI Description

166977 Seq. No.

LIB3234-017-P1-K1-D7 Seq. ID

Method BLASTX NCBI GI g140551 BLAST score 284 E value 2.0e-25 Match length 79 69 % identity

NCBI Description HYPOTHETICAL 250 KD PROTEIN (ORF 2131)

>gi 81505 pir S01446 hypothetical protein 2131 - spinach chloroplast >gi 12246_emb_CAA30743_ (X07908) ORF 2131 (AA

1-2131) [Spinacia oleracea]

Seq. No. 166978

LIB3234-017-P1-K1-D8 Seq. ID

Method BLASTX NCBI GI g3152562 BLAST score 408 E value 5.0e-40 82 Match length 100 % identity

(AC002986) Similar to proteosome component, micropain NCBI Description

(multi-catalytic endopeptidase complex) subunit Y7, gb_X56731 from S. cerevisiae. EST gb_Z25719 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 166979

Seq. ID LIB3234-017-P1-K1-D9

Method BLASTX NCBI GI q2052379 BLAST score 614 E value 3.0e-64 Match length 116 % identity 98

NCBI Description (U66343) calreticulin [Arabidopsis thaliana]

Seq. No. 166980

Seq. ID LIB3234-017-P1-K1-E10

Method BLASTX NCBI GI g3024434 BLAST score 300 E value 2.0e-27 Match length 80 79 % identity

26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description

PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_(D88663) Tat binding protein 1 [Brassica rapa]



```
Seq. No.
                   166981
Seq. ID
                  LIB3234-017-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2262164
BLAST score
                   287
E value
                   7.0e-26
Match length
                  84
                   70
% identity
NCBI Description
                  (AC002329) putative obtusifoliol 14-alpha demethylase
                   [Arabidopsis thaliana]
Seq. No.
                  166982
Seq. ID
                  LIB3234-017-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4589414
BLAST score
                  282
E value
                  1.0e-157
Match length
                  367
                   99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14B15, complete sequence
Seq. No.
                  166983
Seq. ID
                  LIB3234-017-P1-K1-E3
                  BLASTN
Method
NCBI GI
                  g4432793
BLAST score
                  248
                  1.0e-137
E value
Match length
                  292
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T19K21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166984
Seq. ID
                  LIB3234-017-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g2656026
BLAST score
                  361
E value
                  0.0e + 00
Match length
                  365
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDF20
Seq. No.
                  166985
Seq. ID
                  LIB3234-017-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2598461
```

NCBI GI g2598461
BLAST score 183
E value 1.0e-13
Match length 104
% identity 38

NCBI Description (Z98048) HIP (HSC70-INTERACTING PROTEIN (PROGESTERONE

RECEPTOR-ASSOCIATED P48 PROTEIN) [Homo sapiens] >gi_4049268

(U17714) putative tumor suppressor ST13 [Homo sapiens]

Seq. No. 166986



Seq. ID LIB3234-017-P1-K1-E6
Method BLASTX
NCBI GI g135858
BLAST score 252

E value 1.0e-21 Match length 51 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 166987

Seq. ID LIB3234-017-P1-K1-E7

Method BLASTX
NCBI GI g2224911
BLAST score 218
E value 9.0e-18
Match length 110
% identity 44

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

Seq. No. 166988

Seq. ID LIB3234-017-P1-K1-E8

Method BLASTX
NCBI GI g3367520
BLAST score 209
E value 1.0e-16
Match length 110
% identity 41

NCBI Description (AC004392) Similar to protein kinase APK1A,

tyrosine-serine-threonine kinase gb D12522 from A.

thaliana. [Arabidopsis thaliana]

Seq. No. 166989

Seq. ID LIB3234-017-P1-K1-E9

Method BLASTX
NCBI GI g2129767
BLAST score 643
E value 1.0e-67
Match length 124
% identity 98

NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta

precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_

(D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 166990

Seq. ID LIB3234-017-P1-K1-F10

Method BLASTX
NCBI GI g1526424
BLAST score 433
E value 6.0e-43
Match length 100



% identity 86

NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]

Seq. No. 166991

Seq. ID LIB3234-017-P1-K1-F11

Method BLASTN
NCBI GI g1469227
BLAST score 60
E value 4.0e-25
Match length 116
% identity 88

NCBI Description B.oleracea mRNA for hypothetical protein

Seq. No. 166992

Seq. ID LIB3234-017-P1-K1-F12

Method BLASTN
NCBI GI g3985955
BLAST score 285
E value 1.0e-159
Match length 360
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 166993

Seq. ID LIB3234-017-P1-K1-F2

Method BLASTN
NCBI GI g2062153
BLAST score 257
E value 1.0e-142
Match length 306
% identity 98

NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 166994

Seq. ID LIB3234-017-P1-K1-F3

Method BLASTN
NCBI GI 94467131
BLAST score 347
E value 0.0e+00
Match length 363
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13

(ESSA project)

Seq. No. 166995

Seq. ID LIB3234-017-P1-K1-F4

Method BLASTN
NCBI GI 94582411
BLAST score 292
E value 1.0e-163
Match length 359
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,

complete sequence



Seq. No. 166996

Seq. ID LIB3234-017-P1-K1-F5

Method BLASTX
NCBI GI g118927
BLAST score 145
E value 4.0e-09
Match length 117
% identity 35

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC3-06

>gi_320603_pir__C45509 desiccation-related protein (clone PCC3-06) - Craterostigma plantagineum >gi_167475 (M62989) dessication-related protein [Craterostigma plantagineum] >gi_227779_prf__1710351C abscisic acid responsive protein C

[Craterostigma plantagineum]

Seq. No. 166997

Seq. ID LIB3234-017-P1-K1-F6

Method BLASTX
NCBI GI g421836
BLAST score 370
E value 1.0e-35
Match length 76
% identity 100

NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi 553040

(M96855) GF14 [Arabidopsis thaliana]

Seq. No. 166998

Seq. ID LIB3234-017-P1-K1-F7

Method BLASTX
NCBI GI g3785989
BLAST score 312
E value 9.0e-29
Match length 117
% identity 57

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 166999

Seq. ID LIB3234-017-P1-K1-F8

Method BLASTN
NCBI GI g2459406
BLAST score 350
E value 0.0e+00
Match length 354
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167000

Seq. ID LIB3234-017-P1-K1-F9

Method BLASTX
NCBI GI g1255951
BLAST score 387
E value 1.0e-37
Match length 91
% identity 79

NCBI Description (X96932) PS60 [Nicotiana tabacum]



```
Seq. No.
                  167001
Seq. ID
                  LIB3234-017-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g1296310
BLAST score
                  63
                  7.0e-27
E value
Match length
                  135
                  87
% identity
NCBI Description Arabidopsis thaliana chromosome I cosmid g17311 DNA
Seq. No.
                  167002
Seq. ID
                  LIB3234-017-P1-K1-G12
                  BLASTX
Method
                  g1531762
NCBI GI
BLAST score
                  179
E value
                  4.0e-13
Match length
                  48
% identity
                  73
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  167003
Seq. No.
                  LIB3234-017-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1009234
BLAST score
                  471
E value
                  2.0e-47
                  114
Match length
% identity
                  80
NCBI Description
                 (L38829) SUP2 gene product [Nicotiana tabacum]
Seq. No.
                  167004
                  LIB3234-017-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1531760
BLAST score
                  452
E value
                  3.0e-45
Match length
                  88
% identity
                  100
NCBI Description (X97075) proline oxidase [Arabidopsis thaliana]
Seq. No.
                  167005
Seq. ID
                  LIB3234-017-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1170505
BLAST score
                  494
E value
                  4.0e-50
Match length
                  94
% identity
                  100
                  EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)
NCBI Description
                  >gi 322504 pir JC1453 translation initiation factor
                  eIF-4A2 - Arabidopsis thaliana >gi_16556_emb CAA46189
                  (X65053) eukaryotic translation initiation factor 4A-2
                  [Arabidopsis thaliana] >gi 4585969 gb AAD25605.1 AC005287 7
                  (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis
```

thaliana]



Seq. No. 167006

Seq. ID LIB3234-017-P1-K1-G6

Method BLASTX
NCBI GI g99688
BLAST score 594
E value 7.0e-62
Match length 114
% identity 100

NCBI Description translation elongation factor eEF-1 alpha chain (gene A4) -

Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)

elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No. 167007

Seq. ID LIB3234-017-P1-K1-G8

Method BLASTX
NCBI GI g2435395
BLAST score 274
E value 2.0e-24
Match length 63
% identity 73

NCBI Description (U63550) pectate lyase [Fragaria x ananassa]

Seq. No. 167008

Seq. ID LIB3234-017-P1-K1-H1

Method BLASTX
NCBI GI g4585882
BLAST score 466
E value 8.0e-47
Match length 89
% identity 99

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 167009

Seq. ID LIB3234-017-P1-K1-H11

Method BLASTX
NCBI GI 94587519
BLAST score 548
E value 2.0e-56
Match length 108
% identity 100

NCBI Description (AC007060) Strong similarity to F19I3.7 gi 3033380 putative

coatomer epsilon subunit from Arabidopsis Thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No. 167010

Seq. ID LIB3234-017-P1-K1-H12

Method BLASTN
NCBI GI g4512656
BLAST score 169
E value 4.0e-90
Match length 364
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence



Seq. No. 167011

Seq. ID LIB3234-017-P1-K1-H2

Method BLASTX
NCBI GI 94490330
BLAST score 609
E value 1.0e-63
Match length 120
% identity 94

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis

thaliana]

Seq. No. 167012

Seq. ID LIB3234-017-P1-K1-H3

Method BLASTX
NCBI GI g4115386
BLAST score 497
E value 2.0e-50
Match length 105
% identity 88

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 167013

Seq. ID LIB3234-017-P1-K1-H6

Method BLASTN
NCBI GI g3985952
BLAST score 202
E value 1.0e-110
Match length 318
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 167014

Seq. ID LIB3234-017-P1-K1-H7

Method BLASTN
NCBI GI g3241917
BLAST score 351
E value 0.0e+00
Match length 355
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19B1, complete sequence [Arabidopsis thaliana]

Seq. No. 167015

Seq. ID LIB3234-017-P1-K1-H9

Method BLASTN
NCBI GI g22564
BLAST score 160
E value 9.0e-85
Match length 225
% identity 99

NCBI Description A.thaliana tufA gene for elongation factor Tu

Seq. No. 167016

Seq. ID LIB3234-018-P1-K1-A1

Method BLASTX NCBI GI g2924282



BLAST score 406 E value 9.0e-40 Match length 81 93 % identity

NCBI Description (Z00044) NADH dehydrogenase ND1 subunit [Nicotiana tabacum]

167017 Seq. No.

Seq. ID LIB3234-018-P1-K1-A10

Method BLASTN NCBI GI g2281081 BLAST score 345 0.0e+00E value Match length 357 99 % identity

Arabidopsis thaliana chromosome II BAC F18019 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

167018 Seq. No.

LIB3234-018-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI g881615 BLAST score 471 E value 2.0e-47 Match length 106 90 % identity

(U29142) fatty acid elongase 1 [Arabidopsis thaliana] NCBI Description

>gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase

1 [Arabidopsis thaliana]

Seq. No. 167019

Seq. ID LIB3234-018-P1-K1-A8

Method BLASTX NCBI GI g2160151 BLAST score 480 E value 2.0e-48 Match length 113 % identity 85

NCBI Description (AC000375) Strong similarity to Brassica aspartic protease

(gb X77260). [Arabidopsis thaliana]

Seq. No. 167020

Seq. ID LIB3234-018-P1-K1-B10

Method BLASTN NCBI GI g4512656 BLAST score 37 E value 2.0e-11 Match length 268 % identity 85

Arabidopsis thaliana chromosome II BAC F7D19 genomic NCBI Description

sequence, complete sequence

Seq. No. 167021

Seq. ID LIB3234-018-P1-K1-B12

Method BLASTX NCBI GI g2506139 BLAST score 286 E value 1.0e-25



Match length 80 % identity 75

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 167022

Seq. ID LIB3234-018-P1-K1-B2

Method BLASTX
NCBI GI g3869088
BLAST score 537
E value 4.0e-55
Match length 104
% identity 99

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 167023

Seq. ID LIB3234-018-P1-K1-B4

Method BLASTN
NCBI GI 94335744
BLAST score 102
E value 4.0e-50
Match length 240
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167024

Seq. ID LIB3234-018-P1-K1-B7

Method BLASTX
NCBI GI g112682
BLAST score 573
E value 2.0e-59
Match length 114
% identity 96

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167025

Seq. ID LIB3234-018-P1-K1-C1

Method BLASTN
NCBI GI g2645198
BLAST score 45
E value 4.0e-16

Match length 162 % identity 83

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167026

Seq. ID LIB3234-018-P1-K1-C9

Method BLASTN
NCBI GI g3047060
BLAST score 212



E value 1.0e-116 Match length 359 % identity 47

NCBI Description Arabidopsis thaliana BAC F7N22

Seq. No. 167027

Seq. ID LIB3234-018-P1-K1-D1

Method BLASTX
NCBI GI g1628583
BLAST score 79
E value 2.0e-55
Match length 117
% identity 89

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 167028

Seq. ID LIB3234-018-P1-K1-D10

Method BLASTN
NCBI GI g3985955
BLAST score 268
E value 1.0e-149
Match length 351
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 167029

Seq. ID LIB3234-018-P1-K1-D3

Method BLASTX
NCBI GI g1531762
BLAST score 179
E value 3.0e-13
Match length 48
% identity 73

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thalianal

Seq. No. 167030

Seq. ID LIB3234-018-P1-K1-D5

Method BLASTN
NCBI GI g3292807
BLAST score 138
E value 1.0e-71
Match length 303
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No. 167031

Seq. ID LIB3234-018-P1-K1-D7

Method BLASTN
NCBI GI g4757414
BLAST score 187
E value 1.0e-101
Match length 313

% identity

100



```
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
Seq. No.
                  167032
                  LIB3234-018-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3928086
NCBI GI
BLAST score
                  379
                  1.0e-36
E value
                  76
Match length
                  99
% identity
NCBI Description
                  (AC005770) unknown protein [Arabidopsis thaliana]
                  167033
Seq. No.
Seq. ID
                  LIB3234-018-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  q2281081
BLAST score
                  42
                  2.0e-14
E value
Match length
                  96
                  84
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167034
Seq. ID
                  LIB3234-018-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q4314374
BLAST score
                  47
E value
                  3.0e-17
Match length
                  166
% identity
                  58
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167035
Seq. ID
                  LIB3234-018-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q3449331
BLAST score
                  271
E value
                  1.0e-151
Match length
                  343
                  49
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167036
Seq. ID
                  LIB3234-018-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3834307
BLAST score
                  632
E value
                  3.0e-66
Match length
                  118
```

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712.



ESTs gb N65887 and gb N65627 come from this gene. [Arabidopsis thaliana]

Seq. No. 167037 Seq. ID LIB3234-018-P1-K1-E8 Method BLASTX NCBI GI q1490554 BLAST score 181 E value 2.0e-13 Match length 91 % identity 47 NCBI Description

(U63633) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 167038

Seq. ID LIB3234-018-P1-K1-F10

Method BLASTX NCBI GI q2887500 BLAST score 192 E value 1.0e-14Match length 39 85 % identity

NCBI Description (AC002339) putative AP2 domain-containing protein

[Arabidopsis thaliana]

Seq. No. 167039

Seq. ID LIB3234-018-P1-K1-F4

Method BLASTN NCBI GI g4206788 BLAST score 178 E value 1.0e-95 Match length 182 % identity 99

NCBI Description Arabidopsis thaliana syntaxin-related protein At-SYR1

(At-Syr1) mRNA, complete cds

Seq. No. 167040

Seq. ID LIB3234-018-P1-K1-F6

Method BLASTX NCBI GI g543815 BLAST score 470 E value 3.0e-47Match length 92 95 % identity

NCBI Description FLORAL HOMEOTIC PROTEIN APETALA3 >gi_282855_pir__A42095

homeotic protein AP3 - Arabidopsis thaliana >gi 166608

(M86357) APETELA3 [Arabidopsis thaliana]

167041 Seq. No.

Seq. ID LIB3234-018-P1-K1-F7

Method BLASTX NCBI GI g2501812 BLAST score 475 E value 7.0e-48 Match length 118 % identity

(U91509) glycolate oxidase [Arabidopsis thaliana] NCBI Description

BLAST score

Match length

% identity

E value

63

87

71

3.0e-26



```
167042
Seq. No.
Seq. ID
                  LIB3234-018-P1-K1-G1
Method
                  BLASTN
NCBI GI
                   g1030693
BLAST score
                   71
E value
                   8.0e-32
Match length
                  123
% identity
                   87
NCBI Description
                  Arabidopsis thaliana mRNA for fatty acid desaturase in
                  endoplasmic reticulum, complete cds
Seq. No.
                  167043
Seq. ID
                  LIB3234-018-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g131336
BLAST score
                  339
                   6.0e-32
E value
Match length
                  73
% identity
                   93
NCBI Description
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
                  photosystem II phosphoprotein psbH - common tobacco
                  chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                  phosphoprotein [Nicotiana tabacum]
                  >gi_225225_prf__1211235BG photosystem II 10kD
                  phosphoprotein [Nicotiana tabacum]
Seq. No.
                  167044
Seq. ID
                  LIB3234-018-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  323
E value
                  0.0e+00
Match length
                  359
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167045
Seq. ID
                  LIB3234-018-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g3172156
BLAST score
                  99
E value
                  2.0e-48
                  183
Match length
% identity
                  88
NCBI Description Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167046
Seq. ID
                  LIB3234-018-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g141631
```



NCBI Description ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA >gi_82218_pir__A05196 hypothetical protein 512 common tobacco chloroplast >gi_11842_emb_CAA77362 (Z00044) acetyl-CoA carboxylase beta subunit [Nicotiana tabacum] >gi 225210 prf 1211235AQ ORF 512 [Nicotiana tabacum] Seq. No. 167047 Seq. ID LIB3234-018-P1-K1-H1 Method BLASTN NCBI GI g3269280 BLAST score 342 E value 0.0e + 00Match length 354 99 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project) 167048 Seq. No. LIB3234-018-P1-K1-H2 Seq. ID Method BLASTX NCBI GI g399013 BLAST score 411 E value 2.0e-40 Match length 79 % identity 100 NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 99658 pir S21313 ADP, ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi 445607 prf 1909354A adenylate translocator [Arabidopsis thaliana] Seq. No. 167049 Seq. ID LIB3234-018-P1-K1-H6 Method BLASTX NCBI GI q3135270 BLAST score 400 E value 4.0e-39 Match length 80 % identity 100 NCBI Description (AC003058) putative protein kinase [Arabidopsis thaliana] Seq. No. 167050 LIB3234-018-P1-K1-H8 BLASTN g3273742 184

Seq. ID

Method NCBI GI BLAST score E value 3.0e-99 Match length 269 % identity 96

NCBI Description Arabidopsis thaliana lipid transfer protein 2 precursor

(LTP2) gene, complete cds

Seq. No. 167051

Seq. ID LIB3234-019-P1-K1-A1

Method BLASTX



NCBI GI g112682 BLAST score 477 E value 4.0e-48 Match length 114 % identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167052

Seq. ID LIB3234-019-P1-K1-A12

Method BLASTN
NCBI GI g16450
BLAST score 33
E value 7.0e-10
Match length 62
% identity 85

NCBI Description A.thaliana rab18 gene

Seq. No. 167053

Seq. ID LIB3234-019-P1-K1-A8

Method BLASTN
NCBI GI g16450
BLAST score 78
E value 3.0e-36
Match length 138
% identity 92

NCBI Description A.thaliana rab18 gene

Seq. No. 167054

Seq. ID LIB3234-019-P1-K1-A9

Method BLASTN
NCBI GI g4159703
BLAST score 37

E value 1.0e-11 Match length 129 % identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5F14, complete sequence

Seq. No. 167055

Seq. ID LIB3234-019-P1-K1-B11

Method BLASTX
NCBI GI g21911
BLAST score 196
E value 4.0e-15
Match length 79
% identity 46

NCBI Description (X62625) vicilin [Theobroma cacao]

Seq. No. 167056

Seq. ID LIB3234-019-P1-K1-B2

Method BLASTN NCBI GI g4757414 BLAST score 326



E value 0.0e+00 Match length 362 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 167057

Seq. ID LIB3234-019-P1-K1-B5

Method BLASTN
NCBI GI g3449313
BLAST score 285
E value 1.0e-159
Match length 317
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21P3, complete sequence [Arabidopsis thaliana]

Seq. No. 167058

Seq. ID LIB3234-019-P1-K1-B9

Method BLASTX
NCBI GI g131336
BLAST score 335
E value 2.0e-31
Match length 73
% identity 92

NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P

photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374 (Z00044) PSII 10kD

phosphoprotein [Nicotiana tabacum]

>gi_225225_prf__1211235BG photosystem II 10kD

phosphoprotein [Nicotiana tabacum]

Seq. No. 167059

Seq. ID LIB3234-019-P1-K1-C10

Method BLASTN
NCBI GI g4589445
BLAST score 85
E value 5.0e-40
Match length 225
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWL2, complete sequence

Seq. No. 167060

Seq. ID LIB3234-019-P1-K1-C11

Method BLASTX
NCBI GI g1345973
BLAST score 418
E value 3.0e-41
Match length 92
% identity 84

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)



microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No. 167061

Seq. ID LIB3234-019-P1-K1-C2

Method BLASTN
NCBI GI g3449331
BLAST score 370
E value 0.0e+00
Match length 382
% identity 25

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

Seq. No. 167062

Seq. ID LIB3234-019-P1-K1-C5

Method BLASTN
NCBI GI g2924728
BLAST score 378
E value 0.0e+00
Match length 378
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXH1, complete sequence [Arabidopsis thaliana]

Seq. No. 167063

Seq. ID LIB3234-019-P1-K1-C6

Method BLASTX
NCBI GI g1864017
BLAST score 539
E value 2.0e-55
Match length 102
% identity 100

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 167064

Seq. ID LIB3234-019-P1-K1-C7

Method BLASTN
NCBI GI g2351069
BLAST score 314
E value 1.0e-176
Match length 378
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 167065

Seq. ID LIB3234-019-P1-K1-C8

Method BLASTX
NCBI GI 94204299
BLAST score 509
E value 8.0e-52
Match length 101
% identity 99

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]



Seq. No. 167066

Seq. ID LIB3234-019-P1-K1-D1

Method BLASTN
NCBI GI g2358139
BLAST score 122
E value 4.0e-62
Match length 277
% identity 87

NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete

sequence [Arabidopsis thaliana]

Seq. No. 167067

Seq. ID LIB3234-019-P1-K1-D2

Method BLASTX
NCBI GI g1617274
BLAST score 289
E value 5.0e-26
Match length 78
% identity 74

NCBI Description (Z72152) AMP-binding protein [Brassica napus]

Seq. No. 167068

Seq. ID LIB3234-019-P1-K1-D4

Method BLASTX
NCBI GI g464707
BLAST score 533
E value 1.0e-54
Match length 105
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 167069

Seq. ID LIB3234-019-P1-K1-D5

Method BLASTN
NCBI GI g3150396
BLAST score 349
E value 0.0e+00
Match length 381
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

NCBI Description



```
167070
Seq. No.
                   LIB3234-019-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g114591
BLAST score
                   358
                   2.0e - 34
E value
Match length
                   75
                   99
% identity
                  ATP SYNTHASE EPSILON CHAIN >gi 81663 pir S01903
NCBI Description
                   H+-transporting ATP synthase (\overline{E}C 3.6.1.34) epsilon chain -
                   Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_
                   (X12889) Cf1 ATPase epsilon subunit (AA 1 - 132)
                   [Arabidopsis thaliana]
                   167071
Seq. No.
Seq. ID
                   LIB3234-019-P1-K1-E11
Method
                   BLASTX
                   g3738338
NCBI GI
BLAST score
                   214
E value
                   3.0e-17
Match length
                   75
                   59
% identity
NCBI Description
                  (AC005170) putative polygalacturonase [Arabidopsis
                   thaliana]
                   167072
Seq. No.
Seq. ID
                   LIB3234-019-P1-K1-E12
Method
                   BLASTN
                   g2182289
NCBI GI
BLAST score
                   314
E value
                   1.0e-176
Match length
                   373
% identity
                   98
NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167073
Seq. ID
                   LIB3234-019-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q4432856
BLAST score
                   198
E value
                   4.0e-19
Match length
                   87
% identity
NCBI Description (AC006300) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                   167074
                   LIB3234-019-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1350634
BLAST score
                   419
E value
                   2.0e-41
Match length
                   93
                   89
% identity
```

22545

>gi_12213_emb_CAA46567_ (X65615) ribosomal protein L23

CHLOROPLAST 50S RIBOSOMAL PROTEIN L23

[Sinapis alba]

E value

Match length

NCBI Description

% identity

3.0e - 39

93

80



```
Seq. No.
                   167075
Seq. ID
                  LIB3234-019-P1-K1-F2
Method
                  BLASTN
NCBI GI
                   q3702315
BLAST score
                   250
E value
                   1.0e-138
Match length
                   382
                   98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3F17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167076
Seq. ID
                  LIB3234-019-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g113595
BLAST score
                   413
E value
                  1.0e-40
Match length
                  123
% identity
                   63
                  ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
NCBI Description
                  >gi 100562 pir S15024 aldose reductase-related protein -
                   barley >gi 18891 emb CAA40747 (X57526) aldose
                   reductase-related protein [Hordeum vulgare]
                  167077
Seq. No.
                  LIB3234-019-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3702729
BLAST score
                   365
                  0.0e + 00
E value
Match length
                  365
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167078
Seq. ID
                  LIB3234-019-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  371
E value
                  0.0e + 00
Match length
                  375
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167079
Seq. ID
                  LIB3234-019-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                  401
```

22546

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC



1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No. 167080

Seq. ID LIB3234-019-P1-K1-G3

Method BLASTX
NCBI GI g1885356
BLAST score 302
E value 1.0e-27
Match length 104
% identity 54

NCBI Description (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]

Seq. No. 167081

Seq. ID LIB3234-019-P1-K1-G7

Method BLASTN
NCBI GI g2864607
BLAST score 363
E value 0.0e+00
Match length 367
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 167082

Seq. ID LIB3234-019-P1-K1-G8

Method BLASTN
NCBI GI g2264314
BLAST score 264
E value 1.0e-147

E value 1.0e-1
Match length 360
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 167083

Seq. ID LIB3234-019-P1-K1-G9

Method BLASTN
NCBI GI g2642152
BLAST score 368
E value 0.0e+00
Match length 376
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T517 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167084

Seq. ID LIB3234-019-P1-K1-H1

Method BLASTN
NCBI GI g2477521
BLAST score 105
E value 6.0e-52



Match length 264 % identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167085

Seq. ID LIB3234-019-P1-K1-H12

Method BLASTX
NCBI GI g133960
BLAST score 205
E value 3.0e-16
Match length 49
% identity 86

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi 70876 pir R3NT4

ribosomal protein S4 - common tobacco chloroplast
>gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4
[Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal

protein S4 [Nicotiana tabacum]

Seq. No. 167086

Seq. ID LIB3234-019-P1-K1-H2

Method BLASTX
NCBI GI g112682
BLAST score 676
E value 2.0e-71
Match length 127
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167087

Seq. ID LIB3234-019-P1-K1-H4

Method BLASTN
NCBI GI g563624
BLAST score 72
E value 3.0e-32
Match length 99
% identity 95

NCBI Description S.tuberosum (PU141) mRNA for U14 small nucleolar RNA

Seq. No. 167088

Seq. ID LIB3234-019-P1-K1-H5

Method BLASTX
NCBI GI g1170503
BLAST score 438
E value 2.0e-43
Match length 84
% identity 100

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)

>gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1

[Arabidopsis thaliana]



```
167089
Seq. No.
                   LIB3234-019-P1-K1-H8
Seq. ID
Method
                   BLASTX
                   g4539348
NCBI GI
BLAST score
                   487
                   3.0e-49
E value
Match length
                   116
                   82
% identity
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167090
                   LIB3234-020-P1-K1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4096078
BLAST score
                   113
E value
                   7.0e-57
                   222
Match length
                   95
% identity
                   Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167091
                   LIB3234-020-P1-K1-A2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4096078
BLAST score
                   145
E value
                   9.0e-76
                   348
Match length
                   94
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   167092
Seq. No.
Seq. ID
                   LIB3234-020-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q4455223
BLAST score
                   355
E value
                   1.0e-33
Match length
                   132
                   41
% identity
NCBI Description
                   (AL035440) putative DNA binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   167093
Seq. ID
                   LIB3234-020-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q4049401
BLAST score
                   587
E value
                   5.0e-61
```

Match length 121 % identity 94

NCBI Description

(AJ131580) glutathione transferase AtGST 10 [Arabidopsis

thaliana]

167094 Seq. No.

Seq. ID LIB3234-020-P1-K1-A6

Method BLASTN



NCBI GI q2894591 BLAST score 298 E value 1.0e-167 Match length 374 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21

(ESSAII project)

Seq. No. 167095

Seq. ID LIB3234-020-P1-K1-A7

Method BLASTX NCBI GI g4204263 BLAST score 321 E value 9.0e-30 Match length 102 % identity 65

NCBI Description (AC005223) 40409 [Arabidopsis thaliana]

Seq. No. 167096

Seq. ID LIB3234-020-P1-K1-A8

BLASTN Method NCBI GI g4756963 BLAST score 314 E value 1.0e-176 Match length 358 100 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 167097

LIB3234-020-P1-K1-A9 Seq. ID

Method BLASTN NCBI GI g4756963 BLAST score 147 E value 5.0e-77Match length 315 % identity 87

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 167098

Seq. ID LIB3234-020-P1-K1-B4

Method BLASTX NCBI GI g543712 BLAST score 634 E value 2.0e-66 Match length 122 % identity

1-AMINOCYCLOPROPANE-2-CARBOXYLATE SYNTHASE 2 (ACC SYNTHASE NCBI Description

2) (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE 2) >gi_476924_pir__A47199 1-aminocyclopropane-1-carboxylate

synthase (EC 4.4.1.14) - Arabidopsis thaliana >gi_16148_emb_CAA78260_ (Z12614) 1-aminocyclopropane 1-carboxylate synthase [Arabidopsis thaliana] >gi_166580

(M95595) 1-aminocyclopropane-1-carboxylate synthase

[Arabidopsis thaliana] >gi_2505881_emb_CAA73310_ (Y12776)

ACC-synthase [Arabidopsis thaliana]

Seq. No.

167104



```
Seq. No.
                   167099
Seq. ID
                   LIB3234-020-P1-K1-B5
Method
                  BLASTN
NCBI GI
                   g3420042
BLAST score
                   163
E value
                   1.0e-86
Match length
                   351
% identity
                   98
NCBI Description Arabidopsis thaliana chromosome II BAC T13E15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167100
Seq. ID
                  LIB3234-020-P1-K1-B7
Method
                  BLASTX
                  g4678358
NCBI GI
BLAST score
                  176
E value
                   9.0e-52
Match length
                  127
% identity
                   85
NCBI Description
                  (AL049659) cytochrome p450 like protein [Arabidopsis
                  thaliana]
Seq. No.
                   167101
Seq. ID
                  LIB3234-020-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q3121825
BLAST score
                  161
E value
                   9.0e-17
Match length
                  107
% identity
                   51
NCBI Description
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
                  ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
Seq. No.
                  167102
Seq. ID
                  LIB3234-020-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3808062
BLAST score
                  143
E value
                   6.0e-09
Match length
                  61
% identity
                   44
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  167103
Seq. ID
                  LIB3234-020-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2832707
BLAST score
                  213
E value
                  1.0e-17
Match length
                  45
% identity
                  96
NCBI Description
                  (AL021713) translation initiation factor eIF-2 gamma
```

22551

chain-like protein [Arabidopsis thaliana]



```
LIB3234-020-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g1169598
NCBI GI
BLAST score
                  346
E value
                  1.0e-32
                  77
Match length
                  84
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
                  167105
Seq. No.
                  LIB3234-020-P1-K1-C5
Seq. ID
```

Method BLASTX g3335169 NCBI GI BLAST score 581 3.0e-60 E value 112 Match length

98 % identity

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197 emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

167106 Seq. No.

Seq. ID LIB3234-020-P1-K1-C6

Method BLASTN g2760166 NCBI GI BLAST score 304 E value 1.0e-171 Match length 312 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK20, complete sequence [Arabidopsis thaliana]

Seq. No. 167107

Seq. ID LIB3234-020-P1-K1-C7

Method BLASTN NCBI GI q4159712 BLAST score 218 E value 1.0e-119 Match length 380 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 167108

Seq. ID LIB3234-020-P1-K1-D1

Method BLASTX NCBI GI g1346760 BLAST score 337 E value 1.0e-31 Match length 68 % identity 96

SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 6 NCBI Description

>gi_829255_emb_CAA86339_ (Z46253) protein phosphatase type 1 [Arabidopsis thaliana] >gi_3153203 (U80921)

serine/threonine protein phosphatase type one [Arabidopsis

NCBI Description

thaliana]



thaliana]

```
167109
Seq. No.
Seq. ID
                  LIB3234-020-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4204299
                  72
BLAST score
E value
                  6.0e-31
Match length
                  104
% identity
                  70
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  167110
Seq. ID
                  LIB3234-020-P1-K1-D12
                  BLASTN
Method
NCBI GI
                  g4580745
BLAST score
                  104
                  2.0e-51
E value
Match length
                  381
% identity
                  96
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                  complete sequence
Seq. No.
                  167111
Seq. ID
                  LIB3234-020-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g631291
BLAST score
                  393
E value
                  3.0e-38
Match length
                  89
                  91
% identity
                  MAP kinase-activated protein kinase 2 - human
NCBI Description
                  >gi_407075_emb_CAA53094_ (X75346) MAP kinase activated
                  protein kinase-2 [Homo sapiens]
Seq. No.
                  167112
Seq. ID
                  LIB3234-020-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q3859590
BLAST score
                  135
E value
                  8.0e-70
Match length
                  319
% identity
                  96
NCBI Description Arabidopsis thaliana BAC T15B16
Seq. No.
                  167113
                  LIB3234-020-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961542
BLAST score
                  412
E value
                  2.0e-40
Match length
                  94
% identity
                  84
                  (AF050463) zinc finger transcription factor [Arabidopsis
```



```
Seq. No.
                   167114
                   LIB3234-020-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455223
BLAST score
                   323
                   5.0e-30
E value
Match length
                   124
                   37
% identity
NCBI Description
                   (AL035440) putative DNA binding protein [Arabidopsis
                   thaliana]
                   167115
Seq. No.
                   LIB3234-020-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112681
BLAST score
                   575
E value
                   1.0e-59
Match length
                   125
                   90
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   167116
Seq. No.
                   LIB3234-020-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2961542
                   513
BLAST score
E value
                   3.0e-52
                   93
Match length
                   100
% identity
                   (AF050463) zinc finger transcription factor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   167117
Seq. ID
                   LIB3234-020-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q627537
BLAST score
                   425
E value
                   6.0e-42
Match length
                   91
% identity
                   90
NCBI Description
                   mitogen activated protein kinase activated protein kinase
                   (EC 2.7.1.-) 2 - human >gi_530090 (U12779) MAP kinase activated protein kinase 2 [Homo sapiens]
                   167118
Seq. No.
                   LIB3234-020-P1-K1-E5
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3413718
BLAST score 603
E value 7.0e-63
Match length 117
% identity 98

NCBI Description (AC004747) alpha-vacuolar processing enzyme [Arabidopsis



thaliana] >qi 3643591 (AC005395) alpha-vacuolar processing enzyme [Arabidopsis thaliana]

Seq. No. 167119 Seq. ID LIB3234-020-P1-K1-E7 Method BLASTX NCBI GI g114654 BLAST score 282 E value 3.0e-25 Match length 81 78 % identity NCBI Description ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - common tobacco chloroplast >gi 11812 emb CAA77343 (Z00044) ATPase III subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi 224347 prf 1102209A ATPase III, H translocating [Nicotiana sp.] >gi 225272 prf 1211235G ATPase III [Nicotiana tabacum] Seq. No. 167120 Seq. ID LIB3234-020-P1-K1-F1 Method BLASTX g3834322 NCBI GI BLAST score 378 E value 2.0e-36 Match length 91 78 % identity NCBI Description (AC005679) EST gb R30300 comes from this gene. [Arabidopsis thaliana] Seq. No. 167121 LIB3234-020-P1-K1-F12 Seq. ID Method BLASTN NCBI GI g3859840 BLAST score 356 E value 0.0e + 00Match length 376 % identity 79 NCBI Description Plastid transformation vector pGS31A 16S ribosomal RNA gene, partial sequence; aminoglycoside 3'-adenyltransferase (aadA) gene, complete cds Seq. No. 167122 LIB3234-020-P1-K1-F2 Seq. ID Method BLASTX NCBI GI q494550 BLAST score 255 E value 2.0e-22

Match length 80 % identity 66

NCBI Description Homo sapiens >qi 494551 pdb 1RHG B Homo sapiens

>gi 494552 pdb 1RHG C Homo sapiens

Seq. No. 167123

Seq. ID LIB3234-020-P1-K1-F6

Method BLASTX



NCBI GI q1769905 BLAST score 356 7.0e-34 E value Match length 110 % identity 66 (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) NCBI Description [Arabidopsis thaliana] Seq. No. 167124 LIB3234-020-P1-K1-F7 Seq. ID Method BLASTX NCBI GI g2194125 BLAST score 230 4.0e-19 E value Match length 59 80 % identity (AC002062) ESTs gb R30459, gb N38441 come from this gene. NCBI Description [Arabidopsis thaliana] Seq. No. 167125 LIB3234-020-P1-K1-F8 Seq. ID Method BLASTX NCBI GI g4584528 BLAST score 332 E value 3.0e-31 Match length 78 % identity 83

NCBI Description (AL049607) putative protein [Arabidopsis thaliana]

Seq. No. 167126

Seq. ID LIB3234-020-P1-K1-F9

Method BLASTN NCBI GI q4584519 BLAST score 133 E value 8.0e-69 Match length 237 % identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18

(ESSA project)

Seq. No. 167127

Seq. ID LIB3234-020-P1-K1-G11

Method BLASTN NCBI GI g4454447 BLAST score 89 E value 2.0e-42Match length 269 % identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167128

Seq. ID LIB3234-020-P1-K1-G12

Method BLASTN NCBI GI g12218 BLAST score 211 E value 1.0e-115



Match length 321 % identity 92

NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly

Seq. No. 167129

Seq. ID LIB3234-020-P1-K1-G3

Method BLASTN
NCBI GI g4455290
BLAST score 32
E value 8.0e-09
Match length 60
% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5

(ESSAII project)

Seq. No. 167130

Seq. ID LIB3234-020-P1-K1-G4

Method BLASTX
NCBI GI 94584528
BLAST score 482
E value 1.0e-48
Match length 104
% identity 91

NCBI Description (AL049607) putative protein [Arabidopsis thaliana]

Seq. No. 167131

Seq. ID LIB3234-020-P1-K1-G6

Method BLASTX
NCBI GI g4204298
BLAST score 524
E value 1.0e-53
Match length 121
% identity 83

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 167132

Seq. ID LIB3234-020-P1-K1-G7

Method BLASTX
NCBI GI g541546
BLAST score 499
E value 1.0e-50
Match length 128
% identity 18

NCBI Description ubiquitin precursor - Volvox carteri

>gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox

carteri]

Seq. No. 167133

Seq. ID LIB3234-020-P1-K1-H4

Method BLASTN
NCBI GI g4455290
BLAST score 255
E value 1.0e-141
Match length 347
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5



(ESSAII project)

Seq. No. 167134

Seq. ID LIB3234-020-P1-K1-H6

Method BLASTN
NCBI GI g3702733
BLAST score 333
E value 0.0e+00
Match length 373
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJP23, complete sequence [Arabidopsis thaliana]

Seq. No. 167135

Seq. ID LIB3234-020-P1-K1-H9

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 5.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 167136

Seq. ID LIB3234-021-P1-K1-A1

Method BLASTX
NCBI GI g1592677
BLAST score 193
E value 9.0e-15
Match length 38
% identity 100

NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No. 167137

Seq. ID LIB3234-021-P1-K1-A8

Method BLASTX
NCBI GI g4115386
BLAST score 513
E value 2.0e-52
Match length 114
% identity 83

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 167138

Seq. ID LIB3234-021-P1-K1-A9

Method BLASTX
NCBI GI g1531762
BLAST score 162
E value 4.0e-11
Match length 39
% identity 82

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 167139

Seq. ID LIB3234-021-P1-K1-B1



Method BLASTX
NCBI GI g1490554
BLAST score 438
E value 2.0e-43
Match length 107
% identity 86

NCBI Description (U63633) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 167140

Seq. ID LIB3234-021-P1-K1-B10

Method BLASTX
NCBI GI g4006897
BLAST score 468
E value 4.0e-47
Match length 115
% identity 78

NCBI Description (Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No. 167141

Seq. ID LIB3234-021-P1-K1-B12

Method BLASTX
NCBI GI g585382
BLAST score 578
E value 6.0e-60
Match length 118
% identity 93

NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG)

>gi_322536_pir__S30570 laminin receptor homolog Arabidopsis thaliana >gi_16380_emb_CAA48794_ (X69056)
laminin receptor homologue [Arabidopsis thaliana]

Seq. No. 167142

Seq. ID LIB3234-021-P1-K1-B3

Method BLASTX
NCBI GI g2129767
BLAST score 659
E value 2.0e-69
Match length 123
% identity 100

NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta

precursor - Arabidopsis thaliana >qi 1805364 dbj BAA09615

(D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 167143

Seq. ID LIB3234-021-P1-K1-C1

Method BLASTX
NCBI GI g2738248
BLAST score 282
E value 2.0e-25
Match length 65
% identity 83

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 167144

Seq. ID LIB3234-021-P1-K1-C11

Seq. No.

Seq. ID

167149

LIB3234-021-P1-K1-D12

```
Method
                  BLASTX
NCBI GI
                  q4678347
BLAST score
                  211
E value
                  6.0e-17
Match length
                  71
% identity
                  52
NCBI Description (AL049659) putative protein [Arabidopsis thaliana]
Seq. No.
                  167145
Seq. ID
                  LIB3234-021-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1490554
BLAST score
                  424
E value
                  7.0e-42
Match length
                  103
                  85
% identity
NCBI Description
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  167146
Seq. ID
                  LIB3234-021-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q136739
BLAST score
                  380
E value
                  1.0e-36
Match length
                  122
% identity
                  63
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  167147
Seq. ID
                  LIB3234-021-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g3702739
BLAST score
                  336
E value
                  0.0e + 00
Match length
                  340
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167148
Seq. ID
                  LIB3234-021-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g3108208
BLAST score
                  285
E value
                  1.0e-159
Match length
                  350
                  95
% identity
                  Arabidopsis thaliana eukaryotic cap-binding protein (eIF4E)
NCBI Description
                  mRNA, complete cds
```



```
Method
                  BLASTX
                  g3341679
NCBI GI
BLAST score
                  142
                  2.0e-12
E value
Match length
                  63
                  70
% identity
                  (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  167150
                  LIB3234-021-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  g4704766
NCBI GI
                  367
BLAST score
E value
                  3.0e - 35
Match length
                  102
                  43
% identity
                  (AF131223) protein disulfide isomerase homolog; PDI
NCBI Description
                  [Datisca glomerata]
Seq. No.
                  167151
                  LIB3234-021-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464775
                  357
BLAST score
                   5.0e-34
E value
Match length
                  89
                   74
% identity
                  SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492
NCBI Description
                   superoxide dismutase - Para rubber tree >gi_348137 (L11707)
                   superoxide dismutase (manganese) [Hevea brasiliensis]
Seq. No.
                   167152
                  LIB3234-021-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2244749
BLAST score
                   481
                   1.0e-48
E value
Match length
                   104
% identity
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                   167153
Seq. ID
                   LIB3234-021-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   g3298532
BLAST score
                   281
E value
                   1.0e-157
Match length
                   317
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 167154

Seq. ID LIB3234-021-P1-K1-E11

Method BLASTX NCBI GI g166765



BLAST score 416 6.0e-41 E value Match length 81 % identity 98

(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana] NCBI Description

Seq. No. 167155

LIB3234-021-P1-K1-E12 Seq. ID

Method BLASTN NCBI GI g2244991 BLAST score 224 E value 1.0e-123 Match length 310 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

167156 Seq. No.

LIB3234-021-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI q4388728 BLAST score 260 E value 1.0e-22 Match length 62 87 % identity

NCBI Description (AC006413) putative grr1-like protein [Arabidopsis

thaliana]

167157 Seq. No.

Seq. ID LIB3234-021-P1-K1-E4

Method BLASTN NCBI GI q2244991 BLAST score 148 E value 1.0e-77 Match length 240 % identity 90

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 167158

Seq. ID LIB3234-021-P1-K1-F3

Method BLASTX NCBI GI g2160158 BLAST score 508 E value 1.0e-51 Match length 100 % identity 100

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No. 167159

Seq. ID LIB3234-021-P1-K1-F5

Method BLASTN NCBI GI g1946354 BLAST score 86 7.0e-41 E value



```
Match length
                   166
% identity
                   88
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
                   sequence, complete sequence
Seq. No.
                   167160
Seq. ID
                   LIB3234-021-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   q4580745
BLAST score
                   236
E value
                   1.0e-130
Match length
                   336
% identity
                   94
NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                   complete sequence
Seq. No. Seq. ID
                   167161
                   LIB3234-021-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q4704766
BLAST score
                   289
E value
                   3.0e - 34
Match length
                   99
% identity
                   38
NCBI Description
                   (AF131223) protein disulfide isomerase homolog; PDI
                   [Datisca glomerata]
Seq. No.
                   167162
Seq. ID
                   LIB3234-021-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g4159703
BLAST score
                   181
E value
                   2.0e-97
Match length
                   201
% identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K5F14, complete sequence
                   167163
Seq. No.
Seq. ID
                   LIB3234-021-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   110
E value
                   2.0e-10
Match length
                   76
% identity
                   67
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   167164
Seq. ID
                  LIB3234-021-P1-K1-H12
Method
                  BLASTN
NCBI GI
                   g527636
BLAST score
                   43
```

E value 2.0e-15

Match length 75 % identity 89

NCBI Description Arabidopsis thaliana clone HAT7 homeobox protein mRNA,



complete cds Seq. No. 167165 Seq. ID LIB3234-021-P1-K1-H4 Method BLASTN NCBI GI g4159712 BLAST score 197 E value 1.0e-107 Match length 351 % identity 92 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence Seq. No. 167166 Seq. ID LIB3234-021-P1-K1-H6 Method BLASTX NCBI GI q2129659 BLAST score 276 1.0e-24 E value

% identity 62
NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 167167

Match length

Seq. ID LIB3234-021-P1-K1-H7

92 62

Method BLASTX
NCBI GI g633890
BLAST score 253
E value 7.0e-22
Match length 78
% identity 65

NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum

vulgare]

Seq. No. 167168

Seq. ID LIB3234-021-P1-K1-H8

Method BLASTX
NCBI GI g1946369
BLAST score 241
E value 8.0e-29
Match length 98
% identity 72

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 167169

Seq. ID LIB3234-021-P1-K1-H9

Method BLASTN
NCBI GI 94757392
BLAST score 271
E value 1.0e-151
Match length 302
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 167170



LIB3234-022-P1-K1-A3 Seq. ID

Method BLASTX NCBI GI q3219938 BLAST score 179 4.0e-13E value 107 Match length 37 % identity

HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I NCBI Description

>gi 2058378 emb CAB08174 (Z94864) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 167171

LIB3234-022-P1-K1-A5 Seq. ID

Method BLASTX NCBI GI q267073 BLAST score 618 1.0e-64 E value Match length 118 97 % identity

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin

beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 167172

Seq. ID LIB3234-022-P1-K1-A6

Method BLASTX NCBI GI a115767 BLAST score 629 7.0e-66 E value Match length 123 97 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-165/180) (LHCP) >gi 81603_pir_ A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 167173

Seq. ID LIB3234-022-P1-K1-A7

Method BLASTX NCBI GI g118926 BLAST score 208 E value 2.0e-18 Match length 102 51 % identity

DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR NCBI Description

>gi 320600 pir E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi 227781 prf 1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 167174

Seq. ID LIB3234-022-P1-K1-A9



```
Method BLASTX
NCBI GI g1708025
BLAST score 395
E value 1.0e-38
Match length 97
% identity 81
NCBI Description GLYCEROL-
>gi_8407:
dehydroge
```

iption GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]

>gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate

dehydrogenase (NAD+) [Cuphea lanceolata]

Seq. No. 167175

Seq. ID LIB3234-022-P1-K1-B10

Method BLASTX
NCBI GI g4587680
BLAST score 416
E value 7.0e-41
Match length 107
% identity 71

NCBI Description (AC007197) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No. 167176

Seq. ID LIB3234-022-P1-K1-B11

Method BLASTX
NCBI GI g112682
BLAST score 551
E value 1.0e-56
Match length 131
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167177

Seq. ID LIB3234-022-P1-K1-B2

Method BLASTX
NCBI GI g544285
BLAST score 202
E value 8.0e-16
Match length 43
% identity 86

NCBI Description FIBRILLARIN >gi_422056_pir__S33690 fibrillarin - fission

yeast (Schizosaccharomyces pombe) >gi_296704_emb_CAA49550_

(X69930) fibrillarin [Schizosaccharomyces pombe] >gi_3687500 emb CAA21168 (AL031788) fibrillarin

[Schizosaccharomyces pombe]

Seq. No. 167178

Seq. ID LIB3234-022-P1-K1-B3

Method BLASTX
NCBI GI g629500
BLAST score 485
E value 5.0e-49
Match length 105
% identity 92

NCBI Description 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -



Arabidopsis thaliana >gi_166578 (M95594)
1-aminocyclopropane-1-carboxylate synthase [Arabidopsis thaliana]

Seq. No. 167179

Seq. ID LIB3234-022-P1-K1-B5

Method BLASTN
NCBI GI g12216
BLAST score 37
E value 3.0e-11
Match length 115
% identity 88

NCBI Description Sinapis alba chloroplast rps16 gene

Seq. No. 167180

Seq. ID LIB3234-022-P1-K1-B6

Method BLASTX
NCBI GI g1170373
BLAST score 628
E value 1.0e-65
Match length 138
% identity 91

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi 397482 emb_CAA52684_ (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

Seq. No. 167181

Seq. ID LIB3234-022-P1-K1-B7

Method BLASTX
NCBI GI g2605714
BLAST score 520
E value 4.0e-53
Match length 122
% identity 84

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 167182

Seq. ID LIB3234-022-P1-K1-B9

Method BLASTX
NCBI GI g267073
BLAST score 578
E value 7.0e-60
Match length 106
% identity 99

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin

beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 167183

Seq. ID LIB3234-022-P1-K1-C11

Method BLASTN
NCBI GI g4589434
BLAST score 362
E value 0.0e+00



410 Match length 91 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ7, complete sequence

167184 Seq. No.

LIB3234-022-P1-K1-C3 Seq. ID

Method BLASTN NCBI GI g2088638 BLAST score 38 E value 1.0e-12 Match length 42

% identity 98

Arabidopsis thaliana chromosome II BAC T28M21 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

167185 Seq. No.

LIB3234-022-P1-K1-C4 Seq. ID

Method BLASTN NCBI GI g2182289 BLAST score 278 1.0e-155 E value 278 Match length 100 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

167186 Seq. No.

LIB3234-022-P1-K1-D10 Seq. ID

Method BLASTX NCBI GI g1592677 BLAST score 250 9.0e-22 E value Match length 65 83 % identity

NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No. 167187

Seq. ID LIB3234-022-P1-K1-D2

Method BLASTX NCBI GI g2275211 BLAST score 664 E value 6.0e-70 Match length 134 % identity 99

NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 167188

LIB3234-022-P1-K1-D3 Seq. ID

BLASTX Method NCBI GI g1707364 BLAST score 248 E value 4.0e-21 Match length 106 39 % identity

NCBI Description (X94626) AATP2 [Arabidopsis thaliana]

Seq. ID

Method

NCBI GI



```
167189
Seq. No.
                  LIB3234-022-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g1592677
NCBI GI
BLAST score
                  214
                  3.0e-17
E value
                  113
Match length
% identity
                  43
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167190
                  LIB3234-022-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869064
                  55
BLAST score
                  5.0e-22
E value
                  163
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1013, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167191
                  LIB3234-022-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g2129659
NCBI GI
BLAST score
                  328
E value
                  1.0e-30
                  104
Match length
                   62
% identity
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
NCBI Description
                   (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                   167192
Seq. ID
                  LIB3234-022-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4589435
BLAST score
                  118
E value
                   8.0e-60
Match length
                   222
% identity
                   88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOE17, complete sequence
Seq. No.
                   167193
                  LIB3234-022-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g21911
BLAST score
                  155
E value
                   3.0e-10
Match length
                  64
                   45
% identity
NCBI Description (X62625) vicilin [Theobroma cacao]
                  167194
Seq. No.
```

22569

LIB3234-022-P1-K1-F11

BLASTX

g1619602



```
BLAST score
                   384
E value
                   4.0e-37
Match length
                   96
                   75
% identity
NCBI Description
                   (Y08726) MtN3 [Medicago truncatula]
                   167195
Seq. No.
                   LIB3234-022-P1-K1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4512656
BLAST score
                   64
E value
                   1.0e-27
Match length
                   184
                   87
% identity
                   Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   167196
                   LIB3234-022-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q133788
BLAST score
                   476
E value
                   7.0e-48
Match length
                   100
% identity
                   89
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S14 >gi 70987 pir R3NT14
                   ribosomal protein S14 - common tobacco chloroplast
                   >gi_11828_emb_CAA77350_ (Z00044) ribosomal protein S14
[Nicotiana tabacum] >gi_225196_prf__1211235AA ribosomal
                   protein S14 [Nicotiana tabacum]
                   167197
Seq. No.
Seq. ID
                   LIB3234-022-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g2129570
BLAST score
                   277
E value
                   6.0e-25
Match length
                   71
% identity
                   82
NCBI Description
                   DAD-1 homolog - Arabidopsis thaliana
                   >gi_1184193_emb_CAA64837_ (X95585) DAD-1 homologue
                   [Arabidopsis thaliana]
Seq. No.
                   167198
Seq. ID
                   LIB3234-022-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   q2262155
BLAST score
                   86
E value
                   1.0e-40
```

Match length 240 % identity 91

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

167199 Seq. No.

Seq. ID LIB3234-022-P1-K1-G10

Method BLASTN



NCBI GI g3522932 BLAST score 323 E value 0.0e+00 Match length 407 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167200

Seq. ID LIB3234-022-P1-K1-G3

Method BLASTX
NCBI GI g2062163
BLAST score 95
E value 3.0e-03
Match length 132
% identity 16

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 167201

Seq. ID LIB3234-022-P1-K1-G7

Method BLASTN
NCBI GI g4220644
BLAST score 38
E value 4.0e-12

E value 4.0e
Match length 106
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXL8, complete sequence [Arabidopsis thaliana]

Seq. No. 167202

Seq. ID LIB3234-022-P1-K1-G9

Method BLASTN
NCBI GI g4220638
BLAST score 58
E value 4.0e-24
Match length 162
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIF21, complete sequence [Arabidopsis thaliana]

Seq. No. 167203

Seq. ID LIB3234-022-P1-K1-H1

Method BLASTN
NCBI GI 94760411
BLAST score 305
E value 1.0e-171
Match length 333
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,

complete sequence

Seq. No. 167204

Seq. ID LIB3234-022-P1-K1-H5

MethodBLASTXNCBI GIg112682BLAST score449



E value 6.0e-45 Match length 91 % identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167205

Seq. ID LIB3234-022-P1-K1-H6

Method BLASTN
NCBI GI g1865682
BLAST score 81
E value 7.0e-38

Match length 148 % identity 89

NCBI Description A.thaliana 16 kb chromosome 1 DNA fragment

Seq. No. 167206

Seq. ID LIB3234-022-P1-K1-H9

Method BLASTN
NCBI GI g2618604
BLAST score 259
E value 1.0e-144
Match length 263
% identity 65

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 167207

Seq. ID LIB3234-025-P1-K1-A10

Method BLASTX
NCBI GI g3746809
BLAST score 309
E value 9.0e-29
Match length 65
% identity 92

NCBI Description (AF082882) adenylate kinase [Arabidopsis thaliana]

Seq. No. 167208

Seq. ID LIB3234-025-P1-K1-A12

Method BLASTN
NCBI GI g2262097
BLAST score 40
E value 4.0e-13
Match length 152
% identity 91

NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic

sequence, complete sequence

Seq. No. 167209

Seq. ID LIB3234-025-P1-K1-A2

Method BLASTN
NCBI GI g4510392
BLAST score 40
E value 1.0e-13



64 Match length 91 % identity Arabidopsis thaliana chromosome II BAC T17D12 genomic NCBI Description sequence, complete sequence 167210 Seq. No. LIB3234-025-P1-K1-A4 Seq. ID Method BLASTX g4468813 NCBI GI BLAST score 268 E value 1.0e-23 Match length 111 49 % identity (AL035601) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 167211 LIB3234-025-P1-K1-A6 Seq. ID BLASTN Method NCBI GI q4165340 37 BLAST score 2.0e-11 E value 53 Match length 92 % identity NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 167212 LIB3234-025-P1-K1-A9 Seq. ID BLASTX Method g2522534 NCBI GI BLAST score 154 E value 2.0e-13 113 Match length 45 % identity (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens] NCBI Description Seq. No. 167213 LIB3234-025-P1-K1-B11 Seq. ID Method BLASTX g2342674 NCBI GI BLAST score 370 E value 1.0e-35 Match length 104 % identity (AC000106) Similar to ATP-dependent Clp protease NCBI Description (gb D90915). EST gb N65461 comes from this gene. [Arabidopsis thaliana] Seq. No. 167214 Seq. ID LIB3234-025-P1-K1-B2

Method BLASTX
NCBI GI g3880026
BLAST score 141
E value 1.0e-08
Match length 72
% identity 36

NCBI Description (Z75550) Similarity with Schizosaccharomyces hypothetical



gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from
this gene [Caenorhabditis elegans]

Seq. No. 167215

Seq. ID LIB3234-025-P1-K1-B4

Method BLASTX
NCBI GI g3874214
BLAST score 310
E value 2.0e-28
Match length 122
% identity 53

NCBI Description (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W

(SW:YED1 YEAST); cDNA EST EMBL:D27574 comes from this gene;

cDNA EST EMBL:D33757 comes from this gene; cDNA EST EMBL:D34256 comes from this gene; cDNA EST EMBL:D37288

comes from

Seq. No. 167216

Seq. ID LIB3234-025-P1-K1-B6

Method BLASTN
NCBI GI g2584827
BLAST score 272
E value 1.0e-151
Match length 336
% identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 167217

Seq. ID LIB3234-025-P1-K1-B7

Method BLASTX
NCBI GI g1255448
BLAST score 638
E value 6.0e-67
Match length 130
% identity 96

NCBI Description (D50468) mitogen-activated protein kinase [Arabidopsis

thaliana]

Seq. No. 167218

Seq. ID LIB3234-025-P1-K1-B8

Method BLASTN
NCBI GI g4199934
BLAST score 224
E value 1.0e-123
Match length 364
% identity 90

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 167219

Seq. ID LIB3234-025-P1-K1-B9

Method BLASTN
NCBI GI g4589438
BLAST score 251
E value 1.0e-139
Match length 386

NCBI Description



```
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ2, complete sequence
Seq. No.
                  167220
Seq. ID
                  LIB3234-025-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g3241920
BLAST score
                  193
E value
                  1.0e-104
Match length
                  221
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167221
                  LIB3234-025-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757401
BLAST score
                  286
E value
                  1.0e-160
Match length
                  341
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGH6, complete sequence
Seq. No.
                  167222
                  LIB3234-025-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3510247
BLAST score
                  152
E value
                  3.0e-80
Match length
                  172
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167223
                  LIB3234-025-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115362
BLAST score
                  211
E value
                  3.0e - 39
Match length
                  116
% identity
                  69
NCBI Description
                  (AC005957) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  167224
Seq. ID
                  LIB3234-025-P1-K1-C9
                  BLASTX
Method
NCBI GI
                  g120675
BLAST score
                  480
E value
                  2.0e-48
Match length
                  110
                  83
% identity
```

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66011 pir DEIS3C glyceraldehyde-3-phosphate



dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
>gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
alba]

Seq. No. 167225

Seq. ID LIB3234-025-P1-K1-D10

Method BLASTN
NCBI GI g1050427
BLAST score 344
E value 0.0e+00
Match length 348
% identity 100

NCBI Description A.thaliana mRNA for an exon from SNAP25A protein

Seq. No. 167226

Seq. ID LIB3234-025-P1-K1-D11

Method BLASTX
NCBI GI 94490732
BLAST score 482
E value 1.0e-48
Match length 114
% identity 82

NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like

protein [Arabidopsis thaliana]

Seq. No. 167227

Seq. ID LIB3234-025-P1-K1-D12

Method BLASTX
NCBI GI g1168410
BLAST score 414
E value 1.0e-40
Match length 118
% identity 71

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2

>gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 167228

Seq. ID LIB3234-025-P1-K1-D2

Method BLASTN
NCBI GI g4512656
BLAST score 138
E value 1.0e-71
Match length 281
% identity 83

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No. 167229

Seq. ID LIB3234-025-P1-K1-D3

Method BLASTN
NCBI GI g2196463
BLAST score 287
E value 1.0e-160
Match length 323
% identity 97



NCBI Description Arabidopsis thaliana chloroplast trnC, rpoB & rpoC1 genes

Seq. No. 167230

Seq. ID LIB3234-025-P1-K1-D4

Method BLASTX
NCBI GI g2129641
BLAST score 552
E value 7.0e-57
Match length 101
% identity 100

NCBI Description major latex protein type 1 - Arabidopsis thaliana

>gi_1107493_emb_CAA63026_ (X91960) major latex protein

typel [Arabidopsis thaliana]

Seq. No. 167231

Seq. ID LIB3234-025-P1-K1-D5

Method BLASTX
NCBI GI g2342727
BLAST score 410
E value 3.0e-40
Match length 106
% identity 75

NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 167232

Seq. ID LIB3234-025-P1-K1-D7

Method BLASTN
NCBI GI g4159712
BLAST score 170
E value 1.0e-90
Match length 282
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 167233

Seq. ID LIB3234-025-P1-K1-D9

Method BLASTX
NCBI GI g1592677
BLAST score 220
E value 6.0e-18
Match length 103
% identity 48

NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No. 167234

Seq. ID LIB3234-025-P1-K1-E1

Method BLASTN
NCBI GI g4159712
BLAST score 146
E value 2.0e-76
Match length 202
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 167235



Seq. ID LIB3234-025-P1-K1-E10

Method BLASTX
NCBI GI g4056500
BLAST score 217
E value 1.0e-17
Match length 43
% identity 100

NCBI Description (AC005896) putative acetyltransferase [Arabidopsis

thaliana]

Seq. No. 167236

Seq. ID LIB3234-025-P1-K1-E11

Method BLASTX
NCBI GI g1345973
BLAST score 274
E value 2.0e-24
Match length 81
% identity 65

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167237

Seq. ID LIB3234-025-P1-K1-E12

Method BLASTN
NCBI GI g2623294
BLAST score 169
E value 4.0e-90
Match length 257
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167238

Seq. ID LIB3234-025-P1-K1-E3

Method BLASTX
NCBI GI g2494131
BLAST score 591
E value 2.0e-61
Match length 121
% identity 98

NCBI Description (AC002376) Strong similarity to Lycopersicon aldehyde

oxidase (gb_U82559). [Arabidopsis thaliana]

Seq. No. 167239

Seq. ID LIB3234-025-P1-K1-E4

Method BLASTX
NCBI GI g4263704
BLAST score 267
E value 2.0e-23
Match length 91



% identity 55 (AC006223) putative sugar starvation-induced protein NCBI Description [Arabidopsis thaliana] 167240 Seq. No. LIB3234-025-P1-K1-E6 Seq. ID BLASTN Method g16171 NCBI GI 33 BLAST score 6.0e-09 E value Match length 381 36 % identity Arabodopsis thaliana tandemly repeated sequence AR3 NCBI Description Seq. No. 167241 LIB3234-025-P1-K1-E8 Seq. ID Method BLASTN g2351071 NCBI GI BLAST score 147 5.0e-77E value 368 Match length 95 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MVA3, complete sequence [Arabidopsis thaliana] Seq. No. 167242 Seq. ID LIB3234-025-P1-K1-F1 Method BLASTX NCBI GI g2129641 BLAST score 338 5.0e-45E value Match length 90 99 % identity major latex protein type 1 - Arabidopsis thaliana NCBI Description >gi_1107493_emb_CAA63026_ (X91960) major latex protein typel [Arabidopsis thaliana] 167243 Seq. No. LIB3234-025-P1-K1-F10 Seq. ID Method BLASTX NCBI GI q1362026 BLAST score 501 7.0e-51E value Match length 97 98 % identity probable serine/threonine-specific protein kinase (EC NCBI Description 2.7.1.-) BSK1 - rape >gi_289372 (L12393) serine/threonine protein kinase [Brassica napus] >gi_1097353_prf__2113401A protein kinase [Brassica napus]

Seq. No. 167244

Seq. ID LIB3234-025-P1-K1-F11

Method BLASTN
NCBI GI g12216
BLAST score 84
E value 2.0e-39
Match length 295



```
% identity
NCBI Description Sinapis alba chloroplast rps16 gene
Seq. No.
                  167245
                  LIB3234-025-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159708
BLAST score
                  49
E value
                  1.0e-18
                  156
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MKP6, complete sequence
Seq. No.
                  167246
                  LIB3234-025-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  q902584
NCBI GI
                  478
BLAST score
E value
                   3.0e-48
                  99
Match length
                   14
% identity
NCBI Description
                  (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
                  mays]
Seq. No.
                   167247
                  LIB3234-025-P1-K1-F3
Seq. ID
Method
                  BLASTX
                   g3252816
NCBI GI
BLAST score
                   345
E value
                   1.0e-32
Match length
                   107
                   66
% identity
NCBI Description
                   (AC004705) hypothetical protein [Arabidopsis thaliana]
                   >gi 3810589 (AC005398) hypothetical protein [Arabidopsis
                   thaliana]
                   167248
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g3318617
BLAST score
                   362
E value
                   1.0e-34
                  80
Match length
% identity
                   86
NCBI Description
                  (AB016066) mitochondrial phosphate transporter [Arabidopsis
                   thaliana]
                   167249
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-F8
                  BLASTN
Method
NCBI GI
                   g2618604
BLAST score
                  167
                   6.0e-89
E value
Match length
                  182
                   98
% identity
```

22580

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

~:<u>.</u>



MTG13, complete sequence [Arabidopsis thaliana]

 Seq. No.
 167250

 Seq. ID
 LIB3234-025-P1-K1-G1

 Method
 BLASTX

 NCBI GI
 g2244772

 BLAST score
 578

BLAST score 578
E value 6.0e-60
Match length 104
% identity 99

NCBI Description (Z97335) transport protein [Arabidopsis thaliana]

Seq. No. 167251

Seq. ID LIB3234-025-P1-K1-G10

Method BLASTX
NCBI GI g4006934
BLAST score 546
E value 4.0e-56
Match length 109
% identity 95

NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No. 167252

Seq. ID LIB3234-025-P1-K1-G12

Method BLASTN
NCBI GI 94757395
BLAST score 235
E value 1.0e-129
Match length 310
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 167253

Seq. ID LIB3234-025-P1-K1-G2 Method BLASTN

NCBI GI g4662637 BLAST score 95 E value 6.0e-46 Match length 222 % identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC T25M19 genomic

sequence, complete sequence

Seq. No. 167254

Seq. ID LIB3234-025-P1-K1-G5

Method BLASTX
NCBI GI g166570
BLAST score 165
E value 1.0e-11
Match length 31
% identity 97

NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No. 167255

Seq. ID LIB3234-025-P1-K1-G7

Method BLASTN



NCBI GI g2735774
BLAST score 39
E value 8.0e-13
Match length 115
% identity 83

NCBI Description Corallocarpus bainesii 18S ribosomal RNA gene, complete

sequence

Seq. No. 167256

Seq. ID LIB3234-025-P1-K1-G8

Method BLASTN
NCBI GI g3063438
BLAST score 333
E value 0.0e+00
Match length 369
% identity 98

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 167257

Seq. ID LIB3234-025-P1-K1-H1

Method BLASTN
NCBI GI g4262221
BLAST score 39
E value 1.0e-12
Match length 63
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167258

Seq. ID LIB3234-025-P1-K1-H10

Method BLASTX
NCBI GI g2262113
BLAST score 437
E value 2.0e-43
Match length 129
% identity 68

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 167259

Seq. ID LIB3234-025-P1-K1-H11

Method BLASTN
NCBI GI g3449331
BLAST score 47
E value 2.0e-17
Match length 154
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

Seq. No. 167260

Seq. ID LIB3234-025-P1-K1-H2

Method BLASTX
NCBI GI g2160158
BLAST score 309
E value 2.0e-28



Match length 62 % identity 98

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb_EF1G_XENLA). ESTs gb_T20564, gb_T45940, gb_T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 167261

Seq. ID LIB3234-025-P1-K1-H3

Method BLASTX
NCBI GI g1542941
BLAST score 207
E value 2.0e-16
Match length 106
% identity 41

NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No. 167262

Seq. ID LIB3234-025-P1-K1-H5

Method BLASTX
NCBI GI g135535
BLAST score 350
E value 2.0e-33
Match length 91
% identity 76

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis

thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT

alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 167263

Seq. ID LIB3234-026-Q1-K1-A1

Method BLASTX
NCBI GI g1419090
BLAST score 210
E value 6.0e-17
Match length 93
% identity 47

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 167264

Seq. ID LIB3234-026-Q1-K1-A10

Method BLASTX
NCBI GI g541847
BLAST score 539
E value 2.0e-55
Match length 103
% identity 97

NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No. 167265

Seq. ID LIB3234-026-Q1-K1-A11

Method BLASTX NCBI GI g1429213 BLAST score 603



E value 6.0e-63 Match length 118 % identity 99

NCBI Description (X98773) peroxidase ATP4a [Arabidopsis thaliana]

Seq. No. 167266

Seq. ID LIB3234-026-Q1-K1-A12

Method BLASTX
NCBI GI g136739
BLAST score 308
E value 3.0e-28
Match length 97

Match length 97 % identity 64

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 167267

Seq. ID LIB3234-026-Q1-K1-A2

Method BLASTN
NCBI GI g3510341
BLAST score 319
E value 1.0e-179
Match length 363

% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFC16, complete sequence [Arabidopsis thaliana]

Seq. No. 167268

Seq. ID LIB3234-026-Q1-K1-A8

Method BLASTN
NCBI GI 94587582
BLAST score 53
E value 4.0e-21
Match length 188
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC T16B14 genomic

sequence, complete sequence

Seq. No. 167269

Seq. ID LIB3234-026-Q1-K1-B10

Method BLASTN
NCBI GI g4519190
BLAST score 232
E value 1.0e-128
Match length 345
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K6A12, complete sequence

Seq. No. 167270

Seq. ID LIB3234-026-Q1-K1-B3

Method BLASTN
NCBI GI g2980787
BLAST score 106



E value 1.0e-52
Match length 268
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2

(ESSAII project)

Seq. No. 167271

Seq. ID LIB3234-026-Q1-K1-B6

Method BLASTN
NCBI GI g3738275
BLAST score 237
E value 1.0e-130
Match length 348
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167272

Seq. ID LIB3234-026-Q1-K1-C1

Method BLASTN
NCBI GI g4567290
BLAST score 54
E value 2.0e-21

Match length 102 % identity 64

NCBI Description Arabidopsis thaliana chromosome II BAC F18P14 genomic

sequence, complete sequence

Seq. No. 167273

Seq. ID LIB3234-026-Q1-K1-C11

Method BLASTX
NCBI GI g1170839
BLAST score 567
E value 1.0e-58
Match length 120
% identity 93

NCBI Description LOW-TEMPERATURE-INDUCED 65 KD PROTEIN

>gi_419758_pir__S30153 low-temperature-induced protein 65 Arabidopsis thaliana >gi_16388_emb_CAA47902_ (X67670) lti65

[Arabidopsis thaliana]

Seq. No. 167274

Seq. ID LIB3234-026-Q1-K1-C3

Method BLASTX
NCBI GI g418473
BLAST score 385
E value 3.0e-37
Match length 119
% identity 60

NCBI Description GTP-BINDING PROTEIN TYPA/BIPA (TYROSINE PHOSPHORYLATED

PROTEIN A) >gi_628735_pir__S40816 hypothetical protein o591 - Escherichia coli >gi_304976 (L19201) matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to elongation factor G, TetM/TetO tetracycline-resistance proteins [Escherichia coli] >gi 1790302 (AE000462) putative

GTP-binding factor [Escherichia coli]

Method

NCBI GI

BLAST score

BLASTN

306

g4199934



```
Seq. No.
                  167275
Seq. ID
                  LIB3234-026-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  q2584827
BLAST score
                  266
E value
                  1.0e-148
                  336
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167276
                  LIB3234-026-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4584528
BLAST score
                  418
E value
                  3.0e-41
Match length
                  120
                  72
% identity
NCBI Description
                  (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  167277
                  LIB3234-026-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16450
BLAST score
                  50
E value
                  4.0e-19
Match length
                  204
% identity
                  89
NCBI Description A.thaliana rab18 gene
Seq. No.
                  167278
                  LIB3234-026-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678205
BLAST score
                  99
E value
                  4.0e-43
Match length
                  116
% identity
                  81
                  (AC007134) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167279
                  LIB3234-026-Q1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q511598
BLAST score
                  89
E value
                  2.0e-42
Match length
                  263
% identity
                  86
NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,
                  complete cds
Seq. No.
                  167280
Seq. ID
                  LIB3234-026-Q1-K1-D11
```



E value 1.0e-172 Match length 362 % identity 89

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 167281

Seq. ID LIB3234-026-Q1-K1-D12

Method BLASTX
NCBI GI g462147
BLAST score 99
E value 2.0e-53
Match length 120
% identity 93

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase

(EC 5.3.1.9) - Arabidopsis thaliana

>gi 415923 emb CAA48940 (X69195) glucose-6-phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 167282

Seq. ID LIB3234-026-Q1-K1-D2

Method BLASTX
NCBI GI g2117612
BLAST score 483
E value 8.0e-49
Match length 108

% identity 88

NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No. 167283

Seq. ID LIB3234-026-Q1-K1-D3

Method BLASTN
NCBI GI 94220468
BLAST score 185
E value 1.0e-99
Match length 339
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T8011 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167284

Seq. ID LIB3234-026-Q1-K1-D4

Method BLASTX
NCBI GI g2435522
BLAST score 178
E value 4.0e-13
Match length 77
% identity 44

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 167285

Seq. ID LIB3234-026-Q1-K1-D7

Method BLASTN NCBI GI g4757417

Seq. No.

Seq. ID

Method NCBI GI



```
39
BLAST score
                   9.0e-13
E value
                  94
Match length
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  T30G6, complete sequence
                  167286
Seq. No.
                  LIB3234-026-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g133750
NCBI GI
BLAST score
                  477
                  4.0e-48
E value
                  95
Match length
                  97
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi_320170_pir__A26574 ribosomal protein S12 - soybean
                  chloroplast >gi_11572_emb_CAA28661_ (X05013) rps12 [Glycine
                  max]
                  167287
Seq. No.
                  LIB3234-026-Q1-K1-E10
Seq. ID
Method
                  {\tt BLASTN}
                  g2264306
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  159
                  84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167288
                  LIB3234-026-Q1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159708
BLAST score
                   150
E value
                   5.0e-79
Match length
                  182
                   96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MKP6, complete sequence
Seq. No.
                   167289
                   LIB3234-026-Q1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4220640
BLAST score
                  108
E value
                   1.0e-53
Match length
                   308
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPE11, complete sequence [Arabidopsis thaliana]
```

22588

167290

BLASTX

g3193222

LIB3234-026-Q1-K1-E4

```
171
BLAST score
                  3.0e-12
E value
                  65
Match length
% identity
                  72
NCBI Description
                  (AF068687) malate dehydrogenase [Glycine max]
                  167291
Seq. No.
                  LIB3234-026-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138179
                  452
BLAST score
E value
                  4.0e-45
Match length
                  92
                  93
% identity
                  (AJ223969) elongation factor 1 alpha subunit [Malus
NCBI Description
                  domestica]
                  167292
Seq. No.
                  LIB3234-026-Q1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119350
BLAST score
                  276
                  1.0e-24
E value
                  72
Match length
                  78
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                   [Arabidopsis thaliana]
```

>gi 4581151 gb AAD24635.1 AC006919 13 (AC006919) enolase

(2-phospho-D-glycerate hydroylase); identical to P25696

Seq. No. 167293

Seq. ID LIB3234-026-Q1-K1-F10

Method BLASTN NCBI GI g2275194 BLAST score 242 1.0e-134 E value Match length 307 % identity 98

Arabidopsis thaliana chromosome II BAC T08I13 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

167294 Seq. No.

Seq. ID LIB3234-026-Q1-K1-F3

Method BLASTN NCBI GI g4159705 BLAST score 73 E value 5.0e-33 Match length 244

% identity 83 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MGD8, complete sequence

Seq. No. 167295



Seq. ID LIB3234-026-Q1-K1-F6 Method BLASTX NCBI GI g3327204 BLAST score 271 E value 5.0e-24 Match length 106 % identity 57 (AB014595) KIAA0695 protein [Homo sapiens] NCBI Description 167296 Seq. No. LIB3234-026-Q1-K1-F7 Seq. ID Method BLASTN NCBI GI q1800278 BLAST score 55 3.0e-22 E value Match length 184 % identity 86 NCBI Description Arabidopsis thaliana putative Cys3His zinc finger protein (ATCTH) mRNA, complete cds Seq. No. 167297 Seq. ID LIB3234-026-Q1-K1-G11 Method BLASTN NCBI GI g4096078 BLAST score 86 E value 9.0e-41Match length 224 84 % identity NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana] 167298 Seq. No. LIB3234-026-Q1-K1-G6 Seq. ID Method BLASTX NCBI GI g1170149 BLAST score 200 1.0e-15 E value

Match length 104 % identity 64

NCBI Description HEAT SHOCK PROTEIN 101 >gi 537446 (U13949) AtHSP101

[Arabidopsis thaliana]

Seq. No. 167299

LIB3234-026-Q1-K1-H10 Seq. ID

Method BLASTN NCBI GI g4757395 BLAST score 183 E value 2.0e-98 Match length 369 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 167300

LIB3234-026-Q1-K1-H11 Seq. ID

Method BLASTX NCBI GI g4510349



BLAST score 167 E value 1.0e-11 Match length 74 % identity 62

NCBI Description (AC006921) putative bZIP transcription factor [Arabidopsis

thaliana]

Seq. No. 167301

Seq. ID LIB3234-026-Q1-K1-H12

Method BLASTX
NCBI GI g1345973
BLAST score 567
E value 1.0e-58
Match length 109
% identity 98

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167302

Seq. ID LIB3234-026-Q1-K1-H2

Method BLASTN
NCBI GI g3386593
BLAST score 133
E value 1.0e-68
Match length 326
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167303

Seq. ID LIB3234-026-Q1-K1-H7

Method BLASTX
NCBI GI g4371279
BLAST score 136
E value 1.0e-08
Match length 46
% identity 61

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 167304

Seq. ID LIB3234-030-P1-K1-A1

Method BLASTN
NCBI GI g2262097
BLAST score 190
E value 1.0e-102
Match length 357
% identity 89

NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic

sequence, complete sequence



Seq. No. 167305 Seq. ID LIB3234-030-P1-K1-A10 Method BLASTX NCBI GI g4406787 BLAST score 525 E value 1.0e-53 Match length 103 99 % identity NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana] 167306 Seq. No. LIB3234-030-P1-K1-A11 Seq. ID Method BLASTX NCBI GI g2947060 BLAST score 477 E value 4.0e-48 Match length 102 % identity 81 NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana] Seq. No. 167307 LIB3234-030-P1-K1-A12 Seq. ID Method BLASTX NCBI GI g3281868 BLAST score 645 E value 8.0e-68 Match length 124 % identity NCBI Description (AL031004) putative protein [Arabidopsis thaliana] Seq. No. 167308 LIB3234-030-P1-K1-A5 Seq. ID Method BLASTX NCBI GI q114532 BLAST score 561 E value 6.0e-58 Match length 125 % identity NCBI Description ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum] >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum] Seq. No. 167309

Seq. ID LIB3234-030-P1-K1-A9

Method BLASTX
NCBI GI g131164
BLAST score 163
E value 3.0e-11
Match length 48
% identity 67

NCBI Description PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_65727_pir__FERZA photosystem I iron-sulfur protein psaC - rice chloroplast



>gi_65728_pir__FEWT1 photosystem I iron-sulfur protein psaC
- wheat chloroplast >gi_12051_emb_CAA33954_ (X15901) PSI
9kDa protein [Oryza sativa] >gi_12350_emb_CAA31555_
(X13158) photosystem I 8 kDa subunit [Triticum aestivum]
>gi_167038 (L06607) photosystem I subunit C [Hordeum vulgare] >gi_4150873_emb_CAA09816_ (AJ011848) PSI 9 kDa protein [Hordeum vulgare] >gi_226558_prf_1601522B photosystem I 8kD protein [Triticum aestivum]
>gi_226671_prf__1603356CY photosystem I 9kD protein [Oryza sativa]

Seq. No. 167310

Seq. ID LIB3234-030-P1-K1-B1

Method BLASTX
NCBI GI g2781345
BLAST score 507
E value 2.0e-51
Match length 133
% identity 75

NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

Seq. No. 167311

Seq. ID LIB3234-030-P1-K1-B2

Method BLASTX
NCBI GI g2213607
BLAST score 273
E value 4.0e-24
Match length 108
% identity 60

NCBI Description (AC000103) F21J9.1 [Arabidopsis thaliana]

Seq. No. 167312

Seq. ID LIB3234-030-P1-K1-B4

Method BLASTX
NCBI GI g1628583
BLAST score 102
E value 1.0e-28
Match length 92
% identity 80

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 167313

Seq. ID LIB3234-030-P1-K1-B6

Method BLASTN
NCBI GI g4415905
BLAST score 60
E value 4.0e-25
Match length 290

Match length 290 % identity 79

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167314

Seq. ID LIB3234-030-P1-K1-C12

Method BLASTX



NCBI GI g82232 BLAST score 530 E value 3.0e-54 Match length 125 % identity 83

NCBI Description rpoC protein homolog - common tobacco chloroplast

Seq. No. 167315

Seq. ID LIB3234-030-P1-K1-C2

Method BLASTN
NCBI GI g4757401
BLAST score 174
E value 4.0e-93
Match length 218
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 167316

Seq. ID LIB3234-030-P1-K1-C3

Method BLASTN
NCBI GI g4220635
BLAST score 52
E value 3.0e-20

E value 3.0e-Match length 254 % identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 167317

Seq. ID LIB3234-030-P1-K1-C5

Method BLASTX
NCBI GI g112682
BLAST score 72
E value 5.0e-57
Match length 125
% identity 94

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167318

Seq. ID LIB3234-030-P1-K1-C9

Method BLASTN
NCBI GI g3985958
BLAST score 151
E value 1.0e-79
Match length 203
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 167319

Seq. ID LIB3234-030-P1-K1-D3

Method BLASTX

E value

Match length

2.0e-36

83



```
NCBI GI
                  q3043536
BLAST score
                  175
                  1.0e-12
E value
Match length
                  79
                  53
% identity
                  (AB000708) SAUR [Raphanus sativus]
NCBI Description
Seq. No.
                  167320
Seq. ID
                  LIB3234-030-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4104058
BLAST score
                  238
                  5.0e-20
E value
Match length
                  89
% identity
                  51
                  (AF031195) blue copper-binding protein homolog [Triticum
NCBI Description
                  aestivum]
Seq. No.
                  167321
Seq. ID
                  LIB3234-030-P1-K1-D7
Method
                  BLASTN
                  g2342717
NCBI GI
BLAST score
                  95
E value
                  6.0e-46
                  350
Match length
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167322
Seq. No.
Seq. ID
                  LIB3234-030-P1-K1-D8
Method
                  BLASTX
NCBI GI
                   q2342724
BLAST score
                  617
E value
                   2.0e-64
Match length
                  126
% identity
NCBI Description
                  (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   167323
Seq. ID
                  LIB3234-030-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score
                  49
E value
                   2.0e-18
Match length
                  182
% identity
                   87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167324
Seq. ID
                  LIB3234-030-P1-K1-E4
Method
                  BLASTX
                  g1169598
NCBI GI
BLAST score
                  378
```



% identity 84

OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM NCBI Description

(DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No. 167325

LIB3234-030-P1-K1-E9 Seq. ID

Method BLASTX NCBI GI g112682 BLAST score 349 E value 3.0e-33 Match length 81

% identity 84

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

167326 Seq. No.

Seq. ID LIB3234-030-P1-K1-F12

Method BLASTN g4589437 NCBI GI BLAST score 257 E value 1.0e-142 Match length 378 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 167327

Seq. ID LIB3234-030-P1-K1-F3

Method BLASTX NCBI GI q3738332 BLAST score 619 E value 1.0e-64 Match length 125 % identity 96

NCBI Description (AC005170) putative eukaryotic initiation factor

[Arabidopsis thaliana]

Seq. No. 167328

Seq. ID LIB3234-030-P1-K1-G10

Method BLASTN NCBI GI g3282170 BLAST score 99 E value 2.0e-48 Match length 215 87 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,

complete sequence [Arabidopsis thaliana]

167329 Seq. No.

Seq. ID LIB3234-030-P1-K1-G2

Method BLASTN NCBI GI g3510347 BLAST score 140



```
8.0e-73
E value
                  292
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  167330
Seq. No.
                  LIB3234-030-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g2662343
NCBI GI
                  517
BLAST score
                  8.0e-53
E value
                  104
Match length
                  95
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  167331
Seq. No.
                  LIB3234-030-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656031
BLAST score
                  281
                  1.0e-157
E value
                  354
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
                  167332
Seq. No.
                  LIB3234-033-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  g4262250
NCBI GI
BLAST score
                  373
                   6.0e-36
E value
Match length
                  74
                  100
% identity
NCBI Description
                  (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  167333
                  LIB3234-033-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1881585
BLAST score
                  201
                   9.0e-16
E value
Match length
                  104
% identity
                   48
NCBI Description
                  (U72489) remorin [Solanum tuberosum]
Seq. No.
                   167334
Seq. ID
                  LIB3234-033-P1-K1-A5
Method
                  BLASTN
NCBI GI
                   q3869068
BLAST score
                   200
E value
                   1.0e-108
Match length
                   321
% identity
                   90
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

22597

MDC16, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  167335
                  LIB3234-033-P1-K1-D10
Seq. ID
Method
                  BLASTN
                  g3047074
NCBI GI
BLAST score
                  81
                  6.0e-38
E value
                  167
Match length
                  91
% identity
NCBI Description Arabidopsis thaliana BAC F21E10
                  167336
Seq. No.
```

 Seq. ID
 LIB3234-033-P1-K1-D11

 Method
 BLASTX

 NCBI GI
 g4539459

 BLAST score
 177

BLAST score 177 E value 6.0e-13 Match length 47 % identity 60

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 167337

Seq. ID LIB3234-033-P1-K1-D5

Method BLASTN
NCBI GI g3831448
BLAST score 230
E value 1.0e-126
Match length 351
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167338

Seq. ID LIB3234-033-P1-K1-D8

Method BLASTX
NCBI GI g2252828
BLAST score 489
E value 2.0e-49
Match length 106
% identity 91

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 167339

Seq. ID LIB3234-033-P1-K1-D9

Method BLASTX
NCBI GI g4204298
BLAST score 472
E value 9.0e-48
Match length 93
% identity 95

NCBI Description (AC003027) 1cl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 167340

Seq. ID LIB3234-033-P1-K1-E4

Method BLASTX NCBI GI g4185505

```
365
BLAST score
                  6.0e-35
E value
                  105
Match length
                  70
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
Seq. No.
```

167341

Seq. ID LIB3234-033-P1-K1-E6 Method BLASTN NCBI GI g510237 BLAST score 43 E value 2.0e-15 Match length 152 80 % identity

NCBI Description Arabadopsis thaliana Landsberg NT1 mRNA

167342 Seq. No. LIB3234-033-P1-K1-E9 Seq. ID Method BLASTN NCBI GI g4455262 BLAST score 48

E value 1.0e-18 Match length 76 % identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22

(ESSAII project)

Seq. No. 167343

Seq. ID LIB3234-033-P1-K1-F10

Method BLASTN NCBI GI g3193282 BLAST score 63 E value 7.0e-27

Match length 195 % identity 84

NCBI Description Arabidopsis thaliana BAC T14P8

Seq. No. 167344

LIB3234-033-P1-K1-F4 Seq. ID

Method BLASTN NCBI GI g3785968 BLAST score 75 E value 4.0e-34 Match length 147 97

NCBI Description Arabidopsis thaliana chromosome II BAC F2I9 genomic

sequence, complete sequence [Arabidopsis thaliana]

167345 Seq. No.

% identity

LIB3234-033-P1-K1-F5 Seq. ID

Method BLASTN NCBI GI g3335331 BLAST score 181 E value 1.0e-97 Match length 193 98 % identity



NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167346

Seq. ID LIB3234-033-P1-K1-F9

Method BLASTX
NCBI GI g1107501
BLAST score 440
E value 8.0e-44
Match length 102
% identity 87

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 167347

Seq. ID LIB3234-033-P1-K1-G10

Method BLASTN
NCBI GI g4559319
BLAST score 258
E value 1.0e-143
Match length 303
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F14N22 genomic

sequence, complete sequence

Seq. No. 167348

Seq. ID LIB3234-033-P1-K1-G12

Method BLASTX
NCBI GI g1345973
BLAST score 328
E value 2.0e-37
Match length 96

Match length 96 83

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__ JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis
thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167349

Seq. ID LIB3234-033-P1-K1-G4

Method BLASTN
NCBI GI g4159712
BLAST score 60
E value 4.0e-25
Match length 132

Match length 132 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 167350

Seq. ID

Method



```
LIB3234-033-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3243274
BLAST score
                  161
E value
                  1.0e-11
Match length
                  53
% identity
                  64
NCBI Description
                 (AF072134) TCP3 [Arabidopsis thaliana]
Seq. No.
                  167351
Seq. ID
                  LIB3234-033-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  265
E value
                  1.0e-147
Match length
                  354
% identity
                  91
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167352
Seq. ID
                  LIB3234-033-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q2894574
BLAST score
                  224
E value
                  9.0e-19
Match length
                  51
% identity
                  86
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                  >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
Seq. No.
                  167353
Seq. ID
                  LIB3234-033-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g3046853
BLAST score
                  205
E value
                  1.0e-111
Match length
                  269
% identity
                  94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167354
Seq. ID
                  LIB3234-037-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  q4519195
BLAST score
                  356
E value
                  0.0e+00
Match length
                  363
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  167355
```

22601

LIB3234-037-P1-K1-A11

BLASTX

Seq. ID

Method



```
NCBI GI
                   q419760
BLAST score
                   574
E value
                   2.0e-59
Match length
                  121
                   52
% identity
                  P-glycoprotein atpgp1 - Arabidopsis thaliana
NCBI Description
                  >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                  167356
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q2708741
BLAST score
                  629
E value
                   6.0e-66
Match length
                  124
                  99
% identity
NCBI Description
                 (AC003952) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  167357
                  LIB3234-037-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133750
BLAST score
                  209
                  9.0e-17
E value
Match length
                  78
                   60
% identity
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
                  >gi_320170_pir__A26574 ribosomal protein S12 - soybean
                   chloroplast >gi_11572_emb_CAA28661_ (X05013) rps12 [Glycine
                  max]
Seq. No.
                   167358
Seq. ID
                  LIB3234-037-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2315140
BLAST score
                  374
                  5.0e-36
E value
                  76
Match length
                   93
% identity
NCBI Description
                  (AB006187) S-adenosylmethionine synthase [Nicotiana
                   tabacum]
                  167359
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2832674
BLAST score
                  210
E value
                  5.0e-17
Match length
                  80
% identity
                   64
                  (AL021712) fibrillin precursor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  167360
Seq. No.
```

22602

LIB3234-037-P1-K1-B1

BLASTN



```
NCBI GI
                   q4159712
BLAST score
                   60
E value
                   3.0e-25
Match length
                  172
% identity
                  84
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                  167361
                  LIB3234-037-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g1666171
NCBI GI
BLAST score
                  295
E value
                  1.0e-29
Match length
                  91
% identity
                  69
NCBI Description (Y09105) unknown [Nicotiana plumbaginifolia]
Seq. No.
                  167362
Seq. ID
                  LIB3234-037-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  q4191771
BLAST score
                  119
E value
                  3.0e-60
Match length
                  292
% identity
                  88
NCBI Description Arabidopsis thaliana chromosome II BAC F3P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167363
Seq. ID
                  LIB3234-037-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g2961335
BLAST score
                  33
E value
                  3.0e-09
Match length
                  41
% identity
                  95
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20
                  (ESSAII project)
Seq. No.
                  167364
Seq. ID
                  LIB3234-037-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  137
E value
                  4.0e-71
Match length
                  291
% identity
                  87
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
```

Seq. No. 167365

Seq. ID LIB3234-037-P1-K1-B8

Method BLASTN
NCBI GI g3549651
BLAST score 63
E value 7.0e-27



Match length 177 % identity 88 NCBI Description Arab

NCBI Description Arabidopsis thaliana MAP3K epsilon gene

Seq. No. 167366

Seq. ID LIB3234-037-P1-K1-B9

Method BLASTX
NCBI GI g4376233
BLAST score 327
E value 2.0e-30
Match length 65
% identity 94

NCBI Description (X00798) L2 protein [Nicotiana debneyi]

Seq. No. 167367

Seq. ID LIB3234-037-P1-K1-C1

Method BLASTX
NCBI GI g2914703
BLAST score 623
E value 4.0e-65
Match length 132
% identity 64

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 167368

Seq. ID LIB3234-037-P1-K1-C2

Method BLASTX
NCBI GI g1546694
BLAST score 250
E value 2.0e-21
Match length 57
% identity 88

NCBI Description (X98806) peroxidase ATP20a [Arabidopsis thaliana]

Seq. No. 167369

Seq. ID LIB3234-037-P1-K1-C5

Method BLASTX
NCBI GI g4582468
BLAST score 434
E value 5.0e-43
Match length 95
% identity 94

NCBI Description (AC007071) putative 40S ribosomal protein; contains

C-terminal domain [Arabidopsis thaliana]

Seq. No. 167370

Seq. ID LIB3234-037-P1-K1-C7

Method BLASTN
NCBI GI g4559375
BLAST score 133
E value 1.0e-68
Match length 265
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic

sequence, complete sequence

Seq. No. 167371



LIB3234-037-P1-K1-D1 Seq. ID Method BLASTX g1619602 NCBI GI BLAST score 338 9.0e - 32E value 77 Match length 83 % identity (Y08726) MtN3 [Medicago truncatula] NCBI Description 167372 Seq. No. LIB3234-037-P1-K1-D10 Seq. ID BLASTN Method NCBI GI g3241927 BLAST score 341 0.0e+00 E value Match length 365 98 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MTE17, complete sequence [Arabidopsis thaliana] Seq. No. 167373 Seq. ID LIB3234-037-P1-K1-D2 Method BLASTN NCBI GI g2570223 BLAST score 40 3.0e-13 E value Match length 86 86 % identity Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 167374 LIB3234-037-P1-K1-D7 Seq. ID Method BLASTN NCBI GI g4580745 BLAST score 136 E value 2.0e-70 Match length 283 89 % identity NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence, complete sequence 167375 Seq. No. Seq. ID LIB3234-037-P1-K1-D8 Method BLASTN NCBI GI g4589410 BLAST score 37 E value 2.0e-11 Match length 119 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 167376

Seq. ID LIB3234-037-P1-K1-D9

Method BLASTN NCBI GI g3128136



BLAST score 310 E value 1.0e-174 Match length 366 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 167377

Seq. ID LIB3234-037-P1-K1-E10

Method BLASTX
NCBI GI g2827139
BLAST score 244
E value 8.0e-21
Match length 105
% identity 50

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 167378

Seq. ID LIB3234-037-P1-K1-E2

Method BLASTN
NCBI GI g2924652
BLAST score 42
E value 2.0e-14
Match length 172
% identity 64

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9L2, complete sequence [Arabidopsis thaliana]

Seq. No. 167379

Seq. ID LIB3234-037-P1-K1-E5

Method BLASTN
NCBI GI g3985957
BLAST score 260
E value 1 0e-144

E value 1.0e-144
Match length 352
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYN8, complete sequence [Arabidopsis thaliana]

Seq. No. 167380

Seq. ID LIB3234-037-P1-K1-E7

Method BLASTN
NCBI GI g4063756
BLAST score 122
E value 4.0e-62
Match length 214
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC T9F8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167381

Seq. ID LIB3234-037-P1-K1-E8

Method BLASTN NCBI GI g4580745



```
BLAST score
                   52
                   2.0e-20
E value
Match length
                   264
% identity
                   80
                   Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
NCBI Description
                   complete sequence
                   167382
Seq. No.
Seq. ID
                   LIB3234-037-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   q1785673
                   75
BLAST score
E value
                   3.0e - 34
Match length
                   202
                   81
% identity
NCBI Description A.thaliana mitochondrial genome, part A
                   167383
Seq. No.
                   LIB3234-037-P1-K1-F10
Seq. ID
Method
                   BLASTX
                   g2454182
NCBI GI
                   559
BLAST score
E value
                   1.0e-57
Match length
                   124
% identity
                   89
NCBI Description
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                   167384
                   LIB3234-037-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q91152
BLAST score
                   198
                   2.0e-15
E value
Match length
                   81
% identity
                   23
NCBI Description nuclear protein, 25K - mouse
Seq. No.
                   167385
Seq. ID
                   LIB3234-037-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g1710530
BLAST score
                   651
E value
                   2.0e-68
Match length
                   120
% identity
                   97
NCBI Description
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
Seq. No.
                   167386
Seq. ID
                   LIB3234-037-P1-K1-F8
```

Method BLASTX NCBI GI g231586 BLAST score 68 E value 5.0e-14



Match length 73 % identity 66

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82027_pir__S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree
>gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

Seq. No. 167387

Seq. ID LIB3234-037-P1-K1-G6

Method BLASTN
NCBI GI g4544435
BLAST score 367
E value 0.0e+00
Match length 379
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F14M13 genomic

sequence, complete sequence

Seq. No. 167388

Seq. ID LIB3234-037-P1-K1-H12

Method BLASTX
NCBI GI g4455272
BLAST score 377
E value 2.0e-36
Match length 119
% identity 61

NCBI Description (AL035527) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 167389

Seq. ID LIB3234-037-P1-K1-H3

Method BLASTX
NCBI GI g3776005
BLAST score 130
E value 3.0e-24
Match length 100
% identity 61

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 167390

Seq. ID LIB3234-038-P1-K1-A1

Method BLASTX
NCBI GI g1531762
BLAST score 161
E value 4.0e-11
Match length 45
% identity 71

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 167391

Seq. ID LIB3234-038-P1-K1-A10

Method BLASTX
NCBI GI g1709379
BLAST score 157
E value 1.0e-10
Match length 34



% identity 85

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST >gi 881441 (UZ7653) NADH-plastoquinone oxidoreductase

[Lupinus luteus]

Seq. No. 167392

Seq. ID LIB3234-038-P1-K1-A11

Method BLASTX
NCBI GI 94586053
BLAST score 159
E value 1.0e-10
Match length 56

Match length 56 % identity 61

NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana]

Seq. No. 167393

Seq. ID LIB3234-038-P1-K1-A2

Method BLASTN
NCBI GI g4589410
BLAST score 310
E value 1.0e-174
Match length 332
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 167394

Seq. ID LIB3234-038-P1-K1-A4

Method BLASTX
NCBI GI g2507222
BLAST score 496
E value 2.0e-50
Match length 111
% identity 87

NCBI Description KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi 1709236 (U09505)

kinase associated protein phosphatase [Arabidopsis

thaliana]

Seq. No. 167395

Seq. ID LIB3234-038-P1-K1-A6

Method BLASTX
NCBI GI g633890
BLAST score 264
E value 3.0e-23
Match length 82
% identity 66

NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum

vulgare]

Seq. No. 167396

Seq. ID LIB3234-038-P1-K1-A8

Method BLASTN
NCBI GI 94589410
BLAST score 196
E value 1.0e-106
Match length 240
% identity 95



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2015, complete sequence
                  167397
Seq. No.
                  LIB3234-038-P1-K1-A9
Seq. ID
                  BLASTN
Method
                  g2828182
NCBI GI
BLAST score
                  323
                  0.0e+00
E value
Match length
                  348
                  98
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
                  167398
Seq. No.
                  LIB3234-038-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  163
                  1.0e-86
E value
                  221
Match length
% identity
                  96
NCBI Description Arabidopsis thaliana BAC IG002N01
                  167399
Seq. No.
                  LIB3234-038-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g633890
NCBI GI
BLAST score
                  277
E value
                  1.0e-24
Match length
                  85
% identity
                  66
NCBI Description
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  167400
Seq. ID
                  LIB3234-038-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  q3402745
BLAST score
                  182
E value
                  7.0e-98
Match length
                  342
% identity
                  95
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                  (ESSAII project)
```

Seq. No. 167401 Seq. ID LIB3234-038-P1-K1-B4

Method BLASTX
NCBI GI g3309082
BLAST score 259
E value 1.0e-22
Match length 54

% identity 94 NCBI Description (AF076251)

tion (AF076251) calcineurin B-like protein 1 [Arabidopsis

thaliana]



```
Seq. No.
                   167402
Seq. ID
                  LIB3234-038-P1-K1-B5
Method
                  BLASTX
NCBI GI
                   q1742955
BLAST score
                   347
E value
                   7.0e - 33
Match length
                   67
                  100
% identity
NCBI Description
                  (Z71446) CLC-b chloride channel protein [Arabidopsis
                  thaliana]
                  167403
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2781394
BLAST score
                  451
E value
                  4.0e-45
Match length
                  93
% identity
                  100
NCBI Description (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
Seq. No.
                  167404
Seq. ID
                  LIB3234-038-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2118307
BLAST score
                  494
E value
                  4.0e-50
Match length
                  99
% identity
                  100
NCBI Description
                  cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
                  >gi_804950_emb_CAA58893_ (X84097) cysteine synthase
                   [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                  thiol lyase [Arabidopsis thaliana]
Seq. No.
                  167405
Seq. ID
                  LIB3234-038-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g4581161
BLAST score
                  46
E value
                  7.0e-17
Match length
                  46
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic
                  sequence, complete sequence
Seq. No.
                  167406
Seq. ID
                  LIB3234-038-P1-K1-B9
Method
                  BLASTN
```

Method BLASTN
NCBI GI 94467094
BLAST score 64
E value 1.0e-27

Match length 64 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10

(ESSA project)

Seq. No. 167407



Seq. ID LIB3234-038-P1-K1-C1 Method BLASTX NCBI GI g4467114 BLAST score 260 1.0e-22 E value Match length 104 % identity 59 (AL035538) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 167408 LIB3234-038-P1-K1-C2 Seq. ID Method BLASTX NCBI GI g4467114 BLAST score 239 E value 3.0e-20 Match length 104 % identity 55 NCBI Description (AL035538) putative protein [Arabidopsis thaliana] Seq. No. 167409 LIB3234-038-P1-K1-C5 Seq. ID Method BLASTX NCBI GI g4262250 BLAST score 241 1.0e-20 E value 70 Match length 73 % identity NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana] Seq. No. 167410 LIB3234-038-P1-K1-C7 Seq. ID Method BLASTN NCBI GI q1279568 BLAST score 41 9.0e-14 E value Match length 49 % identity 96 NCBI Description Nicotiana acuminata chloroplast JLB region, 1-250bp Seq. No. 167411 Seq. ID LIB3234-038-P1-K1-D10 Method BLASTN NCBI GI q2832667 BLAST score 46 E value 9.0e-17Match length 114 % identity 85 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project) Seq. No. 167412 Seq. ID LIB3234-038-P1-K1-D12

Method BLASTX NCBI GI g231586 BLAST score 146 3.0e-09 E value Match length 89

Method

NCBI GI

E value

BLAST score

BLASTN

g12219

1.0e-89

168



```
% identity
                  46
NCBI Description
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 82027 pir S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi_18831_emb_CAA41401 (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
                  167413
Seq. No.
                  LIB3234-038-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1448941
BLAST score
                  512
                  3.0e-52
E value
Match length
                  109
                  91
% identity
                 (L48181) ypt-related protein [Brassica campestris]
NCBI Description
Seq. No.
                  167414
                  LIB3234-038-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377819
BLAST score
                  211
E value
                  6.0e-17
                  67
Match length
                  70
% identity
NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]
Seq. No.
                  167415
                  LIB3234-038-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119975
                  468
BLAST score
E value
                  4.0e-47
Match length
                  100
% identity
                  93
NCBI Description FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi 166698 (M35868) ferrodoxin A
                  [Arabidopsis thaliana]
Seq. No.
                  167416
Seq. ID
                  LIB3234-038-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4467132
BLAST score
                  447
E value
                  1.0e-44
Match length
                  116
                  77
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                  167417
Seq. ID
                  LIB3234-038-P1-K1-D9
```

NCBI Description



```
Match length
                  341
                  86
% identity
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.
                  167418
                  LIB3234-038-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g12219
BLAST score
                  44
E value
                  8.0e-16
Match length
                  183
                  86
% identity
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.
                  167419
Seq. ID
                  LIB3234-038-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q2832620
BLAST score
                  375
E value
                  3.0e-36
Match length
                  106
% identity
                  68
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  167420
Seq. ID
                  LIB3234-038-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q1620986
BLAST score
                  353
E value
                  1.0e-33
Match length
                  97
% identity
                  69
NCBI Description (Y08858) 40S ribosomal protein S17 [Nicotiana
                  plumbaginifolia]
Seq. No.
                  167421
Seq. ID
                  LIB3234-038-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g2245073
BLAST score
                  333
E value
                  0.0e+00
Match length
                  349
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  167422
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4417271
BLAST score
                  559
E value
                  1.0e-57
Match length
                  119
% identity
                  89
```

22614

[Arabidopsis thaliana]

(AC007019) putative cellulose synthase catalytic subunit



Seq. No. 167423

Seq. ID LIB3234-038-P1-K1-E6

Method BLASTX
NCBI GI g127041
BLAST score 526
E value 7.0e-54
Match length 102
% identity 99

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_81647_pir__JN0131 methionine adenosyltransferase (EC
2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 167424

Seq. ID LIB3234-038-P1-K1-E8

Method BLASTN
NCBI GI g4512656
BLAST score 150
E value 8.0e-79
Match length 259
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No. 167425

Seq. ID LIB3234-038-P1-K1-F10

Method BLASTX
NCBI GI g119143
BLAST score 159
E value 3.0e-48
Match length 103
% identity 85

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 167426

Seq. ID LIB3234-038-P1-K1-F11

Method BLASTX
NCBI GI g3582329
BLAST score 450
E value 6.0e-45
Match length 119
% identity 74

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 167427

Seq. ID LIB3234-038-P1-K1-F12

Method BLASTX

NCBI GI

E value

BLAST score

Match length

g2914688

1.0e-145

261

346



```
g3582329
NCBI GI
                   69
BLAST score
                   3.0e-20
E value
Match length
                   90
 % identity
                   61
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   167428
Seq. No.
                   LIB3234-038-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924258
BLAST score
                   475
E value
                   7.0e-48
Match length
                   116
                   80
 % identity
NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
                   167429
Seq. No.
                   LIB3234-038-P1-K1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2980757
                   274
BLAST score
E value
                   1.0e-153
Match length
                   313
                   97
 % identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
                   (ESSAII project)
                   167430
Seq. No.
Seq. ID
                   LIB3234-038-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g226120
BLAST score
                   186
E value
                   5.0e-14
Match length
                   83
 % identity
                   45
NCBI Description vicilin gene B [Saguinus oedipus]
 Seq. No.
                   167431
 Seq. ID
                   LIB3234-038-P1-K1-F8
Method
                   BLASTX
 NCBI GI
                   g1628583
BLAST score
                   567
E value
                   1.0e-58
Match length
                   111
 % identity
                   99
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
 Seq. No.
                   167432
 Seq. ID
                   LIB3234-038-P1-K1-G2
Method
                   BLASTN
```



98

% identity

```
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167433
Seq. ID
                   LIB3234-038-P1-K1-G3
                   BLASTN
Method
NCBI GI
                   g3047074
BLAST score
                   71
E value
                   1.0e-31
Match length
                   150
                   87
% identity
NCBI Description Arabidopsis thaliana BAC F21E10
                   167434
Seq. No.
Seq. ID
                   LIB3234-038-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   g3241920
BLAST score
                   192
E value
                   1.0e-104
Match length
                   364
                   97
% identity
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167435
                  LIB3234-038-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1864017
BLAST score
                   528
E value
                   4.0e-54
Match length
                   100
% identity
                   100
NCBI Description
                 (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   167436
Seq. ID
                  LIB3234-038-P1-K1-H1
Method
                  BLASTX
NCBI GI
                   q140285
BLAST score
                   207
E value
                   2.0e-16
Match length
                   42
% identity
                   95
                  HYPOTHETICAL 19 KD PROTEIN (ORF 168)
NCBI Description
                   >gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana
                   tabacum]
Seq. No.
                   167437
Seq. ID
                  LIB3234-038-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  q2618605
BLAST score
                  306
E value
                   1.0e-172
Match length
                  326
```

22617

MUK11, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



167438

Seq. No.

```
LIB3234-038-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3980412
BLAST score
                  216
E value
                  2.0e-17
Match length
                  58
                  20
% identity
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                  167439
                  LIB3234-038-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570223
BLAST score
                  42
E value
                  1.0e-14
Match length
                  74
                  89
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167440
Seq. ID
                  LIB3234-038-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3955041
BLAST score
                  261
E value
                  8.0e-23
Match length
                  98
                  52
% identity
NCBI Description (AJ010068) nhp2+ protein [Schizosaccharomyces pombe]
Seq. No.
                  167441
Seq. ID
                  LIB3234-038-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  350
E value
                  3.0e - 33
Match length
                  81
% identity
                  85
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  167442
Seq. ID
                  LIB3234-038-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g4519187
BLAST score
                  319
E value
                  1.0e-179
Match length
                  351
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

97

% identity



K1G2, complete sequence

Seq. No. 167443 Seq. ID LIB3234-038-P1-K1-H9 Method BLASTX NCBI GI q3258569 BLAST score 105 E value 8.0e-28 Match length 70

% identity NCBI Description (U89959) Similar to yeast general negative regulator of

transcription subunit 1 [Arabidopsis thaliana]

167444 Seq. No.

Seq. ID LIB3234-039-P1-K1-A10

93

Method BLASTN NCBI GI q1313927 BLAST score 35 E value 3.0e-10 Match length 128 % identity 88

NCBI Description B.oleracea mRNA for IFA binding protein (sp10)

167445 Seq. No.

LIB3234-039-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI q4678259 BLAST score 212 4.0e-17 E value Match length 115

% identity 15

NCBI Description (AL049657) putative protein [Arabidopsis thaliana]

Seq. No. 167446

Seq. ID LIB3234-039-P1-K1-A3

Method BLASTN NCBI GI q2760170 BLAST score 96 E value 1.0e-46 284 Match length % identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 167447

Seq. ID LIB3234-039-P1-K1-A6

Method BLASTX NCBI GI g2501021 BLAST score 100 E value 7.0e-14Match length 66 % identity 62

LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) NCBI Description

>gi_1652562 dbj BAA17483 (D90906) lysyl-tRNA synthetase

[Synechocystis sp.]

167448 Seq. No.



```
LIB3234-039-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935151
BLAST score
                  562
E value
                  4.0e-58
Match length
                  108
                  97
% identity
NCBI Description
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                  167449
                  LIB3234-039-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760170
                  65
BLAST score
E value
                  4.0e-28
Match length
                  187
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167450
                  LIB3234-039-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  525
E value
                  9.0e-54
                  101
Match length
% identity
                  99
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  167451
Seq. ID
                  LIB3234-039-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q625977
BLAST score
                  456
E value
                  1.0e-45
Match length
                  90
% identity
                  99
NCBI Description
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  167452
Seq. ID
                  LIB3234-039-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g132863
BLAST score
                  45
E value
                  3.0e-52
Match length
                  109
% identity
                  91
NCBI Description
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
                  >gi 12214 emb CAA46568 (X65615) ribosomal protein L2
                  [Sinapis alba]
```

Seq. No. 167453

Seq. ID LIB3234-039-P1-K1-B2

Method BLASTX



```
NCBI GI
                  g3132475
BLAST score
                  472
E value
                  2.0e-47
                  115
Match length
                  82
% identity
NCBI Description
                  (AC003096) similar to proline-rich protein [Arabidopsis
                  thaliana]
                  167454
Seq. No.
                  LIB3234-039-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281868
BLAST score
                  54
                  3.0e-40
E value
                  112
Match length
                  76
% identity
NCBI Description
                  (AL031004) putative protein [Arabidopsis thaliana]
                  167455
Seq. No.
                  LIB3234-039-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3132469
BLAST score
                  57
                  3.0e-23
E value
                  256
Match length
% identity
                  86
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T29F13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  167456
Seq. No.
                  LIB3234-039-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618683
BLAST score
                  154
E value
                  3.0e-81
Match length
                  359
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167457
Seq. ID
                  LIB3234-039-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4406780
BLAST score
                  572
E value
                  3.0e-59
Match length
                  115
% identity
NCBI Description
                  (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  167458
Seq. ID
                  LIB3234-039-P1-K1-C11
```

Method BLASTN NCBI GI g4159707 BLAST score 322 E value 0.0e+00



Match length 352 % identity 98 NCBI Description Ara

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJK13, complete sequence

Seq. No. 167459

Seq. ID LIB3234-039-P1-K1-C12

Method BLASTX
NCBI GI g399013
BLAST score 314
E value 4.0e-29
Match length 108
% identity 62

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis

thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)

adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator

[Arabidopsis thaliana]

Seq. No. 167460

Seq. ID LIB3234-039-P1-K1-C2

Method BLASTN
NCBI GI 94559375
BLAST score 279
E value 1.0e-156
Match length 358
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic

sequence, complete sequence

Seq. No. 167461

Seq. ID LIB3234-039-P1-K1-C4

Method BLASTX
NCBI GI g1531762
BLAST score 191
E value 1.0e-14
Match length 50
% identity 74

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 167462

Seq. ID LIB3234-039-P1-K1-C6

Method BLASTX
NCBI GI g113171
BLAST score 474
E value 9.0e-48
Match length 102
% identity 96

NCBI Description ACYL CARRIER PROTEIN 1 PRECURSOR (ACP)

>gi_81596_pir__S03267 acyl carrier protein precursor Arabidopsis thaliana >gi_16152_emb_CAA31991_ (X13708) acyl

carrier protein [Arabidopsis thaliana]

Seq. No. 167463

NCBI GI

E value

BLAST score

g3142294

6.0e-37

382



LIB3234-039-P1-K1-C7 Seq. ID Method BLASTN NCBI GI q4559375 BLAST score 276 E value 1.0e-154 Match length 343 97 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence Seq. No. 167464 Seq. ID LIB3234-039-P1-K1-C8 Method BLASTN NCBI GI g4559375 BLAST score 277 E value 1.0e-154 344 Match length 98 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence Seq. No. 167465 LIB3234-039-P1-K1-C9 Seq. ID Method BLASTX g3335171 NCBI GI BLAST score 172 E value 2.0e-12 Match length 67 % identity 55 NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana] Seq. No. 167466 LIB3234-039-P1-K1-D1 Seq. ID Method BLASTX NCBI GI q4586053 BLAST score 244 E value 8.0e-21 Match length 114 % identity 48 NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana] Seq. No. 167467 Seq. ID LIB3234-039-P1-K1-D10 Method BLASTX NCBI GI g4704613 BLAST score 356 E value 6.0e-34 Match length 82 88 % identity NCBI Description (AF109695) monodehydroascorbate reductase [Brassica juncea] Seq. No. 167468 Seq. ID LIB3234-039-P1-K1-D11 Method BLASTX



```
Match length
                  88
% identity
                   (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb_U37354 from S. pombe. ESTs gb_T41979, gb N37284 and
                  gb N37529 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  167469
                  LIB3234-039-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075394
BLAST score
                  559
E value
                  9.0e-58
Match length
                  115
                  95
% identity
NCBI Description
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana] >gi_3559809_emb_CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis Thaliana]
Seq. No.
                  167470
Seq. ID
                  LIB3234-039-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                  273
E value
                  1.0e-152
                  273
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167471
Seq. ID
                  LIB3234-039-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g3805962
BLAST score
                  259
E value
                  1.0e-22
Match length
                  112
% identity
                  53
NCBI Description
                  (Y13772) laccase [Populus balsamifera subsp. trichocarpa]
Seq. No.
                  167472
Seq. ID
                  LIB3234-039-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2459446
BLAST score
                  448
E value
                  9.0e-45
Match length
                  116
% identity
                  78
NCBI Description
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
Seq. No.
                  167473
```

Seq. ID LIB3234-039-P1-K1-D9

Method BLASTN
NCBI GI g4757412
BLAST score 286
E value 1.0e-160
Match length 349



% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK23, complete sequence

Seq. No. 167474

Seq. ID LIB3234-039-P1-K1-E1

Method BLASTX
NCBI GI g1172599
BLAST score 451
E value 4.0e-45
Match length 88
% identity 100

NCBI Description PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX SUBUNIT C5) (TAS-F22/FAFP98)

>gi_600387_emb_CAA47753_ (X67338) proteosome subunit

[Arabidopsis thaliana]

Seq. No. 167475

Seq. ID LIB3234-039-P1-K1-E10

Method BLASTN
NCBI GI 94092472
BLAST score 34
E value 1.0e-09
Match length 46

% identity 96
NCBI Description Arabidopsis thaliana BAC F1K3 from chromosome IV near 21

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 167476

Seq. ID LIB3234-039-P1-K1-E11

Method BLASTX
NCBI GI g2501056
BLAST score 450
E value 6.0e-45
Match length 101
% identity 92

NCBI Description SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)

>gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis

thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA

Synthetase [Arabidopsis thaliana]

Seq. No. 167477

Seq. ID LIB3234-039-P1-K1-E12

Method BLASTN
NCBI GI g4512690
BLAST score 282
E value 1.0e-157
Match length 352
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic

sequence, complete sequence

Seq. No. 167478

Seq. ID LIB3234-039-P1-K1-E4

Method BLASTN
NCBI GI g3510347
BLAST score 203



```
1.0e-110
E value
Match length
                   354
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167479
Seq. ID
                  LIB3234-039-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  259
E value
                   2.0e-22
Match length
                  79
% identity
                   65
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                  167480
Seq. ID
                  LIB3234-039-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g584998
BLAST score
                  149
E value
                  1.0e-09
Match length
                  64
% identity
                  44
NCBI Description FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450
                  LXXVA2) (P-450EG1) >gi_629713_pir__S43342 flavonoid
                  hydroxylase cytochrome P450 - eggplant
                  >gi_395261_emb_CAA50155_ (X70824) flavonoid hydroxylase
                   (P450) [Solanum melongena]
Seq. No.
                  167481
Seq. ID
                  LIB3234-039-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  283
E value
                  2.0e-25
Match length
                  89
% identity
                  64
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
NCBI Description
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  167482
Seq. ID
                  LIB3234-039-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g585536
BLAST score
                  534
E value
                  8.0e-55
Match length
                  111
% identity
                  91
```

NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)

>gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -Arabidopsis thaliana >qi 304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi 871990 emb_CAA55786 (X79194)

thioglucosidase [Arabidopsis thaliana]

Seq. No. 167483



```
Seq. ID
                  LIB3234-039-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q2642215
BLAST score
                  191
                  1.0e-14
E value
Match length
                  36
                  97
% identity
NCBI Description
                 (AF030386) NOI protein [Arabidopsis thaliana]
Seq. No.
                  167484
Seq. ID
                  LIB3234-039-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q485514
                  258
BLAST score
E value
                  2.0e-22
Match length
                  77
                  64
% identity
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
Seq. No.
                  167485
Seq. ID
                  LIB3234-039-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q2921158
BLAST score
                  526
                  7.0e-54
E value
Match length
                  117
                  91
% identity
NCBI Description
                 (AF022909) ClpC [Arabidopsis thaliana]
                  167486
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1053047
BLAST score
                  460
E value
                  4.0e-46
Match length
                  92
% identity
                  100
NCBI Description
                  (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
                  histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                  [Glycine max]
                  167487
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g2760164
BLAST score
                  69
                  2.0e-30
E value
Match length
                  209
% identity
                  89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18P6, complete sequence [Arabidopsis thaliana]
```

Seq. No. 167488

Seq. ID LIB3234-039-P1-K1-G12

Method BLASTX



```
NCBI GI
                    q3273743
BLAST score
                    345
E value
                    1.0e-32
Match length
                    88
% identity
                    81
NCBI Description
                    (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                    thaliana] >gi 3786019 (AC005499) unknown protein
                    [Arabidopsis thaliana]
                    167489
Seq. No.
Seq. ID
                    LIB3234-039-P1-K1-G2
Method
                    BLASTX
NCBI GI
                    q266989
BLAST score
                    90
E value
                    7.0e-33
Match length
                    118
% identity
                    69
NCBI Description
                    GTP-BINDING PROTEIN SAR1B >gi 322517 pir S28603
                    GTP-binding protein - Arabidopsis thaliana >gi_166734
                    (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                    167490
Seq. ID
                    LIB3234-039-P1-K1-G3
Method
                    BLASTX
NCBI GI
                    q131336
BLAST score
                    53
E value
                    6.0e-24
Match length
                    72
% identity
                    89
NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715 pir F2NT0P
                    photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum]
                    >gi_225225_prf__1211235BG photosystem II 10kD
phosphoprotein [Nicotiana tabacum]
Seq. No.
                    167491
Seq. ID
                    LIB3234-039-P1-K1-G5
                    BLASTN
Method
NCBI GI
                    g2618599
BLAST score
                    310
E value
                    1.0e-174
Match length
                    362
                    96
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MBD2, complete sequence [Arabidopsis thaliana]
                    167492
Seq. No.
Seq. ID
                    LIB3234-039-P1-K1-G7
Method
                    BLASTN
```

NCBI GI g2689438 BLAST score 166 E value 2.0e-88 Match length 301 % identity 96

NCBI Description Arabidopsis thaliana BAC F2401 chromosome 1, complete

sequence [Arabidopsis thaliana]



Seq. No. 167493

Seq. ID LIB3234-039-P1-K1-H11

47

Method BLASTX
NCBI GI g3776559
BLAST score 145
E value 1.0e-09
Match length 77

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 167494

% identity

Seq. ID LIB3234-039-P1-K1-H12

Method BLASTN
NCBI GI g984307
BLAST score 34
E value 1.0e-09
Match length 34
% identity 100

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 167495

Seq. ID LIB3234-039-P1-K1-H2

Method BLASTX
NCBI GI g112682
BLAST score 94
E value 4.0e-25
Match length 106
% identity 59

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167496

Seq. ID LIB3234-039-P1-K1-H4

Method BLASTN
NCBI GI g4079614
BLAST score 102
E value 4.0e-50
Match length 310
% identity 90

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167497

Seq. ID LIB3234-039-P1-K1-H5

Method BLASTX NCBI GI g3776559



BLAST score 253 E value 5.0e-22 Match length 98 % identity 52

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 167498

Seq. ID LIB3234-039-P1-K1-H6

Method BLASTN
NCBI GI g3522932
BLAST score 319
E value 1.0e-179
Match length 364
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167499

Seq. ID LIB3234-039-P1-K1-H7

Method BLASTX
NCBI GI g1854445
BLAST score 376
E value 3.0e-36
Match length 87
% identity 79

NCBI Description (D83971) CPRD14 protein [Vigna unquiculata]

Seq. No. 167500

Seq. ID LIB3234-039-P1-K1-H8

Method BLASTX
NCBI GI 94204299
BLAST score 583
E value 1.0e-60
Match length 116
% identity 99

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 167501

Seq. ID LIB3234-040-P1-K1-A11

Method BLASTX
NCBI GI 94580460
BLAST score 600
E value 2.0e-62
Match length 125
% identity 94

NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis

thaliana]

Seq. No. 167502

Seq. ID LIB3234-040-P1-K1-A2

Method BLASTX NCBI GI g3695023 BLAST score 269



E value 1.0e-23 Match length 98 % identity 52 NCBI Description (AF055850) unknown [Arabidopsis thaliana] 167503 Seq. No. Seq. ID LIB3234-040-P1-K1-A5 Method BLASTX NCBI GI q2894574 BLAST score 556 E value 2.0e-57 Match length 106 100 % identity NCBI Description (AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana] 167504 Seq. No. Seq. ID LIB3234-040-P1-K1-A6 Method BLASTN NCBI GI q3702722 BLAST score 37 2.0e-11 E value Match length 137 % identity 82 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K12B20, complete sequence [Arabidopsis thaliana] Seq. No. 167505 Seq. ID LIB3234-040-P1-K1-A7 Method BLASTN NCBI GI q4589430 BLAST score 209 E value 1.0e-114 Match length 375 % identity 94 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence Seq. No. 167506 Seq. ID LIB3234-040-P1-K1-A9 Method BLASTX NCBI GI g4468993 BLAST score 597 E value 4.0e-62 Match length 113 % identity 100 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 167507

Seq. ID LIB3234-040-P1-K1-B1

Method BLASTX
NCBI GI g399298
BLAST score 199
E value 2.0e-15
Match length 66
% identity 65



NCBI Description STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 -

Arabidopsis thaliana >gi_16230_emb_CAA38894 (X55053) cold

regulated [Arabidopsis thaliana]

Seq. No.

167508

Seq. ID

LIB3234-040-P1-K1-B10 BLASTX

Method NCBI GI

q3334404

BLAST score

616

E value Match length

2.0e-64 128

% identity

93

NCBI Description

VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb N96435, gb N96106, gb N96189, gb_N96091, gb_AA042286, gb F14324, gb W43643, gb N96027,

gb_N96299, gb_R29943, gb $T\overline{4}3460$, gb $T\overline{4}3544$, gb $T\overline{2}2472$

Seq. No.

167509

Seq. ID

LIB3234-040-P1-K1-B11

Method NCBI GI BLASTX q112682

BLAST score

163

E value

3.0e-11

Match length % identity

112 40

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

167510 Seq. ID

LIB3234-040-P1-K1-B12

Method

BLASTX

NCBI GI

q1345132

BLAST score

620

E value

8.0e-65

Match length

128

% identity

93

NCBI Description

(U47029) ERECTA [Arabidopsis thaliana]

>gi_1389566_dbj_BAA11869 (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.

167511

Seq. ID Method

LIB3234-040-P1-K1-B3

NCBI GI

BLASTX

g1402904

BLAST score

93

E value Match length 1.0e-22

% identity

113

NCBI Description (X98313) peroxidase [Arabidopsis thaliana]



```
Seq. No.
                   167512
                   LIB3234-040-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g133812
BLAST score
                   113
E value
                   3.0e-16
Match length
                   61
                   84
% identity
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S16 >gi 71000 pir R3IS16
                   ribosomal protein S16 - white mustard chloroplast
                   >gi_12217_emb_CAA31944_ (X13609) 16S ribosomal protein
                   [Sinapis alba]
                   167513
Seq. No.
Seq. ID
                   LIB3234-040-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q1531762
BLAST score
                   195
E value
                   5.0e-15
Match length
                   51
                   75
% identity
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                   thaliana]
                   167514
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-B7
Method
                  BLASTX
NCBI GI
                   q4704730
BLAST score
                   166
E value
                   1.0e-11
Match length
                   55
% identity
                   60
NCBI Description
                 (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]
Seq. No.
                  167515
Seq. ID
                  LIB3234-040-P1-K1-B8
Method
                  BLASTN
NCBI GI
                   q2494110
BLAST score
                   321
E value
                   0.0e+00
Match length
                   351
% identity
                   98
NCBI Description
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167516
Seq. ID
                  LIB3234-040-P1-K1-B9
Method
                  BLASTN
NCBI GI
                   g1429212
BLAST score
                  169
E value
                   4.0e-90
Match length
                  258
% identity
                  94
```

Seq. No. 167517

NCBI Description A.thaliana mRNA for peroxidase ATP4a, EST clone 4G6T7P



```
Seq. ID
                  LIB3234-040-P1-K1-C12
Method
                  BLASTX
NCBI GI
                   g231660
BLAST score
                   257
                   3.0e-22
E value
Match length
                  132
% identity
                   48
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.
                  167518
Seq. ID
                  LIB3234-040-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3983125
BLAST score
                   453
E value
                   3.0e-45
Match length
                  117
% identity
                   77
NCBI Description (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  167519
Seq. ID
                  LIB3234-040-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q2656029
BLAST score
                  356
E value
                  0.0e + 00
Match length
                  372
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQB2
Seq. No.
                  167520
Seq. ID
                  LIB3234-040-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  187
E value
                  1.0e-101
Match length
                  367
% identity
                   96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
Seq. No.
                  167521
Seq. ID
                  LIB3234-040-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4584519
BLAST score
                  294
E value
                  1.0e-165
Match length
                  339
% identity
                  96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18
                  (ESSA project)
```

Seq. No. 167522

Seq. ID LIB3234-040-P1-K1-C7

Method BLASTN NCBI GI g1402933



```
BLAST score
                   115
E value
                   7.0e-58
Match length
                   204
% identity
                   86
```

NCBI Description A.thaliana genomic DNA fragment (ecotype DIJON-0/LANDSBERG

ERECTA/ LEIDEN-0/LLAGOSTERA-0)

167523 Seq. No.

Seq. ID LIB3234-040-P1-K1-C9

Method BLASTX NCBI GI g2673917 BLAST score 524 E value 1.0e-53 Match length 130 % identity 57

NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 167524

Seq. ID LIB3234-040-P1-K1-D10

Method BLASTN NCBI GI g3047100 BLAST score 286 1.0e-160 E value Match length 378 % identity 93

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 167525

Seq. ID LIB3234-040-P1-K1-D11

Method BLASTX NCBI GI g112739 BLAST score 208 E value 7.0e-21 Match length 108 % identity 56

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 167526

Seq. ID LIB3234-040-P1-K1-D12

Method BLASTX NCBI GI g4406820 BLAST score 354 E value 1.0e-33 Match length 68 100 % identity

NCBI Description (AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No. 167527

Seq. ID LIB3234-040-P1-K1-D2



Method BLASTX NCBI GI g4262250 BLAST score 404 E value 2.0e-39 Match length 81 100 % identity

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 167528

Seq. ID LIB3234-040-P1-K1-D3

Method BLASTN NCBI GI g2182289 BLAST score 81 E value 1.0e-37 Match length 247 92 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167529

Seq. ID LIB3234-040-P1-K1-D8

Method BLASTX NCBI GI g3150404 BLAST score 229 E value 5.0e-19 Match length 66 % identity 74

NCBI Description (AC004165) putative mitochondrial carrier protein

[Arabidopsis thaliana]

Seq. No. 167530

Seq. ID LIB3234-040-P1-K1-D9

Method BLASTX NCBI GI g3850978 BLAST score 259 E value 2.0e-22 Match length 54 % identity 91

NCBI Description (AF060429) ATP synthase beta subunit [Embothrium coccineum]

Seq. No. 167531

Seq. ID LIB3234-040-P1-K1-E1

Method BLASTN NCBI GI g4490291 BLAST score 342 E value 0.0e+00Match length 373 98 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5

(ESSA project)

Seq. No. 167532

Seq. ID LIB3234-040-P1-K1-E10

Method BLASTX NCBI GI g1498053 BLAST score 446 E value 2.0e-44



Match length 110 % identity 80

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. Seq. ID

167533 LIB323 BLASTN

Method

LIB3234-040-P1-K1-E11

NCBI GI BLAST score E value

g4199934 257 1.0e-142

Match length % identity

364

% identity 91

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No.

167534

Seq. ID

LIB3234-040-P1-K1-E12

Method BLASTX
NCBI GI g1345973
BLAST score 69
E value 2.0e-59
Match length 122
% identity 93

% identity NCBI Description

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No.

167535

Seq. ID LI

LIB3234-040-P1-K1-E2 BLASTX

Method BLASTX
NCBI GI g1628583
BLAST score 473
E value 1.0e-47
Match length 122
% identity 76

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

167536

Seq. ID LIB3234-040-P1-K1-E3

Method BLASTN
NCBI GI g3869065
BLAST score 285
E value 1.0e-159
Match length 312
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.



```
Seq. ID
                  LIB3234-040-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  a1864017
BLAST score
                   535
E value
                   7.0e-55
Match length
                  106
% identity
                   96
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  167538
Seq. ID
                  LIB3234-040-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3236254
BLAST score
                  149
E value
                  1.0e-09
Match length
                  65
% identity
                  48
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                  167539
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-F2
Method
                  BLASTX
                  g2129767
NCBI GI
BLAST score
                  598
E value
                  3.0e-62
Match length
                  121
                  93
% identity
NCBI Description
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
                  precursor - Arabidopsis thaliana >gi_1805364 dbj BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  167540
Seq. ID
                  LIB3234-040-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2129767
BLAST score
                  469
E value
                  2.0e-47
Match length
                  94
                  91
% identity
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
NCBI Description
                  precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  167541
Seq. ID
                  LIB3234-040-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q4662647
BLAST score
                  56
E value
                  3.0e-23
Match length
                  124
% identity
                  87
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3K12 genomic
                  sequence, complete sequence
```

Seq. No. 167542

Seq. ID LIB3234-040-P1-K1-F6

Method BLASTX



NCBI GI g137580
BLAST score 214
E value 3.0e-17
Match length 121
% identity 36

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)

>gi_72286_pir__FWCNAB alpha-globulin B precursor (clone
C72) - upland cotton >gi_167375 (M16891) vicilin precursor

[Gossypium hirsutum]

Seq. No. 167543

Seq. ID LIB3234-040-P1-K1-F8

Method BLASTN
NCBI GI 94699904
BLAST score 38
E value 3.0e-12
Match length 162
% identity 81

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,

complete sequence

Seq. No. 167544

Seq. ID LIB3234-040-P1-K1-G1

Method BLASTX
NCBI GI g1113941
BLAST score 367
E value 3.0e-35
Match length 109
% identity 71

NCBI Description (U40713) Pv42p [Phaseolus vulgaris]

Seq. No. 167545

Seq. ID LIB3234-040-P1-K1-G10

Method BLASTN
NCBI GI g4589434
BLAST score 231
E value 1.0e-127

E value 1.0e-Match length 302 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ7, complete sequence

Seq. No. 167546

Seq. ID LIB3234-040-P1-K1-G12

Method BLASTN
NCBI GI g4581138
BLAST score 290
E value 1.0e-162
Match length 374
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 167547

Seq. ID LIB3234-040-P1-K1-G2

Method BLASTX NCBI GI g1592677



```
BLAST score
                  265
E value
                  3.0e-23
Match length
                  102
                  55
% identity
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                  167548
Seq. ID
                  LIB3234-040-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g3150396
BLAST score
                  257
E value
                  1.0e-142
Match length
                  346
% identity
                  97
NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  167549
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1086249
BLAST score
                  302
E value
                  1.0e-27
Match length
                  126
% identity
                  44
                  subtilisin-like protease - Alnus glutinosa
NCBI Description
                  >gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease
                  [Alnus glutinosa]
Seq. No.
                  167550
Seq. ID
                  LIB3234-040-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  288
E value
                  1.0e-161
                  375
Match length
% identity
                  94
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  167551
Seq. ID
                  LIB3234-040-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4455329
BLAST score
                  588
E value
                  4.0e-61
Match length
                  124
```

96 % identity

NCBI Description (AL035525) lysine-ketoglutarate reductase/saccharopine

[Arabidopsis thaliana]

167552 Seq. No.

Seq. ID LIB3234-040-P1-K1-H10

Method BLASTX q3885334 NCBI GI BLAST score 593 E value 1.0e-61



Match length 123 % identity 93

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

167553 Seq. No.

Seq. ID LIB3234-040-P1-K1-H11

Method BLASTX NCBI GI q3885334 BLAST score 270 E value 5.0e-24Match length 60 % identity

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thalianal

Seq. No. 167554

Seq. ID LIB3234-040-P1-K1-H12

Method BLASTX NCBI GI q1703375 BLAST score 410 E value 2.0e-40 Match length 88 % identity 91

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)

DcARF1 [Daucus carota]

Seq. No. 167555

Seq. ID LIB3234-040-P1-K1-H2

Method BLASTX NCBI GI g2924262 BLAST score 617 E value 2.0e-64 Match length 122 % identity 92

NCBI Description (Z00044) PSII 44kd protein [Nicotiana tabacum]

Seq. No. 167556

Seq. ID LIB3234-040-P1-K1-H3

Method BLASTX NCBI GI g120675 BLAST score 452 E value 4.0e-45 Match length 88 % identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis

alba]

Seq. No. 167557

Seq. ID LIB3234-040-P1-K1-H5

Method BLASTX NCBI GI g3135751 BLAST score 228 E value 6.0e-19



Match length 44 % identity 95

NCBI Description (AJ006095) 26S protease regulatory subunit 6 [Cicer

arietinum]

Seq. No. 167558

Seq. ID LIB3234-040-P1-K1-H6

Method BLASTX
NCBI GI g543841
BLAST score 481
E value 2.0e-48
Match length 96
% identity 97

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir___\$28875

ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)

ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 167559

Seq. ID LIB3234-040-P1-K1-H7

Method BLASTX
NCBI GI g1345973
BLAST score 431
E value 1.0e-42
Match length 97
% identity 81

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167560

Seq. ID LIB3234-040-P1-K1-H8

Method BLASTX
NCBI GI g3169172
BLAST score 403
E value 2.0e-39
Match length 89
% identity 82

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi 3445214 (AC004786) putative serine

carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 167561

Seq. ID LIB3234-040-P1-K1-H9

Method BLASTX
NCBI GI g3695023
BLAST score 292
E value 2.0e-26
Match length 107

% identity (AF055850) unknown [Arabidopsis thaliana] NCBI Description 167562 Seq. No. LIB3234-041-P1-K1-A1 Seq. ID BLASTX Method NCBI GI g4584536 358 BLAST score 4.0e-34 E value Match length 100 % identity 63 (AL049608) cytochrome p450 like protein [Arabidopsis NCBI Description thaliana] 167563 Seq. No. LIB3234-041-P1-K1-A10 Seq. ID BLASTN Method q4757662 NCBI GI BLAST score 322 0.0e+00E value 374 Match length 97 % identity Genomic sequence for Arabidopsis thaliana BAC F10B6 from NCBI Description chromosome I, complete sequence 167564 Seq. No. Seq. ID LIB3234-041-P1-K1-A11 BLASTX Method NCBI GI q1864017 BLAST score 530 3.0e-54E value

Match length 104 97 % identity

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

167565 Seq. No.

Seq. ID LIB3234-041-P1-K1-A12

Method BLASTN NCBI GI g2656031 BLAST score 349 E value 0.0e + 00Match length 369 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC20

Seq. No. 167566

Seq. ID LIB3234-041-P1-K1-A2

Method BLASTX NCBI GI g1841399 BLAST score 441 E value 8.0e-44Match length 97 % identity 89

(Z34661) AtTFIIB2 [Arabidopsis thaliana] NCBI Description

Seq. No. 167567



Seq. ID LIB3234-041-P1-K1-A3 Method BLASTN NCBI GI q2564048 BLAST score 343 E value 0.0e + 00Match length 379 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana] Seq. No. 167568 Seq. ID LIB3234-041-P1-K1-A5 Method BLASTX NCBI GI q4204299 BLAST score 528 E value 5.0e-54Match length 108 % identity 96 NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana] Seq. No. 167569 Seq. ID LIB3234-041-P1-K1-A6 Method BLASTX NCBI GI q1531762 BLAST score 195 E value 5.0e-15Match length 51 % identity 75 NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana] Seq. No. 167570 Seq. ID LIB3234-041-P1-K1-A9 Method BLASTX NCBI GI g3738288 BLAST score 652 E value 1.0e-68 Match length 123 % identity 98 (AC005309) auxin-responsive GH3-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 167571 Seq. ID LIB3234-041-P1-K1-B10 Method BLASTN g3241916 286 1.0e-160 323 % identity 100

NCBI GI BLAST score E value Match length

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15N18, complete sequence [Arabidopsis thaliana]

Seq. No. 167572

Seq. ID LIB3234-041-P1-K1-B11

Method BLASTN



```
NCBI GI
                   q1490552
BLAST score
                   207
E value
                   1.0e-113
Match length
                  283
% identity
                   93
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
NCBI Description
                   (SAMdc) mRNA, complete cds
Seq. No.
                  167573
```

Seq. ID LIB3234-041-P1-K1-B12 Method BLASTX

NCBI GI q3413718 BLAST score 159 E value 1.0e-46 Match length 113 87 % identity

NCBI Description (AC004747) alpha-vacuolar processing enzyme [Arabidopsis thaliana] >gi 3643591 (AC005395) alpha-vacuolar processing

enzyme [Arabidopsis thaliana]

Seq. No. 167574 LIB3234-041-P1-K1-B3 Seq. ID

Method BLASTX NCBI GI q3249107 BLAST score 484 E value 7.0e-49

Match length 101 92 % identity

NCBI Description (AC003114) Contains similarity to phloem-specific lectin

PP2 gb Z17331 from Cucubita maxima. [Arabidopsis thaliana]

Seq. No. 167575

Seq. ID LIB3234-041-P1-K1-B4

Method BLASTX NCBI GI q3335171 BLAST score 475 E value 8.0e-48 Match length 117 % identity 78

NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No. 167576

Seq. ID LIB3234-041-P1-K1-B6

Method BLASTN NCBI GI g3985950 BLAST score 140 E value 9.0e-73 Match length 386 95 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI10, complete sequence [Arabidopsis thaliana]

Seq. No. 167577

Seq. ID LIB3234-041-P1-K1-B7

Method BLASTX NCBI GI g1561730 BLAST score 157

Match length

% identity

371

99



```
E value
                  1.0e-10
Match length
                  61
% identity
                  46
NCBI Description
                  (U65491) Dreg-3 protein [Drosophila melanogaster]
Seq. No.
                  167578
                  LIB3234-041-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395432
BLAST score
                  261
E value
                  9.0e-23
                  90
Match length
% identity
                  56
NCBI Description
                 (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  167579
                  LIB3234-041-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131360
BLAST score
                  232
E value
                  2.0e-19
Match length
                  60
                  78
% identity
NCBI Description
                  PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                  >gi_81727_pir__S02115 photosystem II protein psbK precursor
                  white mustard chloroplast >gi_12209_emb_CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.
                  167580
Seq. ID
                  LIB3234-041-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q82040
BLAST score
                  469
E value
                  3.0e-47
Match length
                  97
% identity
                  25
NCBI Description ubiquitin precursor - flax (fragment) >gi 168304 (M57895)
                  ubiquitin [Linum usitatissimum]
Seq. No.
                  167581
Seq. ID
                  LIB3234-041-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  474
E value
                  1.0e-47
Match length
                  113
% identity
                  82
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  167582
Seq. ID
                  LIB3234-041-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g2623294
BLAST score
                  278
E value
                  1.0e-155
```

Seq. ID



```
NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167583
Seq. ID
                  LIB3234-041-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q633890
BLAST score
                  272
E value
                  5.0e-24
Match length
                  82
% identity
                  67
NCBI Description
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  167584
Seq. ID
                  LIB3234-041-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  63
E value
                  4.0e-09
Match length
                  58
% identity
                  60
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  167585
Seq. ID
                  LIB3234-041-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4773885
BLAST score
                  495
E value
                  4.0e-50
Match length
                  95
% identity
                  98
NCBI Description
                  (AF076243) putative aspartic protease [Arabidopsis
                  thaliana]
Seq. No.
                  167586
Seq. ID
                  LIB3234-041-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4539005
BLAST score
                  231
E value
                  3.0e-19
Match length
                  120
% identity
                  42
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  167587
Seq. ID
                  LIB3234-041-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2924258
BLAST score
                  413
E value
                  1.0e-40
Match length
                  124
% identity
                  65
NCBI Description
                  (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                  167588
```

22647

LIB3234-041-P1-K1-D1



```
Method
                  BLASTN
NCBI GI
                  g3869069
BLAST score
                  353
                  0.0e + 00
E value
                  365
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
                  167589
Seq. No.
                  LIB3234-041-P1-K1-D10
Seq. ID
Method
                  BLASTN
                  g3985933
NCBI GI
BLAST score
                  224
E value
                  1.0e-123
Match length
                  264
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9E15, complete sequence [Arabidopsis thaliana]
                  167590
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4204277
                  596
BLAST score
                  5.0e-62
E value
                  110
Match length
% identity
                  100
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  167591
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-D3
Method
                  BLASTX
                  g881615
NCBI GI
BLAST score
                  618
E value
                  1.0e-64
Match length
                  124
% identity
                   96
NCBI Description
                  (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                  >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
                   167592
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g881614
BLAST score
                  42
E value
                  2.0e-14
Match length
                  138
% identity
NCBI Description
                  Arabidopsis thaliana fatty acid elongase 1 (Fae1) gene,
```

complete cds

167593 Seq. No.

Seq. ID LIB3234-041-P1-K1-D5

Method BLASTX NCBI GI g1628583



BLAST score 360 E value 2.0e-34 Match length 128 % identity 68

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 167594

Seq. ID LIB3234-041-P1-K1-D9

Method BLASTN
NCBI GI g3985933
BLAST score 353
E value 0.0e+00
Match length 376
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9E15, complete sequence [Arabidopsis thaliana]

Seq. No. 167595

Seq. ID LIB3234-041-P1-K1-E1

Method BLASTX
NCBI GI g1071913
BLAST score 77
E value 2.0e-21
Match length 72
% identity 76

NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial

- spinach >gi 1066153 dbj BAA07177 (D37963) cysteine

synthase [Spinacia oleracea]

Seq. No. 167596

Seq. ID LIB3234-041-P1-K1-E12

Method BLASTN
NCBI GI g4580745
BLAST score 104
E value 2.0e-51
Match length 361
% identity 95

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence,

complete sequence

Seq. No. 167597

Seq. ID LIB3234-041-P1-K1-E2

Method BLASTX
NCBI GI g2494842
BLAST score 265
E value 3.0e-23
Match length 97
% identity 52

NCBI Description GLUCOSYLTRANSFERASE ALG6 >gi_2131171_pir__S61985 ALG6

protein - yeast (Saccharomyces cerevisiae) >gi_1150997 (U43491) hypothetical protein UNA544 [Saccharomyces

cerevisiae] >gi 1420090 emb CAA99190 (Z74910) ORF YOR002w

[Saccharomyces cerevisiae]

Seq. No. 167598

% identity



```
LIB3234-041-P1-K1-E3
Seq. ID
Method
                  BLASTX
                  a544424
NCBI GI
BLAST score
                  55
                  9.0e-39
E value
                  85
Match length
                  100
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147
NCBI Description
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                  [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                  167599
                  LIB3234-041-P1-K1-E5
Seq. ID
Method
                  BLASTN
                  g2337888
NCBI GI
BLAST score
                  207
E value
                  1.0e-113
Match length
                  354
                  97
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,
                  complete sequence [Arabidopsis thaliana]
                  167600
Seq. No.
                  LIB3234-041-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3985949
BLAST score
                  304
                  1.0e-170
E value
Match length
                  368
                  95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167601
                  LIB3234-041-P1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q511598
BLAST score
                  345
E value
                  0.0e+00
Match length
                  377
% identity
                  26
NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,
                  complete cds
                  167602
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-F10
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  156
                  2.0e-10
E value
Match length
                  78
```

22650

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510



cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

167603 Seq. No. Seq. ID LIB3234-041-P1-K1-F11 Method BLASTX NCBI GI g1084476 BLAST score 322 5.0e-37 E value Match length 94 78 % identity NCBI Description catalase (EC 1.11.1.6) - maize >gi 311239 emb CAA42720 (X60135) catalase-1 [Zea mays] 167604 Seq. No. LIB3234-041-P1-K1-F12 Seq. ID Method BLASTX NCBI GI g2117612 352 BLAST score E value 2.0e-33 Match length 62 98 % identity NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana Seq. No. 167605 LIB3234-041-P1-K1-F2 Seq. ID Method BLASTX NCBI GI q1864017 BLAST score 561 6.0e-58 E value Match length 109 % identity NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum] 167606 Seq. No. LIB3234-041-P1-K1-F3 BLASTX q1669668 306 3.0e-28

Seq. ID

Method NCBI GI BLAST score E value Match length 88

% identity 72

NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]

Seq. No. 167607

Seq. ID LIB3234-041-P1-K1-F5

Method BLASTX NCBI GI g3873743 BLAST score 251 E value 1.0e-21 Match length 112 46 % identity

NCBI Description (Z66519) similar to Thiamine pyrophosphate enzymes; cDNA

EST EMBL:D36315 comes from this gene; cDNA EST EMBL:D33464

comes from this gene [Caenorhabditis elegans]

NCBI GI

E value

BLAST score

Match length

g4756963

4.0e-53

107

307



```
167608
Seq. No.
                  LIB3234-041-P1-K1-F6 ~
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  221
E value
                  5.0e-18
Match length
                  43
                  93
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  167609
Seq. No.
                  LIB3234-041-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548655
BLAST score
                  361
                  2.0e-34
E value
Match length
                  83
                  90
% identity
                  50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
NCBI Description
                  >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast
                   - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046)
                  ribosomal protein L12 [Arabidopsis thaliana]
                  167610
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4557061
BLAST score
                  140
E value
                  8.0e-73
Match length
                  164
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC F23M2 genomic
                  sequence, complete sequence
Seq. No.
                  167611
Seq. ID
                  LIB3234-041-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4063552
BLAST score
                  594
E value
                  8.0e-62
Match length
                  126
% identity
NCBI Description (AF035908) ATP synthase beta subunit [Muntingia calabura]
                  167612
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-G10
                  BLASTN
Method
```

NCBI Description



```
88
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                  (ESSA project)
                  167613
Seq. No.
                  LIB3234-041-P1-K1-G11
Seq. ID
Method
                  BLASTN
                  g4220510
NCBI GI
BLAST score
                  333
E value
                  0.0e+00
                  373
Match length
                  97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                  (ESSAII project)
                  167614
Seq. No.
                  LIB3234-041-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  277
E value
                  1.0e-154
                  289
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                  (ESSAII project)
Seq. No.
                  167615
                  LIB3234-041-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206556
BLAST score
                  377
                  2.0e-36
E value
Match length
                  114
                  68
% identity
                 (AF066824) ATP synthase beta subunit [Simaba baileyana]
NCBI Description
Seq. No.
                  167616
Seq. ID
                  LIB3234-041-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  635
E value
                  1.0e-66
Match length
                  126
                  96
% identity
                  (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  167617
                  LIB3234-041-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335169
BLAST score
                  665
E value
                   4.0e-70
                  127
Match length
                  97
% identity
```

(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific



protein 1 (ATS1) [Arabidopsis thaliana]

```
Seq. No.
                  167618
                  LIB3234-041-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g4006833
NCBI GI
BLAST score
                  148
E value
                  2.0e-09
Match length
                  57
                  46
% identity
                  (AC005970) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167619
                  LIB3234-041-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3242787
BLAST score
                  480
                  2.0e-48
E value
Match length
                  125
                  78
% identity
                  (AF055356) respiratory burst oxidase protein E [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167620
                  LIB3234-041-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g4586053
NCBI GI
BLAST score
                  243
E value
                  1.0e-20
Match length
                  125
% identity
                  46
NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana]
                  167621
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q4586098
BLAST score
                  349
E value
                  0.0e+00
Match length
                  377
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                   (ESSA project)
Seq. No.
                  167622
Seq. ID
                  LIB3234-041-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  77
E value
                  1.0e-35
Match length
                  137
                  89
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

Seq. No. 167623

MSL1, complete sequence [Arabidopsis thaliana]



LIB3234-041-P1-K1-H12 Seq. ID Method BLASTX NCBI GI g120675 BLAST score 424 E value 7.0e-42Match length 100 81 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba] 167624 Seq. No. LIB3234-041-P1-K1-H4 Seq. ID Method BLASTN NCBI GI g3242700 BLAST score 183 E value 9.0e-99 Match length 191 % identity 63 Arabidopsis thaliana chromosome II BAC F26B6 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 167625 LIB3234-041-P1-K1-H5 Seq. ID Method BLASTX NCBI GI q2160694 BLAST score 492 8.0e-50 E value Match length 125 78 % identity (U73528) B' regulatory subunit of PP2A [Arabidopsis NCBI Description thaliana] Seq. No. 167626 Seq. ID LIB3234-041-P1-K1-H6 Method BLASTN NCBI GI q403417 BLAST score 107 E value 2.0e-53 Match length 118 % identity 97 Arabidopsis thaliana Columbia bZIP protein GBF4 gene, NCBI Description complete cds Seq. No. 167627 Seq. ID LIB3234-041-P1-K1-H7 Method BLASTX NCBI GI g3522943 BLAST score 360 2.0e-34E value 124 Match length % identity

Seq. No. 167628

NCBI Description

(AC004411) putative p-glycoprotein [Arabidopsis thaliana]



```
LIB3234-041-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023934
BLAST score
                  213
E value
                  2.0e-17
                  80
Match length
                  50
% identity
                  HISTONE DEACETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR
NCBI Description
                  BINDING PROTEIN) >gi_1667396 (U31758) transcriptional
                  regulator homolog RPD3 [Mus musculus]
Seq. No.
                  167629
                  LIB3234-043-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  356
                  0.0e+00
E value
Match length
                  411
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  167630
Seq. No.
                  LIB3234-043-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4691223
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
                  167631
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4678299
BLAST score
                  622
E value
                  5.0e-65
Match length
                  122
% identity
                  99
NCBI Description
                  (AL049655) cysteine proteinase precursor-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  167632
Seq. ID
                  LIB3234-043-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3869088
BLAST score
                  599
E value
                  2.0e-62
Match length
                  117
                  98
% identity
                 (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
```

NCBI Description

Seq. No. 167633

Seq. ID LIB3234-043-P1-K1-A4

Method BLASTN



```
NCBI GI
                  g2264316
                  288
BLAST score
                  1.0e-161
E value
Match length
                  405
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167634
                  LIB3234-043-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  148
                  1.0e-77
E value
Match length
                  303
                  65
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167635
Seq. ID
                  LIB3234-043-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4490733
BLAST score
                  468
E value
                  5.0e-47
Match length
                  96
% identity
                  100
NCBI Description
                  (AL035709) putative protein [Arabidopsis thaliana]
                  167636
Seq. No.
                  LIB3234-043-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4559396
                  600
BLAST score
                  2.0e-62
E value
                  129
Match length
                  96
% identity
NCBI Description
                  (AC006526) unknown protein [Arabidopsis thaliana]
                  167637
Seq. No.
                  LIB3234-043-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656030
BLAST score
                  345
E value
                  0.0e + 00
Match length
                  406
                  86
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  167638
Seq. No.
                  LIB3234-043-P1-K1-B4
Seq. ID
```

Method BLASTN
NCBI GI g2494110
BLAST score 331
E value 0.0e+00
Match length 367



% identity 98

NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 167639

Seq. ID LIB3234-043-P1-K1-B5

Method BLASTN
NCBI GI g3337347
BLAST score 43
E value 6.0e-15
Match length 67
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F13P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167640

Seq. ID LIB3234-043-P1-K1-B9

Method BLASTN
NCBI GI g4589445
BLAST score 372
E value 0.0e+00
Match length 396
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWL2, complete sequence

Seq. No. 167641

Seq. ID LIB3234-043-P1-K1-C1

Method BLASTN
NCBI GI g3133272
BLAST score 301
E value 1.0e-169
Match length 405
% identity 92

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T17H7,

complete sequence [Arabidopsis thaliana]

Seq. No. 167642

Seq. ID LIB3234-043-P1-K1-C10

Method BLASTN
NCBI GI g2828188
BLAST score 160
E value 6.0e-85
Match length 232
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K3, complete sequence [Arabidopsis thaliana]

Seq. No. 167643

Seq. ID LIB3234-043-P1-K1-C11

Method BLASTX
NCBI GI g3033375
BLAST score 281
E value 5.0e-25
Match length 103
% identity 88

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis



thaliana]

167644 Seq. No. LIB3234-043-P1-K1-C12 Seq. ID Method BLASTN g3894179 NCBI GI BLAST score 305 E value 1.0e-171 393 Match length 94 % identity Arabidopsis thaliana chromosome II BAC F13H10 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 167645 LIB3234-043-P1-K1-C3 Seq. ID Method BLASTN g4666247 NCBI GI BLAST score 66 1.0e-28 E value Match length 220 83 % identity Arabidopsis thaliana DNA for germin-like protein precursor, NCBI Description complete cds Seq. No. 167646 LIB3234-043-P1-K1-C7 Seq. ID Method BLASTX g4115377 NCBI GI BLAST score 152 6.0e-10E value Match length 102 % identity 38 (AC005967) unknown protein [Arabidopsis thaliana] NCBI Description 167647 Seq. No. Seq. ID LIB3234-043-P1-K1-C9 Method BLASTX NCBI GI g1143322 BLAST score 295 E value 7.0e-27 Match length 102 % identity 61 (U40979) alfa-carboxyltransferase precursor [Glycine max] NCBI Description Seq. No. 167648 Seq. ID LIB3234-043-P1-K1-D2 Method BLASTX NCBI GI g82207 BLAST score 602 1.0e-62 E value Match length 134 87 % identity NCBI Description hypothetical protein 1708 - common tobacco chloroplast

Seq. No. 167649

Seq. ID LIB3234-043-P1-K1-D3

Method BLASTX



NCBI GI g4185507 BLAST score 466 E value 1.0e-46 Match length 121 % identity 81

NCBI Description (AF100163) EZA1 [Arabidopsis thaliana]

Seq. No. 167650

Seq. ID LIB3234-043-P1-K1-D5

Method BLASTN
NCBI GI g3449332
BLAST score 214
E value 1.0e-117
Match length 331
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSF19, complete sequence [Arabidopsis thaliana]

Seq. No. 167651

Seq. ID LIB3234-043-P1-K1-D8

Method BLASTX
NCBI GI g1107501
BLAST score 393
E value 3.0e-38
Match length 99
% identity 80

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 167652

Seq. ID LIB3234-043-P1-K1-E10

Method BLASTN
NCBI GI g336274
BLAST score 90
E value 6.0e-43
Match length 257
% identity 88

NCBI Description Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA,

tRNA-Arg, and tRNA-Asn genes

Seq. No. 167653

Seq. ID LIB3234-043-P1-K1-E11

Method BLASTN
NCBI GI g1448916
BLAST score 359
E value 0.0e+00
Match length 399
% identity 97

NCBI Description Arabidopsis thaliana threonine synthase mRNA, 3' end of cds

Seq. No. 167654

Seq. ID LIB3234-043-P1-K1-E12

Method BLASTN NCBI GI g4580732

BLAST score 53



E value 7.0e-21 Match length 101 88

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F5J5,

complete sequence

Seq. No. 167655

Seq. ID LIB3234-043-P1-K1-E2

Method BLASTX
NCBI GI g1169515
BLAST score 625
E value 2.0e-65
Match length 121
% identity 98

NCBI Description EM-LIKE PROTEIN GEA1 >gi 2119768 pir S34819 embryonic

abundant protein Em1 - Arabidopsis thaliana

>gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1

protein [Arabidopsis thaliana]

Seq. No. 167656

Seq. ID LIB3234-043-P1-K1-E3

Method BLASTX
NCBI GI g3335171
BLAST score 528
E value 5.0e-54
Match length 122
% identity 84

NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No. 167657

Seq. ID LIB3234-043-P1-K1-E5

Method BLASTX
NCBI GI g2384956
BLAST score 231
E value 3.0e-19
Match length 134
% identity 34

NCBI Description (AF022985) No definition line found [Caenorhabditis

elegans]

Seq. No. 167658

Seq. ID LIB3234-043-P1-K1-E7

Method BLASTN
NCBI GI g12218
BLAST score 224
E value 1.0e-123
Match length 264
% identity 96

NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly

Seq. No. 167659

Seq. ID LIB3234-043-P1-K1-E8

Method BLASTX NCBI GI g131360 BLAST score 241

NCBI GI

E value Match length

BLAST score

g3157930

82 7.7e-02

113

```
E value
                  2.0e-20
Match length
                  61
                  80
% identity
NCBI Description
                 PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                  >gi 81727 pir__S02115 photosystem II protein psbK precursor
                  - white mustard chloroplast >gi_12209_emb CAA31909
                  (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
                  167660
Seq. No.
                  LIB3234-043-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g728873
                  168
BLAST score
                  7.0e-12
E value
Match length
                  37
                  81
% identity
NCBI Description
                  L-ASCORBATE PEROXIDASE, CYTOSOLIC (AP)
                  >gi 322534 pir_ S28856 L-ascorbate peroxidase (EC
                  1.11.1.11), cytosolic - Arabidopsis thaliana
                  >gi 16173 emb CAA42168 (X59600) L-ascorbate peroxidase
                  [Arabidopsis thaliana] >gi_217833_dbj_BAA03334_ (D14442)
                  ascorbate peroxidase [Arabidopsis thaliana] >gi 1532170
                  (U63815) ascorbate peroxidase [Arabidopsis thalīana]
                  167661
Seq. No.
                  LIB3234-043-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  193
                  3.0e-15
E value
                  62
Match length
                  61
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  167662
                  LIB3234-043-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q117820
BLAST score
                  245
                  8.0e-21
E value
Match length
                  50
% identity
                  100
NCBI Description CYTOCHROME B6 >gi_625192_pir__CBSP6
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  cytochrome b6 - spinach chloroplast >gi 12285 emb CAA30128
                  (X07106) petB [Spinacia oleracea]
                  167663
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-G12
Method
                  BLASTX
```

Match length

% identity

396 77



```
% identity
                  90
NCBI Description
                  (AC002131) Strong similarity to
                  amino-cyclopropane-carboxylic acid oxidase gb L27664 from
                  Brassica napus. ESTs gb Z48548 and gb Z48549 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  167664
                  LIB3234-043-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  g3327196
NCBI GI
BLAST score
                  281
                  5.0e-25
E value
                  75
Match length
                  71
% identity
NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]
Seq. No.
                  167665
                  LIB3234-043-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245110
BLAST score
                  271
E value
                  7.0e-24
                  54
Match length
                  98
% identity
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                  167666
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-G6
                  BLASTN
Method
                  g2244788
NCBI GI
BLAST score
                  150
E value
                  9.0e-79
Match length
                  333
% identity
                  94
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  167667
                  LIB3234-043-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2605714
BLAST score
                  438
                  2.0e-43
E value
Match length
                  107
% identity
                  81
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167668
Seq. ID
                  LIB3234-043-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q3985955
BLAST score
                  303
E value
                  1.0e-170
```

22663

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



100

[Arabidopsis thaliana]

% identity

NCBI Description

MTH16, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  167669
                  LIB3234-043-P1-K1-H1
Seq. ID
Method
                  BLASTN
                  g4589950
NCBI GI
BLAST score
                  367
                  0.0e + 00
E value
                  408
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                  sequence, complete sequence
                  167670
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-H11
Method
                  BLASTN
                  q3757512
NCBI GI
BLAST score
                  121
                  1.0e-61
E value
Match length
                  171
% identity
                   62
                  Arabidopsis thaliana chromosome II BAC F12A24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167671
                  LIB3234-043-P1-K1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4309747
BLAST score
                   292
                  1.0e-163
E value
                   312
Match length
                   28
% identity
                  Arabidopsis thaliana chromosome II BAC T13E11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   167672
Seq. No.
                  LIB3234-043-P1-K1-H2
Seq. ID
Method
                   BLASTN
                   g3402695
NCBI GI
                   50
BLAST score
E value
                   4.0e-19
                   155
Match length
% identity
                   87
                  Arabidopsis thaliana chromosome II BAC T3K9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   167673
Seq. No.
Seq. ID
                   LIB3234-043-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4678307
BLAST score
                   580
E value
                   4.0e-60
Match length
                   116
```

(AL049655) vacuolar protein sorting-like protein

Seq. ID Method

NCBI GI



```
Seq. No.
                  167674
                  LIB3234-043-P1-K1-H4
Seq. ID
                  BLASTN
Method
                  g1946354
NCBI GI
                  230
BLAST score
                  1.0e-126
E value
                  406
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                  sequence, complete sequence
                  167675
Seq. No.
                  LIB3234-046-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  q3785999
NCBI GI
                  470
BLAST score
                  3.0e-47
E value
Match length
                  107
                  84
% identity
                  (AC005499) putative peptidyl-prolyl cis-trans isomerase
NCBI Description
                   [Arabidopsis thaliana]
                  167676
Seq. No.
                  LIB3234-046-P1-K1-A10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2924257
BLAST score
                  66
E value
                  1.0e-28
                  191
Match length
                   90
% identity
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  167677
                  LIB3234-046-P1-K1-A11
Seq. ID
Method
                  BLASTN
                   g3327867
NCBI GI
BLAST score
                   389
E value
                   0.0e + 00
Match length
                   389
                   100
% identity
                  Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein
NCBI Description
                   7, complete cds
                   167678
Seq. No.
                   LIB3234-046-P1-K1-A12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2154718
BLAST score
                   340
E value
                   0.0e + 00
Match length
                   390
% identity
                   97
NCBI Description A.thaliana nit2 gene, nit1 gene and nit3 gene
Seq. No.
                   167679
```

22665

LIB3234-046-P1-K1-A2

BLASTX

g2317902

E value

Match length

3.0e-18

77



```
BLAST score
                  714
                  7.0e-76
E value
Match length
                  130
                  100
% identity
                  (U89959) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167680
                  LIB3234-046-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g2262167
NCBI GI
BLAST score
                  578
E value
                  7.0e-60
Match length
                  110
                  100
% identity
                  (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
                  167681
Seq. No.
                  LIB3234-046-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  g99992
NCBI GI
BLAST score
                  485
E value
                  5.0e-49
Match length
                  129
% identity
                  53
                  protein disulfide-isomerase (EC 5.3.4.1) precursor -
NCBI Description
                  alfalfa (clone B2) >gi 166418 (M82973) putative
                  endomembrane protein; putative [Medicago sativa]
                  167682
Seq. No.
                  LIB3234-046-P1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1531762
                  195
BLAST score
                  5.0e-15
E value
                  51
Match length
                   75
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                  167683
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g3808062
BLAST score
                   153
                   4.0e-10
E value
Match length
                   66
% identity
                   44
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
                   167684
Seq. No.
                   LIB3234-046-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1814424
BLAST score
                   223
```



```
% identity
                  55
                  (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
NCBI Description
                  167685
Seq. No.
                  LIB3234-046-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678299
                  661
BLAST score
                  1.0e-69
E value
                  126
Match length
                  100
% identity
                  (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  167686
Seq. No.
                  LIB3234-046-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2262116
BLAST score
                  664
                  5.0e-70
E value
                  129
Match length
% identity
                  98
                  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                  167687
Seq. No.
                  LIB3234-046-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1592675
BLAST score
                  313
                  8.0e-29
E value
                  108
Match length
                  61
% identity
                  (X91919) LEA76 homologue typel [Arabidopsis thaliana]
NCBI Description
                  167688
Seq. No.
                  LIB3234-046-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g1619602
NCBI GI
                   369
BLAST scoré
E value
                   2.0e-35
Match length
                  87
                   79
% identity
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                  167689
Seq. No.
                  LIB3234-046-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1592677
BLAST score
                   193
                   9.0e-15
E value
                   38
Match length
                   100
% identity
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
```

22667

167690

BLASTN

LIB3234-046-P1-K1-B4

Seq. No.

Seq. ID Method

BLAST score

Match length

E value

269

117

1.0e-23



```
NCBI GI
                  g4589969
BLAST score
                  147
                  6.0e-77
E value
Match length
                  262
                  61
% identity
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
NCBI Description
                  sequence, complete sequence
                  167691
Seq. No.
                  LIB3234-046-P1-K1-B5
Seq. ID
                  BLASTN
Method
                  g2213606
NCBI GI
                  390
BLAST score
                  0.0e + 00
E value
Match length
                  390
                  100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F21J9,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  167692
Seq. No.
                  LIB3234-046-P1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1592677
NCBI GI
                  201
BLAST score
                   9.0e-16
E value
                  92
Match length
                   49
% identity
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
                  167693
Seq. No.
                  LIB3234-046-P1-K1-B8
Seq. ID
                  BLASTX
Method
                   g3176874
NCBI GI
BLAST score
                   545
E value
                   4.0e-56
Match length
                   121
% identity
                   89
                  (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   167694
Seq. No.
Seq. ID
                   LIB3234-046-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2511725
BLAST score
                   674
                   4.0e-71
E value
Match length
                   128
% identity
                   100
NCBI Description
                  (AF021937) catalase 1 [Arabidopsis thaliana]
                   167695
Seq. No.
Seq. ID
                   LIB3234-046-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g112740
```



% identity 52 NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN) NCBI Description >gi 81691 pir A25997 napin precursor (napA) - rape >gi 167153 (J02586) prepronapin [Brassica napus] >gi 167155 $(J0\overline{2}798)$ napin [Brassica napus] 167696 Seq. No. Seq. ID LIB3234-046-P1-K1-C10 Method BLASTX NCBI GI g2622920 304 BLAST score E value 9.0e-28 123 Match length % identity 44 (AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium NCBI Description thermoautotrophicum] Seq. No. 167697 LIB3234-046-P1-K1-C11 Seq. ID BLASTX Method g2213608 NCBI GI 233 BLAST score E value 2.0e-19 129 Match length 36 % identity NCBI Description (AC000103) F21J9.2 [Arabidopsis thaliana] Seq. No. 167698 LIB3234-046-P1-K1-C12 Seq. ID BLASTX Method NCBI GI g1502428 BLAST score 335 2.0e-31 E value 66 Match length 100 % identity (U62330) phosphate transporter [Arabidopsis thaliana] NCBI Description >gi_2258116_dbj_BAA21503_ (D86591) inorganic phosphate

transporter [Arabidopsis thaliana]

>gi_2258118_dbj_BAA21504_ (D86608) inorganic phosphate

transporter [Arabidopsis thaliana]

Seq. No. 167699

LIB3234-046-P1-K1-C2 Seq. ID

Method BLASTN NCBI GI q4092472 BLAST score 36 E value 3.0e-11 Match length 36 % identity 100

Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 NCBI Description

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 167700

Seq. ID LIB3234-046-P1-K1-C3

Method BLASTN NCBI GI g4220643

BLAST score 50



E value 4.0e-19
Match length 188
% identity 88
NCBI Description Arabido

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 167701

Seq. ID LIB3234-046-P1-K1-C5

Method BLASTX
NCBI GI g1709970
BLAST score 360
E value 2.0e-34
Match length 73
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 167702

Seq. ID LIB3234-046-P1-K1-C6

Method BLASTX
NCBI GI 94704824
BLAST score 359
E value 3.0e-34
Match length 117
% identity 60

NCBI Description (AF139377) stearoyl acyl carrier protein desaturase

Lldd3A20 [Lupinus luteus]

Seq. No. 167703

Seq. ID LIB3234-046-P1-K1-C7

Method BLASTX
NCBI GI g2244905
BLAST score 208
E value 2.0e-16
Match length 54
% identity 80

NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 167704

Seq. ID LIB3234-046-P1-K1-C8

Method BLASTN
NCBI GI g4220643
BLAST score 356
E value 0.0e+00
Match length 384
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 167705

Seq. ID LIB3234-046-P1-K1-C9

Method BLASTX
NCBI GI g343503
BLAST score 183
E value 1.0e-13
Match length 36
% identity 100



(L12250) ribosomal protein S12 [Nicotiana plumbaginifolia] NCBI Description >gi_1334367_emb_CAA27200_ (X03481) rps12-like coding sequence [Nicotiana tabacum] >gi 2924276 emb CAA77429 (Z00044) ribosomal protein S12 [Nicotiana tabacum] >gi 2924283 emb CAA77436 (Z00044) ribosomal protein S12 [Nicotiana tabacum] 167706 Seq. No. LIB3234-046-P1-K1-D1 Seq. ID Method BLASTX g1107501 NCBI GI BLAST score 378 2.0e-36 E value Match length 119 66 % identity (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) NCBI Description Match to gb X91954 orf gene product from A. thaliana. ESTs gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from this gene. [Arabidopsis thaliana] 167707 Seq. No. LIB3234-046-P1-K1-D11 Seq. ID Method BLASTN NCBI GI g4510392 BLAST score 210 E value 1.0e-114 Match length 387 100 % identity Arabidopsis thaliana chromosome II BAC T17D12 genomic NCBI Description sequence, complete sequence Seq. No. 167708 LIB3234-046-P1-K1-D12 Seq. ID Method BLASTN NCBI GI g3135250 BLAST score 56 E value 1.0e-22 Match length 100 89 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana] 167709 Seq. No. LIB3234-046-P1-K1-D2 Seq. ID Method BLASTX NCBI GI q4678306 BLAST score 132 E value 1.0e-11 Match length 83 % identity

NCBI Description (AL049655) kinesin-like protein [Arabidopsis thaliana]

Seq. No. 167710

Seq. ID LIB3234-046-P1-K1-D3

Method BLASTN NCBI GI g4733952 BLAST score 279



E value 1.0e-156 Match length 387 % identity 93

Arabidopsis thaliana chromosome I BAC F23H11 genomic NCBI Description

sequence, complete sequence

Seq. No. 167711

LIB3234-046-P1-K1-D4 Seq. ID

Method BLASTN NCBI GI g2564049 BLAST score 392 0.0e+00E value Match length 392 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE2, complete sequence [Arabidopsis thaliana]

167712 Seq. No.

LIB3234-046-P1-K1-D6 Seq. ID

BLASTX Method NCBI GI q4006827 BLAST score 259 E value 2.0e-22 Match length 130 % identity 44

(AC005970) subtilisin-like protease [Arabidopsis thaliana] NCBI Description

Seq. No. 167713

Seq. ID LIB3234-046-P1-K1-D7

Method BLASTX q2582381 NCBI GI BLAST score 604 6.0e-63E value 127 Match length 87 % identity

(AF021220) cation-chloride co-transporter [Nicotiana NCBI Description

tabacum]

167714 Seq. No.

LIB3234-046-P1-K1-D8 Seq. ID

BLASTX Method NCBI GI q112682 BLAST score 158 4.0e-23 E value 124 Match length 55 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167715

LIB3234-046-P1-K1-D9 Seq. ID

BLASTN Method NCBI GI g4589421

BLAST score 36



E value 9.0e-11 Match length 70 97 % identity Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: NCBI Description K5K13, complete sequence Seq. No. 167716 LIB3234-046-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g1169476 BLAST score 595 7.0e-62 E value Match length 113 100 % identity ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE NCBI Description ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum] Seq. No. 167717 LIB3234-046-P1-K1-E10 Seq. ID Method BLASTN NCBI GI g2264316 BLAST score 38 6.0e-12 E value Match length 156 88 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRO11, complete sequence [Arabidopsis thaliana] Seq. No. 167718 LIB3234-046-P1-K1-E11 Seq. ID Method BLASTX g1184075 NCBI GI BLAST score 153 4.0e-10 E value Match length 129 1 % identity

(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] NCBI Description >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon

esculentum]

167719 Seq. No.

LIB3234-046-P1-K1-E12 Seq. ID

BLASTX Method g633890 NCBI GI 287 BLAST score 8.0e-26 E value 88 Match length % identity 65

(S72926) glucose and ribitol dehydrogenase homolog [Hordeum NCBI Description

vulgare]

167720 Seq. No.

LIB3234-046-P1-K1-E2 Seq. ID

Method BLASTX NCBI GI g82232 562 BLAST score



5.0e-58 E value Match length 129 84 % identity rpoC protein homolog - common tobacco chloroplast NCBI Description Seq. No. 167721 LIB3234-046-P1-K1-E3 Seq. ID Method BLASTX a2708750 NCBI GI 316 BLAST score 3.0e-29 E value 128 Match length % identity 55 (AC003952) putative physical impedence protein [Arabidopsis NCBI Description thaliana] Seq. No. 167722 Seq. ID LIB3234-046-P1-K1-E4 Method BLASTX q1077345 NCBI GI 154 BLAST score 3.0e-10 E value Match length 82 40 % identity NCBI Description hypothetical protein YLR290c - yeast (Saccharomyces cerevisiae) >gi_596046 (U17243) L8003.16 gene product [Saccharomyces cerevisiae] Seq. No. 167723 Seq. ID LIB3234-046-P1-K1-E5 BLASTX Method NCBI GI q2454184 BLAST score 629 7.0e-66 E value Match length 127 % identity 99 NCBI Description (U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] Seq. No. 167724 Seq. ID LIB3234-046-P1-K1-E6 Method BLASTN NCBI GI g3367500 BLAST score 329 E value 0.0e + 00Match length 394 % identity 96 REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 NCBI Description TO: 93489, complete sequence [Arabidopsis thaliana]

167725 Seq. No.

LIB3234-046-P1-K1-E7 Seq. ID

Method BLASTX g3402716 NCBI GI BLAST score 183 1.0e-13 E value 85 Match length



```
% identity
NCBI Description
                  (AC004261) unknown protein [Arabidopsis thaliana]
                  167726
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2529229
BLAST score
                  516
                  1.0e-52
E value
                  127
Match length
                  81
% identity
                 (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                  167727
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-F1
                  BLASTX
Method
                  g465835
NCBI GI
BLAST score
                  443
E value
                  4.0e-44
Match length
                  129
% identity
                  64
                  HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOME III
NCBI Description
                  >gi 630577 pir S44625 C50C3.6 protein - Caenorhabditis
                  elegans >gi 289658 (L14433) putative [Caenorhabditis
                  elegans]
                  167728
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-F10
                  BLASTX
Method
NCBI GI
                  q135406
BLAST score
                  418
                  3.0e-41
E value
                  80
Match length
                  97
% identity
NCBI Description
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
                  alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                  167729
                  LIB3234-046-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119143
BLAST score
                   605
                   4.0e-63
E value
Match length
                  115
                  100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
                   (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                   (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
```

>gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]



167730

LIB3234-046-P1-K1-F12

Seq. No.

```
Seq. ID
Method
                   BLASTX
                   q4204298
NCBI GI
BLAST score
                   558
                   1.0e-57
E value
                   125
Match length
% identity
                   86
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   167731
Seq. No.
                   LIB3234-046-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586109
BLAST score
                   314
E value
                   6.0e-29
Match length
                   58
                   100
% identity
                   (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167732
                   LIB3234-046-P1-K1-F5
Seq. ID
Method
                   BLASTX
                   g2894598
NCBI GI
BLAST score
                   696
E value
                   1.0e-73
Match length
                   131
                   100
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   167733
Seq. No.
                   LIB3234-046-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832703
BLAST score
                    381
E value
                   7.0e-37
Match length
                   79
                    95
% identity
                   (AL021713) potassium channel protein KAT2 [Arabidopsis
NCBI Description
                    thaliana]
                    167734
Seq. No.
                   LIB3234-046-P1-K1-F9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4507311
BLAST score
                    215
E value
                    2.0e-17
Match length
                   103
                    40
% identity
                   suppressor of Ty (S.cerevisiae) 4 homolog 1
NCBI Description
                   >gi_3122873_sp_Q16550_SPT4_HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4_HOMOLOG \overline{1} >gi_1209779 (U43923) similar to
                    Saccharomyces cerevisiae Spt4; protein has potential
                    N-terminal zinc-finger [Homo sapiens] >gi_1401053 (U38818)
                    SUPT4H [Homo sapiens] >gi_1401055 (U38817) SUPT4H [Homo
```



sapiens] >gi_1401066 (U43154) Supt4h [Mus musculus]
>gi_3779194 (U96809) chromatin structural protein homolog
[Mus musculus]

Seq. No. 167735

Seq. ID LIB3234-046-P1-K1-G1

Method BLASTN
NCBI GI g4220643
BLAST score 363
E value 0.0e+00
Match length 388
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 167736

Seq. ID LIB3234-046-P1-K1-G10

Method BLASTX
NCBI GI g1168410
BLAST score 639
E value 5.0e-67
Match length 129
% identity 94

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2

>gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 167737

Seq. ID LIB3234-046-P1-K1-G11

Method BLASTN
NCBI GI 94586065
BLAST score 95
E value 6.0e-46
Match length 231

% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC T17A11 genomic

sequence, complete sequence

Seq. No. 167738

Seq. ID LIB3234-046-P1-K1-G12

Method BLASTN
NCBI GI g2264307
BLAST score 225
E value 1.0e-123
Match length 255
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MED24, complete sequence [Arabidopsis thaliana]

Seq. No. 167739

Seq. ID LIB3234-046-P1-K1-G2

Method BLASTX
NCBI GI g4262250
BLAST score 459
E value 6.0e-46
Match length 91



```
% identity
                  100
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167740
                  LIB3234-046-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1592677
BLAST score
                  382
                   6.0e-37
E value
Match length
                  123
                   69
% identity
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
                  167741
Seq. No.
                  LIB3234-046-P1-K1-G7
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3659491
BLAST score
                   385
E value
                   0.0e + 00
                   385
Match length
                   100
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   167742
Seq. No.
                   LIB3234-046-P1-K1-G9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2924733
BLAST score
                   135
                   7.0e-70
E value
                   207
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                   167743
Seq. No.
                   LIB3234-046-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1916613
                   517
BLAST score
                   9.0e-53
E value
                   108
Match length
                   100
% identity
                  (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
NCBI Description
                   167744
Seq. No.
                   LIB3234-046-P1-K1-H10
Seq. ID
                   BLASTX
Method
                   g3264778
NCBI GI
```

NCBI GI g3264778
BLAST score 562
E value 4.0e-58
Match length 118
% identity 93

NCBI Description (AF072536) H-protein promoter binding factor-1 [Arabidopsis

thaliana]

Seq. No. 167745



```
LIB3234-046-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449327
BLAST score
                  340
E value
                  0.0e + 00
                  379
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCA23, complete sequence [Arabidopsis thaliana]
                  167746
Seq. No.
                  LIB3234-046-P1-K1-H12
Seq. ID
Method
                  BLASTX
                  q3395441
NCBI GI
                  431
BLAST score
                  1.0e-42
E value
Match length
                  110
% identity
                   75
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  167747
Seq. No.
                  LIB3234-046-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204298
                   540
BLAST score
                   2.0e-55
E value
                   112
Match length
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   167748
                   LIB3234-046-P1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519187
BLAST score
                   115
                   5.0e-58
E value
Match length
                   315
                   94
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                   K1G2, complete sequence
                   167749
Seq. No.
                   LIB3234-046-P1-K1-H4
Seq. ID
Method
                   BLASTX
                   g1628583
NCBI GI
                   674
BLAST score
                   4.0e-71
E value
                   129
Match length
% identity
                   100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 167750

Seq. ID LIB3234-046-P1-K1-H5

Method BLASTN



```
NCBI GI
                  g3510339
BLAST score
                   400
                   0.0e+00
E value
Match length
                   400
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K7, complete sequence [Arabidopsis thaliana]
                   167751
Seq. No.
                   LIB3234-046-P1-K1-H6
Seq. ID
                   BLASTN
Method
                   g3241927
NCBI GI
BLAST score
                   227
                   1.0e-125
E value
                   271
Match length
                   86
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167752
Seq. ID
                   LIB3234-046-P1-K1-H8
                   BLASTX
Method
NCBI GI
                   g4490330
BLAST score
                   558
                   1.0e-57
E value
Match length
                   128
                   87
% identity
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   167753
Seq. No.
                   LIB3234-046-P1-K1-H9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1313927
                   45
BLAST score
                   4.0e-16
E value
                   168
Match length
                   83
% identity
                  B.oleracea mRNA for IFA binding protein (sp10)
NCBI Description
                   167754
Seq. No.
                   LIB3234-047-P1-K1-A1
Seq. ID
                   BLASTN
Method
```

Method BLASTN
NCBI GI g3241926
BLAST score 85
E value 2.0e-40
Match length 157
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 167755

Seq. ID LIB3234-047-P1-K1-A10

Method BLASTN
NCBI GI 94757414
BLAST score 322
E value 0.0e+00



```
Match length
                    354
                    98
 % identity
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                    MYF24, complete sequence
Seq. No.
                    167756
 Seq. ID
                    LIB3234-047-P1-K1-A2
                    BLASTX
 Method
                    g1352663
 NCBI GI
 BLAST score
                    478
                    4.0e-48
 E value
                    91
 Match length
                    99
 % identity
 NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC
                    SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase
                    (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana
                    >gi 466441 (M96841) Ser/Thr protein phosphatase
                    [Arabidopsis thaliana]
                    >gi_4559341_gb_AAD23003.1_AC007087 22 (AC007087)
                    serine/threonine protein phosphatase PP2A-3 catalytic
                    subunit [Arabidopsis thaliana]
                    >gi_4567320_gb_AAD23731.1_AC005956_20 (AC005956)
                    serine/threonine protein phosphatase [Arabidopsis thaliana]
                    167757
 Seq. No.
 Seq. ID
                    LIB3234-047-P1-K1-A4
                    BLASTX
 Method
                    g1084351
 NCBI GI
 BLAST score
                    155
 E value
                    9.0e-15
 Match length
                    83
                    58
  % identity
 NCBI Description napin - rape > gi_468018 (U04943) napin [Brassica napus]
                    >gi 468020 (U04944) napin [Brassica napus]
                    167758
  Seq. No.
  Seq. ID .
                    LIB3234-047-P1-K1-A5
                    BLASTX
 Method
                    q1903360
 NCBI GI
  BLAST score
                    184
                    8.0e-14
  E value
 Match length
                    76
                    54
  % identity
  NCBI Description (AC000104) Similar to Arabidopsis 2A6 (gb X83096). EST
                    gb T76913 comes from this gene. [Arabidopsis thaliana]
                    167759
  Seq. No.
                    LIB3234-047-P1-K1-A6
  Seq. ID
                    BLASTX
```

Method BLASTX
NCBI GI g3687228
BLAST score 504
E value 5.0e-51
Match length 112
% identity 95

NCBI Description (AC005169) putative malate dehydrogenase [Arabidopsis

thaliana]



```
Seq. No.
                  167760
                  LIB3234-047-P1-K1-A7
Seq. ID
Method
                  BLASTN
                  g3236234
NCBI GI
                  35
BLAST score
                  3.0e-10
E value
Match length
                  122
                  82
% identity
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167761
                  LIB3234-047-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2583125
BLAST score
                  52
                  5.0e-55
E value
                  118
Match length
                   96
% identity
                  (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   167762
                  LIB3234-047-P1-K1-B1
Seq. ID
Method
                   BLASTN
                  g2351062
NCBI GI
                   404
BLAST score
                   0.0e+00
E value
                   412
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                   167763
Seq. No.
                  LIB3234-047-P1-K1-B10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4544435
BLAST score
                   184
                   4.0e-99
E value
                   333
Match length
                   96
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F14M13 genomic
                   sequence, complete sequence
                   167764
Seq. No.
                   LIB3234-047-P1-K1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519195
BLAST score
                   68
E value
                   8.0e-30
Match length
                   172
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MQC12, complete sequence
```

22682

167765

LIB3234-047-P1-K1-B12

Seq. No. Seq. ID

NCBI Description



```
Method
                   BLASTX
                   q3786005
NCBI GI
BLAST score
                   372
                   8.0e-36
E value
                   87
Match length
% identity
                   63
                   (AC005499) putative phosphoethanolamine
NCBI Description
                   cytidylyltransferase [Arabidopsis thaliana]
                   167766
Seq. No.
                   LIB3234-047-P1-K1-B2
Seq. ID
Method
                   BLASTX
                   g1168972
NCBI GI
                   258
BLAST score
E value
                   2.0e-22
                   56
Match length
                   95
% identity
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
NCBI Description
                   PRECURSOR >gi 480969 pir S37557 clpA protein - rape
                   (fragment) >gi 406311 emb CAA53077 (X75328) clpA [Brassica
                   napus]
                   167767
Seq. No.
                   LIB3234-047-P1-K1-B3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3212102
BLAST score
                   297
E value
                   1.0e-166
                   373
Match length
                   100
% identity
                   Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   167768
Seq. No.
                   LIB3234-047-P1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g120675
BLAST score
                   450
                   6.0e-45
E value
Match length
                   89
% identity
                   94
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   167769
Seq. ID
                   LIB3234-047-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g3335169
BLAST score
                   533
E value
                   1.0e-54
Match length
                   119
% identity
                   83
```

22683

(AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi 4455197 emb CAB36520.1 (AL035440) embryo-specific



protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 167770 LIB3234-047-P1-K1-B6 Seq. ID Method BLASTX q2160133 NCBI GI BLAST score 287 9.0e-26 E value 119 Match length % identity 54 (AC000375) Strong similarity to Arabidopsis NCBI Description gb X91953, F19K23.3, F19K23.15. ESTs gb T21984,gb ATTS0219,gb ATTS0207,gb T21984 come from this gene. [Arabidopsis thaliana] Seq. No. 167771 LIB3234-047-P1-K1-B8 Seq. ID Method BLASTX q3377797 NCBI GI 477 BLAST score 5.0e-48 E value Match length 121 % identity 77 (AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara 167772 Seq. No. LIB3234-047-P1-K1-C10 Seq. ID Method BLASTX NCBI GI g1216389 BLAST score 510 E value 4.0e-52 95 Match length 99 % identity NCBI Description (U39289) myrosinase-associated protein [Brassica napus] >gi 1589009 prf 2209432A myrosinase-associated protein:ISOTYPE=5 [Brassica napus] 167773 Seq. No. Seq. ID LIB3234-047-P1-K1-C12 BLASTX Method NCBI GI g4204298 BLAST score 572 E value 3.0e-59 Match length 127 85 % identity NCBI Description (AC003027) 1cl prt seq No definition line found [Arabidopsis thaliana] Seq. No. 167774

Seq. ID LIB3234-047-P1-K1-C2

Method BLASTX NCBI GI g4510383 BLAST score 421



```
1.0e-41
E value
Match length
                  111
                  76
% identity
NCBI Description
                  (AC007017) unknown protein [Arabidopsis thaliana]
                  167775
Seq. No.
                  LIB3234-047-P1-K1-C3
Seq. ID
Method
                  BLASTN
                  q3327922
NCBI GI
                  119
BLAST score
                  3.0e-60
E value
                  388
Match length
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167776
                  LIB3234-047-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160158
                  466
BLAST score
                  9.0e-47
E value
                  109
Match length
% identity
                  83
                  (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  167777
Seq. ID
                  LIB3234-047-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  q2924779
BLAST score
                  277
E value
                  6.0e-25
Match length
                  84
% identity
                   69
                   (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                   thaliana] >gi 2981616 dbj BAA25248 (AB008854)
                   3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                   >gi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                   thiolase [Arabidopsis thaliana]
                  167778
Seq. No.
                  LIB3234-047-P1-K1-D1
Seq. ID
Method
                  BLASTN
                  g3449313
NCBI GI
                  75
BLAST score
E value
                  5.0e-34
Match length
                  226
                   85
```

% identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21P3, complete sequence [Arabidopsis thaliana]

167779 Seq. No.

LIB3234-047-P1-K1-D11 Seq. ID

Method BLASTX NCBI GI g228416



```
BLAST score 478
E value 3.0e-48
Match length 118
% identity 87
```

NCBI Description oleosin [Brassica napus]

Seq. No. 167780

Seq. ID LIB3234-047-P1-K1-D12

Method BLASTX
NCBI GI g3269286
BLAST score 498
E value 1.0e-50
Match length 120
% identity 89

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 167781

Seq. ID LIB3234-047-P1-K1-D3

Method BLASTX
NCBI GI g1864017
BLAST score 521
E value 3.0e-53
Match length 100
% identity 99

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 167782

Seq. ID LIB3234-047-P1-K1-D4

Method BLASTX
NCBI GI g2118220
BLAST score 405
E value 1.0e-39
Match length 97
% identity 56

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi 3096941 emb CAA18851.1 (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
>gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No. 167783

Seq. ID LIB3234-047-P1-K1-D6

Method BLASTX
NCBI GI g1345973
BLAST score 311
E value 7.0e-29
Match length 61
% identity 97

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)



omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No. 167784 LIB3234-047-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g544134 BLAST score 261 1.0e-22 E value Match length 90 51 % identity

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi 99720 pir S22863 hypothetical protein - Arabidopsis

thaliana >gi 421844 pir A46260 RecA functional analog

DRT100 - Arabidopsis thaliana (fragment)

Seq. No. 167785

Seq. ID LIB3234-047-P1-K1-D8

Method BLASTX
NCBI GI g2199574
BLAST score 560
E value 9.0e-58
Match length 106

% identity 99

NCBI Description (AF004293) aquaporin [Brassica rapa]

Seq. No. 167786

Seq. ID LIB3234-047-P1-K1-E1

Method BLASTN
NCBI GI g3449312
BLAST score 286
E value 1.0e-160
Match length 337
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K16L22, complete sequence [Arabidopsis thaliana]

Seq. No. 167787

Seq. ID LIB3234-047-P1-K1-E10

Method BLASTN
NCBI GI 94589439
BLAST score 344
E value 0.0e+00
Match length 348
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 167788

Seq. ID LIB3234-047-P1-K1-E11

Method BLASTX NCBI GI g115767 BLAST score 568

```
E value
                  9.0e-59
Match length
                  110
% identity
                  98
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >qi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  167789
Seq. ID
                  LIB3234-047-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g729857
BLAST score
                  170
E value
                  3.0e-12
Match length
                  87
% identity
                  38
                  SERINE/THREONINE-PROTEIN KINASE IRE1 PRECURSOR
NCBI Description
                  >qi 539088 pir A47541 protein kinase IRE1 (EC 2.7.1.-)
                  precursor - yeast (Saccharomyces cerevisiae) >gi 393281
                  (L19640) ERN1 [Saccharomyces cerevisiae]
Seq. No.
                  167790
Seq. ID
                  LIB3234-047-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g2454183
BLAST score
                  60
                  4.0e-25
E value
Match length
                  124
                  87
% identity
NCBI Description
                 Arabidopsis thaliana pyruvate dehydrogenase El beta subunit
                  mRNA, nuclear gene encoding plastid protein, complete cds
Seq. No.
                  167791
                  LIB3234-047-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586109
BLAST score
                  169
                  5.0e-12
E value
Match length
                  41
                  71
% identity
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
                  167792
Seq. No.
                  LIB3234-047-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335171
BLAST score
                  549
                  2.0e-56
E value
Match length
                  121
```

(AF067858) embryo-specific protein 3 [Arabidopsis thaliana] Seq. No. 167793

NCBI Description

% identity

LIB3234-047-P1-K1-E7 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g3924596
BLAST score
                  212
E value
                  5.0e-17
Match length
                  106
% identity
                  43
NCBI Description
                  (AF069442) putative phospho-ser/thr phosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  167794
Seq. ID
                  LIB3234-047-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g304040
BLAST score
                  152
E value
                  5.0e-80
Match length
                  172
% identity
                  97
NCBI Description Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene
Seq. No.
                  167795
Seq. ID
                  LIB3234-047-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  285
                  1.0e-25
E value
Match length
                  62
                  90
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >qi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi 471091 dbj_BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  167796
Seq. ID
                  LIB3234-047-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3047082
BLAST score
                  143
E value
                  4.0e-19
Match length
                  104
                  50
% identity
NCBI Description
                  (AF058914) similar to Vigna radiata pectinacetylesterase
                  precursor (GB:X99348) [Arabidopsis thaliana]
Seq. No.
                  167797
Seq. ID
                  LIB3234-047-P1-K1-F11
```

Method BLASTN NCBI GI q4589428 BLAST score 187 1.0e-101 E value Match length 378 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MFH8, complete sequence

```
Seq. No.
                  167798
Seq. ID
                  LIB3234-047-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3132471
BLAST score
                  192
E value
                   9.0e-42
                   91
Match length
                   99
% identity
                  (AC003096) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  167799
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4115387
BLAST score
                  365
E value
                  6.0e-35
Match length
                  71
                  100
% identity
                  (AC005967) putative NADP-dependent
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  167800
Seq. ID
                  LIB3234-047-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  q3869063
BLAST score
                  346
E value
                  0.0e + 00
Match length
                  374
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K17022, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167801
                  LIB3234-047-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q625977
BLAST score
                  534
                  1.0e-54
E value
Match length
                  107
                  96
% identity
NCBI Description
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  167802
                  LIB3234-047-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2586127
BLAST score
                  253
E value
                  8.0e-22
                  99
Match length
                  51
% identity
                  (U89510) b-keto acyl reductase [Hordeum vulgare]
NCBI Description
```



```
Seq. No.
                  167803
Seq. ID
                  LIB3234-047-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3335171
BLAST score
                  555
                  3.0e-57
E value
Match length
                  122
                  88
% identity
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
                  167804
Seq. No.
                  LIB3234-047-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4038039
BLAST score
                  294
E value
                   1.0e-26
Match length
                  72
% identity
                  79
                   (AC005936) putative proteinase inhibitor II [Arabidopsis
NCBI Description
                  thalianal
                   167805
Seq. No.
Seq. ID -
                   LIB3234-047-P1-K1-G10
                   BLASTN
Method
NCBI GI
                   g4538990
BLAST score
                   84
                   1.0e-39
E value
Match length
                   183
% identity
                   98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                   (ESSA project)
Seq. No.
                   167806
                   LIB3234-047-P1-K1-G12
Seq. ID
                   BLASTN
Method
                   g3449312
NCBI GI
                   261
BLAST score
E value
                   1.0e-145
Match length
                   342
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K16L22, complete sequence [Arabidopsis thaliana]
                   167807
Seq. No.
                   LIB3234-047-P1-K1-G2
Seq. ID
                   BLASTX
Method
                   g2894574
NCBI GI
                   495
BLAST score
                   3.0e-50
E value
                   96
Match length
                   98
% identity
                   (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                   >gi 2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
```

22691

167808

Seq. No.



Seq. ID LIB3234-047-P1-K1-G3

Method BLASTX
NCBI GI g118926
BLAST score 276
E value 1.0e-24
Match length 100
% identity 53

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR

>gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 167809

Seq. ID LIB3234-047-P1-K1-G4

Method BLASTX
NCBI GI g4512619
BLAST score 484
E value 7.0e-49
Match length 101
% identity 95

NCBI Description (AC004793) This gene is a member of the formyl transferase

family PF_00551 and may be a pseudogene of gb_X74767 phosphoribosylglycinamide formyl transferase (PUR3) from Arabidopsis thaliana since our sequence differs from

PUR3... >gi 4753662 emb CAA52779.2 (X74767)

phosphoribosylglycinamide formyltransferase [Arabidopsis

thaliana]

Seq. No. 167810

Seq. ID LIB3234-047-P1-K1-G7

Method BLASTN
NCBI GI g3150396
BLAST score 196
E value 1.0e-106
Match length 258
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167811

Seq. ID LIB3234-047-P1-K1-H12

Method BLASTX
NCBI GI g82200
BLAST score 343
E value 2.0e-32
Match length 131
% identity 69

NCBI Description hypothetical protein 1244 - common tobacco chloroplast

Seq. No. 167812

Seq. ID LIB3234-047-P1-K1-H4

Method BLASTN
NCBI GI g4512656
BLAST score 159
E value 4.0e-84



```
Match length
                  314
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  167813
Seq. No.
Seg. ID
                  LIB3234-047-P1-K1-H5
Method
                  BLASTN
                  a3510347
NCBI GI
                  53
BLAST score
                  7.0e-21
E value
                  113
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167814
                  LIB3234-047-P1-K1-H6
Seq. ID
Method
                  BLASTN
                  q4757414
NCBI GI
                  390
BLAST score
                  0.0e + 00
E value
Match length
                  402
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
                  167815
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-H7
Method
                  BLASTX
                  q2292907
NCBI GI
BLAST score
                  246
                  3.0e-21
E value
Match length
                  87
% identity
                  31
NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]
Seq. No.
                  167816
Seq. ID
                  LIB3234-047-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2655008
BLAST score
                  377
                  2.0e-36
E value
Match length
                  118
% identity
                  56
                  (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  167817
Seq. ID
                  LIB3234-048-P1-K1-A1
```

Method BLASTX
NCBI GI g3335169
BLAST score 186
E value 6.0e-57
Match length 123
% identity 89

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

 Seq. No.
 167818

 Seq. ID
 LIB3234-048-P1-K1-A11

 Method
 BLASTX

 NCBI GI
 g1216389

 BLAST score
 123

BLAST score 123 E value 2.0e-56 Match length 114 % identity 97

NCBI Description (U39289) myrosinase-associated protein [Brassica napus]

>gi 1589009 prf 2209432A myrosinase-associated

protein:ISOTYPE=5 [Brassica napus]

Seq. No. 167819

Seq. ID LIB3234-048-P1-K1-A12

Method BLASTN
NCBI GI g4335711
BLAST score 44
E value 1.0e-15

Match length 146 % identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F9013 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167820

Seq. ID LIB3234-048-P1-K1-A2

Method BLASTN
NCBI GI g2160132
BLAST score 186
E value 1.0e-100
Match length 314
% identity 92

NCBI Description Sequence of BAC F19K23 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 167821

Seq. ID LIB3234-048-P1-K1-A4

Method BLASTN
NCBI GI g2583106
BLAST score 173
E value 2.0e-92
Match length 357
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167822

Seq. ID LIB3234-048-P1-K1-A5

Method BLASTX
NCBI GI g3135264
BLAST score 332
E value 4.0e-31
Match length 116
% identity 61

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  167823
                  LIB3234-048-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114649
BLAST score
                  313
                  7.0e-29
E value
Match length
                  81
                  85
% identity
NCBI Description
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                  >gi_67899_pir__LWLVA H+-transporting ATP synthase (EC
                  3.6.1.34) lipid-binding protein - liverwort (Marchantia
                  polymorpha) chloroplast >gi_11653_emb_CAA28066_ (X04465)
                  atpH [Marchantia polymorpha]
Seq. No.
                  167824
                  LIB3234-048-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q485514
BLAST score
                  151
                  8.0e-10
E value
Match length
                  53
% identity
                  51
                  ADR11-2 protein - soybean (fragment)
NCBI Description
                  >gi_296443_emb_CAA49341_ (X69640) auxin down regulated
                  [Glycine max]
Seq. No.
                  167825
                  LIB3234-048-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618688
BLAST score
                  386
E value
                  2.0e-37
Match length
                  118
                  69
% identity
NCBI Description
                 (AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.
                  167826
Seq. ID
                  LIB3234-048-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3036810
BLAST score
                  219
                  7.0e-18
E value
Match length
                  62
% identity
                  65
NCBI Description
                  (AL022373) putative Myc-type transcription factor
                  [Arabidopsis thaliana]
Seq. No.
                  167827
Seq. ID
                  LIB3234-048-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q2264321
BLAST score
                  65
E value
                  4.0e-28
Match length
                  348
                  90
% identity
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 167828

Seq. ID LIB3234-048-P1-K1-B2

Method BLASTX
NCBI GI g2623962
BLAST score 396
E value 2.0e-38
Match length 81
% identity 94

NCBI Description (Y12540) isocitrate dehydrogenase (NADP+) [Apium

graveolens]

Seq. No. 167829

Seq. ID LIB3234-048-P1-K1-B3

Method BLASTX
NCBI GI g136636
BLAST score 316
E value 4.0e-29
Match length 59
% identity 98

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
>gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 167830

Seq. ID LIB3234-048-P1-K1-B4

Method BLASTN
NCBI GI g3327922
BLAST score 67
E value 3.0e-29
Match length 348
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC T31E10 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167831

Seq. ID LIB3234-048-P1-K1-B5

Method BLASTX
NCBI GI g1526424
BLAST score 462
E value 2.0e-46
Match length 105
% identity 88

NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]

Seq. No. 167832

Seq. ID LIB3234-048-P1-K1-B6

Method BLASTN
NCBI GI g4510338
BLAST score 358

```
E value
                   0.0e + 00
Match length
                   370
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F2H17 genomic
                  sequence, complete sequence
Seq. No.
                  167833
Seq. ID
                  LIB3234-048-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1209258
BLAST score
                  302
E value
                  1.0e-27
Match length
                  76
                  79
% identity
NCBI Description (L31937) protease inhibitor II [Brassica rapa]
Seq. No.
                  167834
Seq. ID
                  LIB3234-048-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g129082
BLAST score
                  355
E value
                  8.0e-34
Match length
                  114
% identity
                  69
NCBI Description
                  OLEOSIN BN-III >gi_81692_pir_S22475 oleosin BN-III - rape
                  >gi_17839_emb_CAA43941_ (X61937) oleosin BN-III [Brassica
                  napus] >gi_742387_prf _2009397A oleosin [Brassica napus]
Seq. No.
                  167835
Seq. ID
                  LIB3234-048-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3193308
BLAST score
                  336
E value
                  1.0e-31
Match length
                  118
% identity
NCBI Description
                 (AF069300) similar to Medicago truncatula MtN2 (GB:Y15293)
                  [Arabidopsis thaliana]
Seq. No.
                  167836
Seq. ID
                  LIB3234-048-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1363488
BLAST score
                  340
E value
                  6.0e-32
Match length
                  68
% identity
                  99
NCBI Description
                  IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
                  IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
```

Seq. No. 167837

Seq. ID LIB3234-048-P1-K1-C10

Method BLASTX NCBI GI g112741 BLAST score 207

```
E value
                   6.0e-25
Match length
                  72
% identity
                  82
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  167838
Seq. ID
                  LIB3234-048-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q2956690
BLAST score
                  296
E value
                  7.0e-27
Match length
                  89
% identity
                  75
NCBI Description (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928
                  (AF079800) PsbY precursor [Arabidopsis thaliana]
Seq. No.
                  167839
Seq. ID
                  LIB3234-048-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4220633
BLAST score
                  70
E value
                  5.0e-31
Match length
                  156
% identity
                  92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167840
Seq. ID
                  LIB3234-048-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g543841
BLAST score
                  523
E value
                  2.0e-53
Match length
                  102
% identity
                  99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586
                  (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                  >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                  thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
```

Seq. No. 167841

Seq. ID LIB3234-048-P1-K1-C4

Method BLASTN
NCBI GI g2558511
BLAST score 103
E value 9.0e-51
Match length 107
% identity 99

NCBI Description Arabidopsis thaliana mRNA for proton pump interactor,



partial Seq. No. 167842 Seq. ID LIB3234-048-P1-K1-C5 Method BLASTN NCBI GI q3046856 BLAST score 308 E value 1.0e-173 Match length 371 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana] Seq. No. 167843 LIB3234-048-P1-K1-C6 Seq. ID Method BLASTX NCBI GI q136739 BLAST score 602 E value 9.0e-63 Match length 124 % identity 95 NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum] Seq. No. 167844 Seq. ID LIB3234-048-P1-K1-C8 Method BLASTX NCBI GI g2129648 BLAST score 532 E value 1.0e-54 Match length 98 % identity 100 NCBI Description MYB-related protein 33,3K - Arabidopsis thaliana >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana] Seq. No. 167845 Seq. ID LIB3234-048-P1-K1-D10 Method BLASTX NCBI GI g2129670 BLAST score 229 E value 1.0e-22

Match length 103 % identity 61

NCBI Description phosphoinositide-specific phospholipase C - Arabidopsis

thaliana >gi_857374_dbj_BAA09432 (D50804) phosphoinositide

specific phospholipase C [Arabidopsis thaliana]

Seq. No. 167846

Seq. ID LIB3234-048-P1-K1-D11

Method BLASTN NCBI GI g3420043 BLAST score 319 E value 1.0e-179



Match length 319 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F23F1 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167847

Seq. ID LIB3234-048-P1-K1-D2

Method BLASTX
NCBI GI g112682
BLAST score 571
E value 4.0e-59
Match length 122
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 167848

Seq. ID LIB3234-048-P1-K1-D3

Method BLASTX
NCBI GI g4204298
BLAST score 465
E value 1.0e-46
Match length 120
% identity 72

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 167849

Seq. ID LIB3234-048-P1-K1-D4

Method BLASTN
NCBI GI g2828187
BLAST score 96
E value 1.0e-46
Match length 236
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21C13, complete sequence [Arabidopsis thaliana]

Seq. No. 167850

Seq. ID LIB3234-048-P1-K1-D5

Method BLASTX
NCBI GI g82201
BLAST score 214
E value 3.0e-17
Match length 104
% identity 36

NCBI Description hypothetical protein 131 - common tobacco chloroplast

>gi_11879_emb_CAA77392 (Z00044) hypothetical protein
[Nicotiana tabacum] >gi_1223680_emb_CAA77401 (Z00044)

hypothetical protein [Nicotiana tabacum]

>gi_225249_prf__1211235CH ORF 131 [Nicotiana tabacum]

Seq. No. 167851

Seq. ID LIB3234-048-P1-K1-D6

Seq. ID



```
BLASTN
Method
                  g4558674
NCBI GI
                  134
BLAST score
                  3.0e-69
E value
                  265
Match length
                  92
% identity
                  Arabidopsis thaliana chromosome II BAC F7B19 genomic
NCBI Description
                  sequence, complete sequence
                  167852
Seq. No.
                  LIB3234-048-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  g129083
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  78
Match length
                  50
% identity
                  OLEOSIN BN-V >gi 280390 pir S25089 oleosin Bn-V - rape
NCBI Description
                   (fragment) >gi_808944_emb_CAA45313_ (X63779) oleosin BN-V
                   [Brassica napus]
                  167853
Seq. No.
                  LIB3234-048-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  q4588906
NCBI GI
                  387
BLAST score
                  1.0e-37
E value
                   98
Match length
                  77
% identity
                  (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
                  167854
Seq. No.
                  LIB3234-048-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4185511
                   459
BLAST score
                   5.0e-46
E value
Match length
                   102
                   83
% identity
                  (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                   thaliana]
                   167855
Seq. No.
                   LIB3234-048-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g1076331
NCBI GI
                   632
BLAST score
                   3.0e-66
E value
Match length
                   116
                   100
% identity
                  histidine transport protein - Arabidopsis thaliana
NCBI Description
                   >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
                   1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His
                   transporter [Arabidopsis thaliana]
                   167856
Seq. No.
```

LIB3234-048-P1-K1-E11

Seq. ID

Method

BLASTX



```
Method
                   BLASTX
NCBI GI
                   g2446981
                   496
BLAST score
                   2.0e-50
E value
Match length
                   96
                   98
% identity
                   (AB005560) AtGDI2 [Arabidopsis thaliana]
NCBI Description
                   >gi 2569936 emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis
                   thaliana]
                   167857
Seq. No.
                   LIB3234-048-P1-K1-E12
Seq. ID
Method
                   BLASTX
                   g951453
NCBI GI
                   300
BLAST score
                   2.0e-27
E value
Match length
                   121
% identity
                   52
                   (M95746) initiation factor (iso)4f p82 subunit [Triticum
NCBI Description
                   aestivum]
Seq. No.
                   167858
Seq. ID
                   LIB3234-048-P1-K1-E2
Method
                   BLASTN
                   q3256065
NCBI GI
BLAST score
                   273
                   1.0e-152
E value
                   313
Match length
% identity
                   97
                   Arabidopsis thaliana mRNA for chloroplast NAD-dependent
NCBI Description
                   malate dehydrogenase
                   167859
Seq. No.
                   LIB3234-048-P1-K1-E3
Seq. ID
                   BLASTX
Method
                   g3372645
NCBI GI
                   350
BLAST score
                   3.0e-33
E value
Match length
                   119
                   49
% identity
                   (AF060491) cinnamyl alcohol dehydrogenase [Pinus radiata]
NCBI Description
                   167860
Seq. No.
                   LIB3234-048-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g129082
                   364
BLAST score
                   8.0e-35
E value
                   115
Match length
                   70
% identity
                   OLEOSIN BN-III >gi_81692_pir__S22475 oleosin BN-III - rape
NCBI Description
                   >gi_17839_emb_CAA43941 (X61937) oleosin BN-III [Brassica
napus] >gi_742387_prf__2009397A oleosin [Brassica napus]
                   167861
Seq. No.
                   LIB3234-048-P1-K1-E6
```

BLAST score

208



```
NCBI GI
                   g129082
BLAST score
                   374
                   6.0e-36
E value
Match length
                   117
% identity
                   71
                   OLEOSIN BN-III >qi 81692 pir S22475 oleosin BN-III - rape
NCBI Description
                   >gi_17839 emb CAA43941 (X61937) oleosin BN-III [Brassica napus] >gi_742387_prf__2009397A oleosin [Brassica napus]
                   167862
Seq. No.
                   LIB3234-048-P1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3461848
BLAST score
                   540
                   2.0e-55
E value
                   121
Match length
% identity
                   89
                   (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                   167863
Seq. No.
                   LIB3234-048-P1-K1-F10
Seq. ID
                   BLASTN
Method
                   q511598
NCBI GI
BLAST score
                   368
                   0.0e+00
E value
                   368
Match length
                   28
% identity
                   Arabidopsis thaliana cell wall protein (APTR-1) gene,
NCBI Description
                   complete cds
Seq. No.
                   167864
                   LIB3234-048-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112746
                   378
BLAST score
                   2.0e-36
E value
                   101
Match length
                   74
% identity
NCBI Description
                   NAPIN B PRECURSOR (1.7S SEED STORAGE PROTEIN)
                   >gi 99818 pir S15382 napin napB - rape
                   >gi 17835 emb CAA41150 (X58142) napin [Brassica napus]
                   167865
Seq. No.
                   LIB3234-048-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2149640
BLAST score
                   632
                   3.0e-66
E value
Match length
                   122
% identity
                   99
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                   167866
Seq. No.
                   LIB3234-048-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   g4006888
NCBI GI
```

NCBI GI

```
A No. 64
```

```
1.0e-16
E value
Match length
                    82
                    50
% identity
                    (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    167867
                    LIB3234-048-P1-K1-F4
Seq. ID
Method
                    BLASTN
NCBI GI
                    q600854
BLAST score
                    72
                    3.0e-32
E value
                    130
Match length
% identity
                    96
                    Arabidopsis thaliana bZIP protein mRNA, complete cds
NCBI Description
                    167868
Seq. No.
                    LIB3234-048-P1-K1-F5
Seq. ID
                    BLASTX
Method
NCBI GI
                    q112742
BLAST score
                    113
                    1.0e-39
E value
                    111
Match length
                    77
% identity
                    NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                    >gi_81687_pir__S10018 napin (clone BngNAP1) - rape
                    >gi 1084352 pir S52027 napin - rape
                    >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica
                    napus] >gi 46\overline{8}022 (U04\overline{9}45) napin [Brassica napus]
                    167869
Seq. No.
                    LIB3234-048-P1-K1-F6
Seq. ID
                    BLASTN
Method
                    g557693
NCBI GI
BLAST score
                    248
                     1.0e-137
E value
                     252
Match length
                     100
% identity
                    Arabidopsis thaliana Columbia GTP binding protein beta
NCBI Description
                    subunit (AGB1) mRNA, complete cds
                     167870
Seq. No.
                    LIB3234-048-P1-K1-F7
Seq. ID
                    BLASTX
Method
                     g266693
NCBI GI
                     543
BLAST score
                     7.0e-56
E value
                     120
Match length
                     90
% identity
                    OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
NCBI Description
                     (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                     167871
Seq. No.
                     LIB3234-048-P1-K1-F8
Seq. ID
                     BLASTN
Method
```

22704

g2564044



```
BLAST score 90
E value 5.0e-43
Match length 232
% identity 94
NCBI Description Arabido,
K19P17,
```

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 167872

Seq. ID LIB3234-048-P1-K1-F9

Method BLASTX
NCBI GI g4507311
BLAST score 199
E value 2.0e-15
Match length 103
% identity 38

NCBI Description suppressor of Ty (S.cerevisiae) 4 homolog 1

>gi_3122873_sp_Q16550_SPT4_HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi_1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi_1401053 (U38818) SUPT4H [Homo sapiens] >qi_1401055 (U38817) SUPT4H [Homo

SUPT4H [Homo sapiens] >gi_1401055 (U38817) SUPT4H [Homo sapiens] >gi_1401066 (U43154) Supt4h [Mus musculus]

>gi 3779194 (U96809) chromatin structural protein homolog

[Mus musculus]

Seq. No. 167873

Seq. ID LIB3234-048-P1-K1-G1

Method BLASTX
NCBI GI g134025
BLAST score 446
E value 2.0e-44
Match length 110
% identity 81

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8

ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No. 167874

Seq. ID LIB3234-048-P1-K1-G10

Method BLASTX
NCBI GI g1707857
BLAST score 484
E value 6.0e-49
Match length 120
% identity 75

NCBI Description (Y09291) obtusifoliol 14-alpha-demethylase [Triticum

aestivum]

Seq. No. 167875

Seq. ID LIB3234-048-P1-K1-G12

Method BLASTX
NCBI GI g2384671
BLAST score 302
E value 9.0e-36
Match length 88



% identity NCBI Description (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana] 167876 Seq. No. LIB3234-048-P1-K1-G2 Seq. ID Method BLASTN NCBI GI q3659491 BLAST score 193 1.0e-104 E value 315 Match length 99 % identity Sequence of BAC T22H22 from Arabidopsis thaliana chromosome NCBI Description 1, complete sequence [Arabidopsis thaliana] 167877 Seq. No. Seq. ID LIB3234-048-P1-K1-G3 Method BLASTX NCBI GI q112681 264 BLAST score 4.0e-23 E value 95 Match length 56 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 167878 LIB3234-048-P1-K1-G5 Seq. ID BLASTX Method NCBI GI q421826 529 BLAST score E value 4.0e-54 124 Match length % identity 81 chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana] Seq. No. 167879 Seq. ID LIB3234-048-P1-K1-G6 Method BLASTX NCBI GI g421826 BLAST score 271 E value 6.0e-24 Match length 95 59 % identity NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 167880

Seq. ID LIB3234-048-P1-K1-G9

Method BLASTX NCBI GI g2982437



```
200
BLAST score
E value
                  6.0e-26
                  101
Match length
% identity
                  (AL022224) terpene cyclase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167881
                  LIB3234-048-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  g1706256
NCBI GI
                  351
BLAST score
E value
                  2.0e-33
                  108
Match length
                  61
% identity
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN-10) >gi 733577 (U23453) similar to
                  peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN)
                   [Caenorhabditis elegans] >qi 1155225 (U34954) cyclophilin
                  isoform 10 [Caenorhabditis elegans]
                  167882
Seq. No.
                  LIB3234-048-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g2252857
NCBI GI
BLAST score
                  315
                   4.0e-29
E value
                  101
Match length
% identity
                   68
NCBI Description
                   (AF013294) similar to acidic ribosomal protein p1
                   [Arabidopsis thaliana]
                  167883
Seq. No.
                  LIB3234-048-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
                  567
BLAST score
                   1.0e-58
E value
Match length
                   113
                   96
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   167884
Seq. No.
                  LIB3234-049-P1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1352463
                   452
BLAST score
E value
                   4.0e-45
                   109
```

Match length 83 % identity

MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi 1161312 NCBI Description

(U04876) myo-inositol-1-phosphate synthase [Arabidopsis

thaliana]

167885 Seq. No.



LIB3234-049-P1-K1-A10 Seq. ID BLASTX Method g267081 NCBI GI 675 BLAST score 3.0e-71 E value 126 Match length 100 % identity TUBULIN BETA-7 CHAIN >qi 320188 pir JQ1591 tubulin beta-7 NCBI Description chain - Arabidopsis thaliana >gi 166906 (M84704) beta-7 tubulin [Arabidopsis thaliana] >gi 3980381 (AC004561) tubulin beta-7 chain [Arabidopsis thaliana] 167886 Seq. No. LIB3234-049-P1-K1-A11 Seq. ID BLASTX Method g2605714 NCBI GI 465 BLAST score 1.0e-46 E value Match length 113 82 % identity (AF026275) beta-tonoplast intrinsic protein [Arabidopsis NCBI Description thaliana] 167887 Seq. No. Seq. ID LIB3234-049-P1-K1-A12 Method BLASTX g4539316 NCBI GI 275 BLAST score E value 7.0e-40Match length 96 86 % identity (AL035679) putative fructose-bisphosphate aldolase NCBI Description [Arabidopsis thaliana] Seq. No. 167888 LIB3234-049-P1-K1-A2 Seq. ID BLASTN Method NCBI GI g4199934 BLAST score 181 3.0e-97 E value Match length 303 % identity 99 Genomic sequence for Arabidopsis thaliana BAC T3P18, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 167889 LIB3234-049-P1-K1-A3 Seq. ID Method BLASTN g4206762 NCBI GI 89 BLAST score 2.0e-42 E value Match length 257 94 % identity NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker

Seq. No. 167890

protein homolog (CWLP) mRNA, complete cds



LIB3234-049-P1-K1-A4 Seq. ID Method BLASTX NCBI GI q2829904 BLAST score 244 1.0e-26 E value 116 Match length 63 % identity (AC002311) Hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 167891 Seq. ID LIB3234-049-P1-K1-A5 BLASTX Method g1490554 NCBI GI BLAST score 93 4.0e-10 E value 49 Match length 72 % identity (U63633) S-adenosylmethionine decarboxylase [Arabidopsis NCBI Description thaliana] 167892 Seq. No. LIB3234-049-P1-K1-A6 Seq. ID BLASTN Method g633027 NCBI GI BLAST score 257 1.0e-142 E value 285 Match length 98 % identity NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C 167893 Seq. No. Seq. ID LIB3234-049-P1-K1-A7 Method BLASTX NCBI GI a135858 BLAST score 408 5.0e-40 E value 100 Match length % identity TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) NCBI Description >gi 99760 pir S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >qi 16182 emb CAA45114 (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi 166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana] Seq. No. 167894 LIB3234-049-P1-K1-B12 Seq. ID Method BLASTN NCBI GI g4584519 BLAST score 374

0.0e + 00E value Match length 374 % identity 100

NCBI Description 'Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18

(ESSA project)



```
Seq. No.
                  167895
Seq. ID
                  LIB3234-049-P1-K1-B3
                  BLASTX
Method
NCBI GI
                  g2583131
BLAST score
                  141
                  3.0e-09
E value
                  62
Match length
                  52
% identity
                  (AC002387) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167896
                  LIB3234-049-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4314374
                  32
BLAST score
                  2.0e-08
E value
Match length
                  326
% identity
                  18
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  167897
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-C1
Method
                  BLASTN
                  q3135250
NCBI GI
BLAST score
                  141
                  2.0e-73
E value
                  343
Match length
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167898
                  LIB3234-049-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618683
                  91
BLAST score
                  1.0e-43
E value
Match length
                  323
% identity
                  88
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167899
                  LIB3234-049-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267082
```

Method BLASTX
NCBI GI g267082
BLAST score 145
E value 6.0e-27
Match length 121
% identity 60

NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8

chain - Arabidopsis thalīana >gī_166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

Seq. No. 167900

Seq. ID LIB3234-049-P1-K1-C2



Method BLASTX
NCBI GI g4538906
BLAST score 452
E value 3.0e-45
Match length 91
% identity 97
NCBI Description (AL04948)

NCBI Description (AL049482) choline kinase GmCK2p-like protein [Arabidopsis

thaliana]

Seq. No. 167901

Seq. ID LIB3234-049-P1-K1-C3

Method BLASTX
NCBI GI g4538906
BLAST score 250
E value 2.0e-21
Match length 101
% identity 58

NCBI Description (AL049482) choline kinase GmCK2p-like protein [Arabidopsis

thaliana]

Seq. No. 167902

Seq. ID LIB3234-049-P1-K1-C5

Method BLASTX
NCBI GI g4417310
BLAST score 593
E value 1.0e-61
Match length 130
% identity 88

NCBI Description (AC006446) putative Athila retroelement ORF1 protein

[Arabidopsis thaliana]

Seq. No. 167903

Seq. ID LIB3234-049-P1-K1-C7

Method BLASTN
NCBI GI g4760411
BLAST score 344
E value 0.0e+00
Match length 367
% identity 89

NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,

complete sequence

Seq. No. 167904

Seq. ID LIB3234-049-P1-K1-C8

Method BLASTN
NCBI GI g436919
BLAST score 268
E value 1.0e-149
Match length 268
% identity 100

NCBI Description Arabidopsis thaliana Landsburg lipoxygenase 1 gene,

complete cds

Seq. No. 167905

Seq. ID LIB3234-049-P1-K1-C9

Method BLASTN NCBI GI g4006885

```
BLAST score
                  81
                  8.0e-38
E value
Match length
                  202
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
                  167906
Seq. No.
                  LIB3234-049-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q226120
                  222
BLAST score
                  3.0e-18
E value
Match length
                  122
                  39
% identity
NCBI Description vicilin gene B [Saguinus oedipus]
                  167907
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-D10
Method
                  BLASTX
                  g1531762
NCBI GI
BLAST score
                  195
                  5.0e-15
E value
                  51
Match length
                  75
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167908
Seq. ID
                  LIB3234-049-P1-K1-D11
                  BLASTX
Method
                  q112740
NCBI GI
BLAST score
                   260
                   1.0e-22
E value
Match length
                   115
                   51
% identity
                  NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                   >gi 81691 pir A25997 napin precursor (napA) - rape
                   >qi 167153 (J02586) prepronapin [Brassica napus] >gi_167155
                   (J02798) napin [Brassica napus]
Seq. No.
                   167909
                   LIB3234-049-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169598
BLAST score
                   369
                   2.0e-35
E value
Match length
                   81
```

85 % identity

OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM NCBI Description (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

167910 Seq. No.

LIB3234-049-P1-K1-D2 Seq. ID

Method BLASTX NCBI GI q629500



BLAST score 585 E value 1.0e-60 Match length 107 % identity 100

NCBI Description 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -

Arabidopsis thaliana >gi_166578 (M95594)

1-aminocyclopropane-1-carboxylate synthase [Arabidopsis

thaliana]

Seq. No. 167911

Seq. ID LIB3234-049-P1-K1-D3

Method BLASTN
NCBI GI g2244788
BLAST score 320
E value 1.0e-180
Match length 386
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 167912

Seq. ID LIB3234-049-P1-K1-D4

Method BLASTX
NCBI GI g3287693
BLAST score 304
E value 9.0e-28
Match length 81
% identity 70

NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from

the genome of Synechocystis sp. gb D90916. [Arabidopsis

thaliana]

Seq. No. 167913

Seq. ID LIB3234-049-P1-K1-D5

Method BLASTX
NCBI GI g1345973
BLAST score 474
E value 1.0e-47
Match length 104
% identity 83

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis
thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167914

Seq. ID LIB3234-049-P1-K1-D6

Method BLASTX
NCBI GI g2827002
BLAST score 479
E value 3.0e-48
Match length 116



92

% identity

% identity (AF005993) HSP70 [Triticum aestivum] NCBI Description 167915 Seq. No. Seq. ID LIB3234-049-P1-K1-D7 Method BLASTN g2465924 NCBI GI 359 BLAST score E value 0.0e + 00382 Match length 98 % identity NCBI Description Arabidopsis thaliana receptor-like serine/threonine kinase (RKF2) mRNA, complete cds 167916 Seq. No. Seq. ID LIB3234-049-P1-K1-D8 BLASTX Method g2652938 NCBI GI BLAST score 508 E value 1.0e-51 112 Match length 45 % identity (Z47554) orf [Zea mays] NCBI Description Seq. No. 167917 LIB3234-049-P1-K1-D9 Seq. ID BLASTX Method NCBI GI q4204315 BLAST score 682 E value 4.0e-72 128 Match length % identity 100 (AC003027) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 167918 LIB3234-049-P1-K1-E10 Seq. ID BLASTX Method NCBI GI g1706749 BLAST score 495 E value 4.0e-50 Match length 102 % identity 99 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR NCBI Description (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi 780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana] 167919 Seq. No. LIB3234-049-P1-K1-E11 Seq. ID Method BLASTX g586036 NCBI GI BLAST score 593 E value 1.0e-61 Match length 130

>gi 629560 pir S42550 signal recognition particle 54K

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 1 (SRP54)



protein - Arabidopsis thaliana >gi_304111 (L19997) signal recognition particle 54 kDa subunit [Arabidopsis thaliana]

167920 Seq. No. Seq. ID LIB3234-049-P1-K1-E12 BLASTN Method g3212846 NCBI GI 383 BLAST score 0.0e+00E value 391 Match length 99 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana] 167921 Seq. No. LIB3234-049-P1-K1-E3 Seq. ID BLASTX Method g3128180 NCBI GI BLAST score 600 E value 2.0e-62 126 Match length 91 % identity (AC004521) citrate synthetase [Arabidopsis thaliana] NCBI Description 167922 Seq. No. Seq. ID LIB3234-049-P1-K1-E4 BLASTN Method NCBI GI g3212846 BLAST score 352 E value 0.0e+00Match length 380 98 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. . 167923 LIB3234-049-P1-K1-E5 Seq. ID BLASTX Method g1169273 NCBI GI BLAST score 203 6.0e-16 E value Match length 116 42 % identity NCBI Description DEOXYCYTIDINE KINASE (DCK) >gi 1083283 pir A55122 deoxycytidine kinase (EC 2.7.1.74) - mouse >gi 456677 emb CAA54787 (X77731) deoxycytidine kinase [Mus musculus] Seq. No. 167924 Seq. ID LIB3234-049-P1-K1-E6 Method BLASTN NCBI GI g3885325 BLAST score 178 8.0e-96 E value 194 Match length

22715

NCBI Description Arabidopsis thaliana chromosome II BAC T20P8 genomic

98

% identity



sequence, complete sequence [Arabidopsis thaliana]

167925 Seq. No. LIB3234-049-P1-K1-E7 Seq. ID Method BLASTX g3776558 NCBI GI BLAST score 471 2.0e-47 E value 109 Match length 90 % identity (ACO05388) Identical to gb L14814 DNA for tissue-specific NCBI Description acyl carrier protein isoform 2 from A. thaliana. ESTs gb_AA597351, gb_T41805, gb H36871, gb R30210, gb AA042549, gb Z47650, gb H76304 and gb AA597348 come from this gene. [Arabidopsi 167926 Seq. No. LIB3234-049-P1-K1-F1 Seq. ID Method BLASTX NCBI GI q3643610 532 BLAST score 2.0e-54E value 103 Match length % identity (AC005395) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] 167927 Seq. No. Seq. ID LIB3234-049-P1-K1-F11 Method BLASTX q2493045 NCBI GI BLAST score 594 9.0e-62 E value Match length 120 % identity 98 ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description >gi 1655484 dbj BAA13601 (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] Seq. No. 167928 LIB3234-049-P1-K1-F12 Seq. ID Method BLASTN NCBI GI g2570223 BLAST score 326 0.0e+00E value Match length 391 % identity 98 NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana] 167929 Seq. No. LIB3234-049-P1-K1-F2 Seq. ID Method BLASTN NCBI GI g2264318 BLAST score 368 0.0e + 00E value

376

Match length

% identity

NCBI Description

66

thaliana]



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
                  167930
Seq. No.
                  LIB3234-049-P1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3184283
BLAST score
                  575
                  1.0e-59
E value
                  128
Match length
                  91
% identity
                  (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  167931
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g2098711
BLAST score
                  237
                  6.0e-20
E value
                  129
Match length
                  41
% identity
                 (U82976) pectinesterase [Citrus sinensis]
NCBI Description
                  167932
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-F6
                  BLASTX
Method
                  g3808062
NCBI GI
BLAST score
                  164
E value
                  6.0e-12
                  68
Match length
                  46
% identity
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  167933
                  LIB3234-049-P1-K1-F9
Seq. ID
                  BLASTN
Method
                  q3298532
NCBI GI
BLAST score
                  349
                  0.0e + 00
E value
Match length
                  369
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T26B15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167934
                  LIB3234-049-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006833
BLAST score
                  288
                  7.0e-37
E value
Match length
                  128
```

22717

(AC005970) putative reverse transcriptase [Arabidopsis



Seq. No. 167935

Seq. ID LIB3234-049-P1-K1-G11

Method BLASTX
NCBI GI g166765
BLAST score 534
E value 9.0e-55
Match length 102
% identity 100

NCBI Description (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No. 167936

Seq. ID LIB3234-049-P1-K1-G12

Method BLASTX
NCBI GI g3157930
BLAST score 602
E value 1.0e-62
Match length 114
% identity 98

NCBI Description (AC002131) Strong similarity to

amino-cyclopropane-carboxylic acid oxidase gb_L27664 from Brassica napus. ESTs gb Z48548 and gb Z48549 come from

this gene. [Arabidopsis thaliana]

Seq. No. 167937

Seq. ID LIB3234-049-P1-K1-G3

Method BLASTN
NCBI GI g3449321
BLAST score 58
E value 7.0e-24
Match length 202
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 167938

Seq. ID LIB3234-049-P1-K1-G4

Method BLASTX
NCBI GI g3445207
BLAST score 728
E value 2.0e-77
Match length 130
% identity 99

NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 167939

Seq. ID LIB3234-049-P1-K1-G5

Method BLASTN
NCBI GI g4092470
BLAST score 43
E value 6.0e-15
Match length 71
% identity 90

NCBI Description Arabidopsis thaliana BAC T24G23 from chromosome IV near 21

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 167940

Seq. ID LIB3234-049-P1-K1-G8

Seq. ID

Method



```
Method
                  BLASTX
NCBI GI
                  g4309730
BLAST score
                  502
                  5.0e-51
E value
Match length
                  113
                  86
% identity
                   (AC006439) putative lipid transfer protein [Arabidopsis
NCBI Description
                  thaliana]
                  167941
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g4325282
BLAST score
                  304
                   9.0e-28
E value
Match length
                   60
% identity
                   92
NCBI Description
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                  >qi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   167942
Seq. No.
                  LIB3234-049-P1-K1-H1
Seq. ID
Method
                   BLASTX
                   q3335169
NCBI GI
                   335
BLAST score
                   1.0e-31
E value
                   63
Match length
% identity
                   97
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                   >qi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                   protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                   167943
                   LIB3234-049-P1-K1-H10
Seq. ID
Method
                   BLASTN
                   g2924729
NCBI GI
                   132
BLAST score
E value
                   4.0e-68
Match length
                   286
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNA5, complete sequence [Arabidopsis thaliana]
                   167944
Seq. No.
                   LIB3234-049-P1-K1-H12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4455801
                   205
BLAST score
                   1.0e-112
E value
                   209
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana prxr3 gene, exons 1-4
                   167945
Seq. No.
```

22719

LIB3234-049-P1-K1-H3

BLASTX

```
g2583108
NCBI GI
BLAST score
                  414
E value
                  7.0e-41
                  100
Match length
                  85
% identity
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                  167946
Seq. No.
                  LIB3234-049-P1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  592
                  2.0e-61
E value
                  125
Match length
                  89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  167947
Seq. No.
                  LIB3234-049-P1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160146
                  277
BLAST score
                  1.0e-24
E value
                   65
Match length
                  86
% identity
                   (AC000375) Strong similarity to Arabidopsis
NCBI Description
                  qb X91953, F21M12.3, F21M12.1. EST gb H36326 comes from this
                   gene. [Arabidopsis thaliana]
                   167948
Seq. No.
                   LIB3234-049-P1-K1-H6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4584351
BLAST score
                   352
                   0.0e + 00
E value
Match length
                   368
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   167949
                   LIB3234-049-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   q4650842
NCBI GI
                   646
BLAST score
                   7.0e-68
E value
                   128
Match length
                   96
% identity
                  (AB026185) elongation factor 2 [Lithospermum erythrorhizon]
NCBI Description
```

22720

167950

BLASTN

LIB3234-049-P1-K1-H9

Seq. No.

Seq. ID

Method



NCBI GI g2281081
BLAST score 334
E value 0.0e+00
Match length 350
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167951

Seq. ID LIB3234-050-P1-K1-A10

Method BLASTN
NCBI GI g3402695
BLAST score 271
E value 1.0e-151
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167952

Seq. ID LIB3234-050-P1-K1-A12

Method BLASTN
NCBI GI g4467094
BLAST score 366
E value 0.0e+00
Match length 370
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10

(ESSA project)

Seq. No. 167953

Seq. ID LIB3234-050-P1-K1-A2

Method BLASTX
NCBI GI g1706186
BLAST score 280
E value 5.0e-25
Match length 119
% identity 46

NCBI Description HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)

(CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS

RECEPTOR) >gi 110721 pir A32742 murine ecotropic

retrovirus receptor protein - mouse >gi_532612 (M26687)

ecotropic retrovirus receptor [Mus musculus]

Seq. No. 167954

Seq. ID LIB3234-050-P1-K1-A3

Method BLASTN
NCBI GI 94468976
BLAST score 377
E value 0.0e+00
Match length 377
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18

(ESSA project)

Seq. No. 167955



Seq. ID LIB3234-050-P1-K1-A4 Method BLASTX NCBI GI q2129753 BLAST score 632 E value 3.0e-66 121 Match length % identity 100 NCBI Description threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi 1448917 (L41666) threonine synthase [Arabidopsis thaliana] 167956 Seq. No. Seq. ID LIB3234-050-P1-K1-A5 BLASTN Method q4510360 NCBI GI BLAST score 373 E value 0.0e + 00373 Match length % identity 100 Arabidopsis thaliana chromosome II BAC F11F19 genomic NCBI Description sequence, complete sequence 167957 Seq. No. Seq. ID LIB3234-050-P1-K1-A6 BLASTN Method NCBI GI q633027 BLAST score 189 1.0e-102 E value Match length 361 % identity 89 Arabidopsis thaliana mRNA for protein phosphatase 2C NCBI Description 167958 Seq. No. LIB3234-050-P1-K1-A7 Seq. ID BLASTN Method NCBI GI g3449318 BLAST score 82 3.0e - 38E value Match length 150 % identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLF18, complete sequence [Arabidopsis thaliana] Seq. No. 167959 LIB3234-050-P1-K1-A9 Seq. ID BLASTX Method NCBI GI g3918 BLAST score 412 2.0e-40 E value 122 Match length

% identity 61

(X58378) mitochondrial elongation factor G [Saccharomyces NCBI Description

cerevisiae]

167960 Seq. No.

LIB3234-050-P1-K1-B12 Seq. ID

Method BLASTN



NCBI GI g4262221 BLAST score 279 E value 1.0e-156 Match length 370 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167961

Seq. ID LIB3234-050-P1-K1-B2

Method BLASTX
NCBI GI g3808062
BLAST score 148
E value 2.0e-09
Match length 61
% identity 46

NCBI Description (AB019195) PV100 [Cucurbita maxima]

Seq. No. 167962

Seq. ID LIB3234-050-P1-K1-B4

Method BLASTN
NCBI GI 94199934
BLAST score 184
E value 4.0e-99
Match length 343
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 167963

Seq. ID LIB3234-050-P1-K1-B6

Method BLASTX
NCBI GI g4503269
BLAST score 190
E value 2.0e-14
Match length 110
% identity 42

NCBI Description deoxycytidine kinase >gi_118447_sp_P27707_DCK_HUMAN

DEOXYCYTIDINE KINASE (DCK) >gi 105829 pir A38585 deoxycytidine kinase (EC 2.7.1.74) - human >gi 181510

(M60527) deoxycytidine kinase [Homo sapiens]

Seq. No. 167964

Seq. ID LIB3234-050-P1-K1-B7

Method BLASTN
NCBI GI g3309276
BLAST score 170
E value 1.0e-90
Match length 272
% identity 99

NCBI Description Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3

cM, complete sequence

Seq. No. 167965

Seq. ID LIB3234-050-P1-K1-B8

Method BLASTX NCBI GI g1592677



BLAST score 193 E value 8.0e-15 Match length 38 % identity 100

NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No. 167966

Seq. ID LIB3234-050-P1-K1-B9

Method BLASTX
NCBI GI g2129532
BLAST score 269
E value 1.0e-23
Match length 83
% identity 66

NCBI Description acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -

Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis

thaliana]

Seq. No. 167967

Seq. ID LIB3234-050-P1-K1-C10

Method BLASTN
NCBI GI g2262155
BLAST score 229
E value 1.0e-126

Match length 289 % identity 97

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 167968

Seq. ID LIB3234-050-P1-K1-C12

Method BLASTN
NCBI GI g4432829
BLAST score 207
E value 1.0e-113
Match length 373
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167969

Seq. ID LIB3234-050-P1-K1-C2

Method BLASTX
NCBI GI g3287691
BLAST score 165
E value 2.0e-11
Match length 65
% identity 55

NCBI Description (AC003979) Contains similarity to RING zinc finger protein

gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No. 167970

Seq. ID LIB3234-050-P1-K1-C3

Method BLASTN
NCBI GI g4159712
BLAST score 371

BLAST score

Match length

E value

134 3.0e-69

270

```
Tele Transferred
```

```
E value
                   0.0e + 00
Match length
                   371
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                  167971
                  LIB3234-050-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2651294
BLAST score
                   305
                   1.0e-171
E value
Match length
                   377
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T2P4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  167972
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-C7
                  BLASTX
Method
NCBI GI
                   q4678285
BLAST score
                   410
E value
                   3.0e-40
Match length
                   122
                   61
% identity
                  (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167973
Seq. ID
                   LIB3234-050-P1-K1-C9
Method
                   BLASTX
                   q3335169
NCBI GI
                   517
BLAST score
                   8.0e-53
E value
Match length
                   121
                   77
% identity
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                   >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                   protein 1 (ATS1) [Arabidopsis thaliana]
                   167974
Seq. No.
                   LIB3234-050-P1-K1-D1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4455348
BLAST score
                   370
E value
                   0.0e+00
                   370
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
                   (ESSAII project)
                   167975
Seq. No.
                   LIB3234-050-P1-K1-D11
Seq. ID
Method
                   BLASTN
                   g4159703
NCBI GI
```



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5F14, complete sequence
Seq. No.
                  167976
                  LIB3234-050-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617268
BLAST score
                  597
                  4.0e-62
E value
                  122
Match length
                  90
% identity
                 (Z72153) acyl CoA synthetase [Brassica napus]
NCBI Description
                  167977
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-D4
                  BLASTX
Method
                  q72827
NCBI GI
BLAST score
                  157
E value
                  1.0e-10
Match length
                  63
                  13
% identity
NCBI Description IgA Fc receptor precursor - Streptococcus agalactiae
                  167978
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4335752
BLAST score
                  324
E value
                  4.0e-30
Match length
                  104
% identity
                  56
                  (AC006284) putative myb transcription factor-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167979
Seq. ID
                  LIB3234-050-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3808062
BLAST score
                  149
E value
                  1.0e-09
Match length
                  62
                  45
% identity
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  167980
                  LIB3234-050-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q399091
BLAST score
                  485
                  5.0e-49
E value
Match length
                  120
% identity
                  80
```

NCBI Description PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized -



Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

167981 Seq. No. Seq. ID LIB3234-050-P1-K1-D8 BLASTX Method g3445209 NCBI GI BLAST score 518 6.0e-53 E value 121 Match length 78 % identity (AC004786) putative serine carboxypeptidase I [Arabidopsis NCBI Description thaliana] 167982 Seq. No. LIB3234-050-P1-K1-D9 Seq. ID BLASTX Method g3603456 NCBI GI BLAST score 477 E value 4.0e-4898 Match length 29 % identity (AF088848) polyubiquitin [Capsicum chinense] NCBI Description 167983 Seq. No. Seq. ID LIB3234-050-P1-K1-E10 BLASTN Method g3482964 NCBI GI BLAST score 359 0.0e+00E value 371 Match length 99 % identity NCBI Description Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project) 167984 Seq. No. LIB3234-050-P1-K1-E11 Seq. ID BLASTN Method NCBI GI q3482964 BLAST score 177 6.0e-95 E value Match length 333 % identity 88 NCBI Description Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project) Seq. No. 167985 LIB3234-050-P1-K1-E12 Seq. ID Method BLASTN NCBI GI g4159708 BLAST score 360 0.0e+00E value Match length 372

MKP6, complete sequence

93

% identity

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:



Seq. No. 167986

Seq. ID LIB3234-050-P1-K1-E2

Method BLASTN
NCBI GI 94757678
BLAST score 33
E value 5.0e-09
Match length 96
% identity 90

NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic

sequence, complete sequence

Seq. No. 167987

Seq. ID LIB3234-050-P1-K1-F1

Method BLASTX
NCBI GI g131297
BLAST score 674
E value 3.0e-71
Match length 124
% identity 98

NCBI Description PHOTOSYSTEM II D2 PROTEIN (PHOTOSYSTEM Q(A) PROTEIN)

>gi_72667_pir__F2SPD2 photosystem II protein D2 - spinach
chloroplast >gi_12280_emb_CAA25863_ (X01724) D2 protein
[Spinacia oleracea] >gi_473511 (M27308) D2 photosystem II
protein [Spinacia oleracea] >gi_552887 (M36833) 32 Kd-like

protein [Spinacia oleracea]

Seq. No. 167988

Seq. ID LIB3234-050-P1-K1-F11

Method BLASTX
NCBI GI g1345973
BLAST score 425
E value 5.0e-42
Match length 96
% identity 81

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis
thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167989

Seq. ID LIB3234-050-P1-K1-F2

Method BLASTX
NCBI GI 94585972
BLAST score 284
E value 2.0e-25
Match length 94
% identity 57

NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No. 167990

Seq. ID LIB3234-050-P1-K1-F3

Method BLASTX



```
NCBI GI
                  q128733
BLAST score
                  270
                  8.0e-24
E value
Match length
                  51
                  96
% identity
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4-LIKE
NCBI Description
                  >gi 97653 pir S14968 ndhD-like protein - Synechocystis sp
                  >gi 581748_emb_CAA37837_ (X53842) ndhD-like ORF
                  [Synechocystis sp.]
                  167991
Seq. No.
                  LIB3234-050-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512673
BLAST score
                  332
                  4.0e-31
E value
Match length
                  64
                  100
% identity
NCBI Description
                  (AC006931) putative phosphoprotein phosphatase [Arabidopsis
                  thaliana]
                  167992
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g166570
BLAST score
                  220
E value
                  6.0e-18
Match length
                  101
% identity
                  47
NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                  167993
                  LIB3234-050-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                  607
                  2.0e-63
E value
Match length
                  117
                  100
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  167994
Seq. ID
                  LIB3234-050-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3695374
BLAST score
                  407
E value
                  7.0e-40
Match length
                  73
% identity
                  97
NCBI Description
                  (AF096370) contains similarity to NAM (no apical meristem)
                  -like proteins [Arabidopsis thaliana]
```

Seq. No. 167995

Seq. ID LIB3234-050-P1-K1-F9

Method BLASTN
NCBI GI g3298532
BLAST score 101



E value 2.0e-49 Match length 205 % identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167996

Seq. ID LIB3234-050-P1-K1-G12

Method BLASTX
NCBI GI 94249382
BLAST score 393
E value 3.0e-38
Match length 95
% identity 81

NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC

gb AC004481. [Arabidopsis thaliana]

Seq. No. 167997

Seq. ID LIB3234-050-P1-K1-G2

Method BLASTN
NCBI GI g2264315
BLAST score 367
E value 0.0e+00
Match length 371
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRN17, complete sequence [Arabidopsis thaliana]

Seq. No. 167998

Seq. ID LIB3234-050-P1-K1-G3

Method BLASTX
NCBI GI g3335171
BLAST score 535
E value 7.0e-55
Match length 114
% identity 89

NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No. 167999

Seq. ID LIB3234-050-P1-K1-G4

Method BLASTX
NCBI GI g3319355
BLAST score 581
E value 3.0e-60
Match length 125
% identity 100

NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex

gamma chain [Arabidopsis thaliana]

Seq. No. 168000

Seq. ID LIB3234-050-P1-K1-G5

Method BLASTN
NCBI GI g3426033
BLAST score 311
E value 1.0e-175
Match length 338

NCBI Description



% identity NCBI Description Arabidopsis thaliana chromosome II BAC F12C2O genomic sequence, complete sequence [Arabidopsis thaliana] 168001 Seq. No. LIB3234-050-P1-K1-G6 Seq. ID Method BLASTX g3808062 NCBI GI BLAST score 143 6.0e-09 E value Match length 61 44% identity (AB019195) PV100 [Cucurbita maxima] NCBI Description 168002 Seq. No. Seq. ID LIB3234-050-P1-K1-G7 Method BLASTX q4581140 NCBI GI BLAST score 325 E value 3.0e - 30121 Match length 57 % identity (AC006919) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 168003 Seq. ID LIB3234-050-P1-K1-G9 BLASTX Method NCBI GI q4325282 BLAST score 272 E value 4.0e-24 Match length 72 72 % identity (AF123310) NAC domain protein NAM [Arabidopsis thaliana] NCBI Description >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana] 168004 Seq. No. LIB3234-050-P1-K1-H1 Seq. ID Method BLASTX NCBI GI q207905 BLAST score 276 2.0e-24 E value Match length 124 41 % identity (M18027) alpha globulin B [Artificial gene] NCBI Description 168005 Seq. No. LIB3234-050-P1-K1-H10 Seq. ID Method BLASTN NCBI GI g4490324 301 BLAST score E value 1.0e-169 313 Match length % identity 99

22731

(ESSA project)

Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

Method

NCBI GI

BLASTX

g136739



```
168006
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2117612
BLAST score
                  687
                  1.0e-72
E value
                  124
Match length
                  99
% identity
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
                  168007
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-H2
                  BLASTX
Method
NCBI GI
                  g1168391
BLAST score
                  173
                  1.0e-12
E value
                  96
Match length
                  38
% identity
                  ALLERGEN ARA H 1, CLONE P41B (ARA H I) >gi 602436 (L34402)
NCBI Description
                  Ara h I [Arachis hypogaea]
                  168008
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-H3
                  BLASTN
Method
NCBI GI
                  g3983533
BLAST score
                  214
                  1.0e-117
E value
Match length
                  318
% identity
                  97
NCBI Description Arabidopsis thaliana BAC T24G3 from chromosome V near 70
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168009
Seq. ID
                  LIB3234-050-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3913648
BLAST score
                  246
E value
                  5.0e-21
Match length
                  96
% identity
                  55
NCBI Description FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
                  168010
Seq. No.
                  LIB3234-050-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4314374
                  45
BLAST score
                  1.0e-16
E value
Match length
                  244
                  10
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168011
                  LIB3234-050-P1-K1-H6
Seq. ID
```



BLAST score 345 E value 1.0e-32 Match length 112 % identity 62

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi 218001_dbj_BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 168012

Seq. ID LIB3234-050-P1-K1-H7

Method BLASTN
NCBI GI g4115930
BLAST score 290
E value 1.0e-162
Match length 366

% identity 94

NCBI Description Arabidopsis thaliana BAC T4B21

Seq. No. 168013

Seq. ID LIB3234-050-P1-K1-H8

Method BLASTX
NCBI GI 94689108
BLAST score 176
E value 8.0e-13
Match length 82

% identity 44

NCBI Description (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]

Seq. No. 168014

Seq. ID LIB3234-052-P1-K1-A1

Method BLASTN
NCBI GI g336917
BLAST score 56
E value 1.0e-22
Match length 104
% identity 95

NCBI Description Epifagus virginiana chloroplast complete genome

Seq. No. 168015

Seq. ID LIB3234-052-P1-K1-A10

Method BLASTN
NCBI GI g2262155
BLAST score 378
E value 0.0e+00
Match length 378
% identity 100

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 168016

Seq. ID LIB3234-052-P1-K1-A11

Method BLASTX
NCBI GI g2827559
BLAST score 361
E value 2.0e-34



Match length 83 % identity 82

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana] >gi 3292808 emb CAA19798 (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 168017

Seq. ID LIB3234-052-P1-K1-A12

Method BLASTX
NCBI GI g1345973
BLAST score 431
E value 1.0e-42
Match length 97
% identity 81

% identity

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis
thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 168018

Seq. ID LIB3234-052-P1-K1-A2

Method BLASTX
NCBI GI g1502428
BLAST score 335
E value 2.0e-31
Match length 66
% identity 100

NCBI Description (U62330) phosphate transporter [Arabidopsis thaliana]

>gi 2258116 dbj BAA21503 (D86591) inorganic phosphate

transporter [Arabidopsis thaliana]

>gi_2258118_dbj_BAA21504_ (D86608) inorganic phosphate

transporter [Arabidopsis thaliana]

Seq. No. 168019

Seq. ID LIB3234-052-P1-K1-A3

Method BLASTN
NCBI GI g4049332
BLAST score 284
E value 1.0e-158
Match length 329
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4

(ESSAII project)

Seq. No. 168020

% identity

Seq. ID LIB3234-052-P1-K1-A4

88

Method BLASTN
NCBI GI g2827698
BLAST score 33
E value 6.0e-09
Match length 164

BLAST score

E value

54 2.0e-21



```
NCBI Description Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11
                  (ESSAII project)
                  168021
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3420004
BLAST score
                  160
                  6.0e-11
E value
                  73
Match length
                  40
% identity
                 (AF000305) steroid sulfotransferase 1 [Brassica napus]
NCBI Description
Seq. No.
                  168022
Seq. ID
                  LIB3234-052-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  q267069
BLAST score
                  526
E value
                  8.0e-54
                  97
Match length
                  100
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >qi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  168023
Seq. No.
                  LIB3234-052-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128205
BLAST score
                  521
                  3.0e-53
E value
                  120
Match length
% identity
                  87
                  (AC004077) putative pyruvate dehydrogenase complex E1 beta
NCBI Description
                  subunit [Arabidopsis thaliana]
                  168024
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g112682
                  566
BLAST score
                  2.0e-58
E value
Match length
                  127
% identity
                  86
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  168025
                  LIB3234-052-P1-K1-B10
Seq. ID
Method
                  BLASTN
                  g4581138
NCBI GI
```



Match length 114 87 % identity Arabidopsis thaliana chromosome II BAC F1011 genomic NCBI Description sequence, complete sequence Seq. No. 168026 Seq. ID LIB3234-052-P1-K1-B11 Method BLASTX NCBI GI g4454482 BLAST score 472 E value 2.0e-47Match length 122 73 % identity (AC006234) hypothetical protein [Arabidopsis thaliana] NCBI Description 168027 Seq. No. Seq. ID LIB3234-052-P1-K1-B2 Method BLASTN NCBI GI g2351061 BLAST score 380 E value 0.0e+00Match length 388 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana] Seq. No. 168028 Seq. ID LIB3234-052-P1-K1-B4 Method BLASTN NCBI GI g3169169 BLAST score 270 E value 1.0e-150 Match length 349 % identity 93 NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168029 LIB3234-052-P1-K1-B5 Seq. ID Method BLASTN NCBI GI g1931636 BLAST score 165 E value 5.0e-88 Match length 219 % identity 92 NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No. 168030

Seq. ID LIB3234-052-P1-K1-B6

Method BLASTN
NCBI GI g511598
BLAST score 375
E value 0.0e+00
Match length 375
% identity 27

NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,

complete cds



```
Seq. No.
                  168031
Seq. ID
                  LIB3234-052-P1-K1-B7
                  BLASTN
Method
NCBI GI
                  g4159703
BLAST score
                  149
E value
                  3.0e-78
Match length
                  347
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5F14, complete sequence
Seq. No.
                  168032
Seq. ID
                  LIB3234-052-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2239089
BLAST score
                  145
                  3.0e-09
E value
Match length
                  53
% identity
                  47
                  (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi 3288180 emb CAB11466 (Z98758)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
                  168033
Seq. No.
                  LIB3234-052-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961107
BLAST score
                  140
                  1.0e-08
E value
Match length
                  69
                  39
% identity
NCBI Description
                  (AF042383) TLS-associated protein with SR repeats [Mus
                  musculus] >gi_2961149 (AF047448) TLS-associated protein
                  TASR [Homo sapiens]
Seq. No.
                  168034
                  LIB3234-052-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4454587
BLAST score
                  58
E value
                  7.0e-24
Match length
                  148
                  89
% identity
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168035
Seq. ID
                  LIB3234-052-P1-K1-C11
Method
                  BLASTN
                  g2244870
```

NCBI GI BLAST score 71 E value 1.0e-31 Match length 228 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig



fragment No

Seq. No. 168036 Seq. ID LIB3234-052-P1-K1-C12 Method BLASTX NCBI GI q140551 BLAST score 212 E value 1.0e-18 Match length 91 63 % identity NCBI Description HYPOTHETICAL 250 KD PROTEIN (ORF 2131) >gi 81505 pir S01446 hypothetical protein 2131 - spinach chloroplast >gi_12246_emb_CAA30743_ (X07908) ORF 2131 (AA 1-2131) [Spinacia oleracea] Seq. No. 168037 Seq. ID LIB3234-052-P1-K1-C3 Method BLASTN NCBI GI g3449321 BLAST score 36

BLAST score 36 E value 9.0e-11 Match length 72 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

 Seq. No.
 168038

 Seq. ID
 LIB3234-052-P1-K1-C4

 Method
 BLASTX

 NCBI GI
 g1703108

 BLAST score
 548

 E value
 2.0e-56

 Match length
 101

Match length 101 % identity 100

NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis

thaliana >gi_2129528 pir___S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 168039

Seq. ID LIB3234-052-P1-K1-C5

Method BLASTX
NCBI GI g2160138
BLAST score 644
E value 1.0e-67
Match length 126
% identity 51

NCBI Description (AC000375) No definition line found [Arabidopsis thaliana]

Seq. No. 168040

Seq. ID LIB3234-052-P1-K1-D1

Method BLASTN
NCBI GI g3193305
BLAST score 383
E value 0.0e+00
Match length 387



100 % identity NCBI Description Arabidopsis thaliana BAC F3D13 168041 Seq. No. LIB3234-052-P1-K1-D10 Seq. ID Method BLASTN g4199934 NCBI GI BLAST score 261 1.0e-145 E value 356 Match length 91 % identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana] 168042 Seq. No. Seq. ID LIB3234-052-P1-K1-D11 Method BLASTN NCBI GI g2264302 20 BLAST score 3.2e-01 E value 378 Match length 92 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MAC12, complete sequence [Arabidopsis thaliana] Seq. No. 168043 Seq. ID LIB3234-052-P1-K1-D12 Method BLASTN NCBI GI g4335744 BLAST score 141 7.0e-74E value Match length 141 100 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168044 LIB3234-052-P1-K1-D2 Seq. ID Method BLASTN g1699056 NCBI GI BLAST score 379 E value 0.0e + 00383 Match length % identity 100 Arabidopsis thaliana 27 kDa unknown protein mRNA, complete NCBI Description cds

Seq. No. 168045

Seq. ID LIB3234-052-P1-K1-D3

Method BLASTX NCBI GI q1709970 BLAST score 452 E value 4.0e-45Match length 114 80 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Method

NCBI GI

BLASTN

g4455321



```
Seq. No.
                  168046
Seq. ID
                  LIB3234-052-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  q4519192
BLAST score
                  173
E value
                  2.0e-92
                  371
Match length -
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MBK21, complete sequence
Seq. No.
                  168047
                  LIB3234-052-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522003
BLAST score
                  477
                  4.0e-48
E value
Match length
                  112
                  85
% identity
                  (AC007069) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  168048
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  545
E value
                  5.0e-56
Match length
                  124
% identity
                  85
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  168049
Seq. No.
                  LIB3234-052-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832620
BLAST score
                  414
E value
                  1.0e-40
Match length
                  115
% identity
                   69
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  168050
Seq. No.
                  LIB3234-052-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3046855
BLAST score
                  219
E value
                   1.0e-120
Match length
                   342
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168051
Seq. ID
                  LIB3234-052-P1-K1-E2
```



BLAST score 157 E value 6.0e-83 Match length 373 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10

(ESSAII project)

Seq. No. 168052

Seq. ID LIB3234-052-P1-K1-E3

Method BLASTN
NCBI GI g4217996
BLAST score 349
E value 0.0e+00
Match length 365
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F24H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168053

Seq. ID LIB3234-052-P1-K1-E4

Method BLASTN
NCBI GI 94519193
BLAST score 128
E value 1.0e-65
Match length 383
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 168054

Seq. ID LIB3234-052-P1-K1-E6

Method BLASTX
NCBI GI 94249391
BLAST score 392
E value 4.0e-38
Match length 112
% identity 73

NCBI Description (AC005966) Similar to gi 3249076 T13D8.16 beta glucosidase

from Arabidopsis thaliana BAC gb AC004473. [Arabidopsis

thalianal

Seq. No. 168055

Seq. ID LIB3234-052-P1-K1-E7

Method BLASTX
NCBI GI g112737
BLAST score 185
E value 8.0e-14
Match length 94
% identity 46

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir_ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]



```
168056
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q3287691
BLAST score
                  153
E value
                  4.0e-10
Match length
                  65
                  52
% identity
NCBI Description
                  (AC003979) Contains similarity to RING zinc finger protein
                  gb X95455 from Gallus gallus. [Arabidopsis thaliana]
Seq. No.
                  168057
                  LIB3234-052-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82051
BLAST score
                  317
E value
                  3.0e-29
Match length
                  119
% identity
                  55
NCBI Description
                  lipid body-associated membrane protein - carrot
                  >gi_259453_bbs_117620 (S47635) lipid body membrane
                  protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                  180 aa] [Daucus carota]
Seq. No.
                  168058
Seq. ID
                  LIB3234-052-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  86
E value
                  2.0e-15
Match length
                  80
                  57
% identity
NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
                   (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  168059
Seq. ID
                  LIB3234-052-P1-K1-F10
                  BLASTX
Method
NCBI GI
                  q1345973
BLAST score
                  435
E value
                  4.0e-43
                  98
Match length
% identity
                  82
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
```

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)

microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

168060 Seq. No.

Seq. ID LIB3234-052-P1-K1-F11

Method BLASTX NCBI GI q3377517

E value

Match length

2.0e-95

384



```
BLAST score
                   225
E value
                   2.0e-18
Match length
                  90
                   43
% identity
NCBI Description
                  (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
                  168061
Seq. No.
                  LIB3234-052-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263646
BLAST score
                  644
                  1.0e-67
E value
Match length
                  126
% identity
                  98
                  (AC006136) putative TA1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
                  168062
Seq. No.
                  LIB3234-052-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1762584
BLAST score
                  473
E value
                  1.0e-47
Match length
                  91
% identity
                  100
NCBI Description
                  (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
Seq. No.
                  168063
                  LIB3234-052-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490749
BLAST score
                  654
E value
                  8.0e-69
Match length
                  125
% identity
                   99
NCBI Description
                   (AL035708) 2-dehydro-3-deoxyphosphoheptonate aldolase
                   [Arabidopsis thaliana]
Seq. No.
                  168064
Seq. ID
                  LIB3234-052-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g3985949
BLAST score
                  378
E value
                  0.0e+00
Match length
                  382
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168065
Seq. ID
                  LIB3234-052-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g4454447
BLAST score
                  178
```



% identity 99 Arabidopsis thaliana chromosome II BAC F5H14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 168066 Seq. No. LIB3234-052-P1-K1-F6 Seq. ID Method BLASTX g4314363 NCBI GI BLAST score 610 1.0e-63 E value Match length 123 % identity 98

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 168067

Seq. ID LIB3234-052-P1-K1-F7

Method BLASTX
NCBI GI g2245378
BLAST score 589
E value 3.0e-61
Match length 125
% identity 91

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 168068

Seq. ID LIB3234-052-P1-K1-F8

Method BLASTN
NCBI GI 94757411
BLAST score 343
E value 0.0e+00
Match length 347
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXC7, complete sequence

Seq. No. 168069

Seq. ID LIB3234-052-P1-K1-G11

Method BLASTN
NCBI GI g3046850
BLAST score 351
E value 0.0e+00
Match length 378
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24G6, complete sequence [Arabidopsis thaliana]

Seq. No. 168070

Seq. ID LIB3234-052-P1-K1-G12

Method BLASTN
NCBI GI g2924729
BLAST score 267
E value 1.0e-148
Match length 379
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.

Seq. ID

Method

168076

BLASTX

LIB3234-052-P1-K1-H11

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And the second s
```

```
Seq. No.
                   168071
                  LIB3234-052-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2961356
BLAST score
                   416
E value
                   6.0e-41
                  113
Match length
                   71
% identity
                   (AL022140) alcohol dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168072
                  LIB3234-052-P1-K1-G3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3805839
BLAST score
                   382
E value
                   0.0e + 00
                   382
Match length
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
NCBI Description
                   (ESSAII project)
                  168073
Seq. No.
                  LIB3234-052-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3172156
BLAST score
                  177
                   7.0e-95
E value
                   387
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                  complete sequence [Arabidopsis thaliana]
                  168074
Seq. No.
                  LIB3234-052-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4678299
BLAST score
                   594
E value
                   8.0e-62
Match length
                   116
% identity
                   100
NCBI Description
                   (AL049655) cysteine proteinase precursor-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   168075
Seq. ID
                  LIB3234-052-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2924258
BLAST score
                  524
E value
                   1.0e-53
Match length
                  126
% identity
                   76
                  (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
NCBI Description
```

```
NCBI GI
                  q3242079
BLAST score
                  226
                  1.0e-18
E value
                  69
Match length
% identity
                   62
                  (AJ006984) proline-rich protein [Capsicum annuum]
NCBI Description
                  168077
Seq. No.
                  LIB3234-052-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129773
BLAST score
                  678
E value
                  1.0e-71
                  125
Match length
                  98
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR3 -
                  Arabidopsis thaliana (fragment) >gi 1244752 (U43485)
                  xyloglucan endotransglycosylase-related protein
                   [Arabidopsis thaliana]
Seq. No.
                  168078
                  LIB3234-052-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4755194
BLAST score
                  693
                   2.0e-73
E value
Match length
                  126
                   100
% identity
                   (AC007018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4755195_gb_AAD29062.1_AC007018_10 (AC007018)
                  hypothetical protein [Arabidopsis thaliana]
                   168079
Seq. No.
Seq. ID
                   LIB3234-052-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q3421378
BLAST score
                   371
E value
                   1.0e-35
Match length
                   125
% identity
NCBI Description (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]
Seq. No.
                   168080
                  LIB3234-052-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4678266
BLAST score
                   379
                   0.0e + 00
E value
Match length
                   383
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
NCBI Description
                   (ESSA project)
```

Seq. No. 168081

Seq. ID LIB3234-052-P1-K1-H5

Method BLASTX NCBI GI g3242079



```
BLAST score
                  145
                  3.0e-09
E value
Match length
                  50
% identity
                  56
                  (AJ006984) proline-rich protein [Capsicum annuum]
NCBI Description
Seq. No.
                  168082
                  LIB3234-052-P1-K1-H6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3659491
BLAST score
                  355
E value
                  0.0e+00
Match length
                  380
                  98
% identity
NCBI Description
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168083
Seq. ID
                  LIB3234-052-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  q3449316
BLAST score
                  380
E value
                  0.0e+00
Match length
                  380
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9D7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168084
                  LIB3234-052-P1-K1-H8
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4662609
BLAST score
                   72
                   2.0e-32
E value
                   168
Match length
                   90
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
NCBI Description
                   complete sequence
                  168085
Seq. No.
                  LIB3234-052-P1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82512
                   538
BLAST score
                   3.0e-55
E value
Match length
                  109
                   43
% identity
                  ubiquitin precursor - rice (fragment)
NCBI Description
                   >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
```

sativa]

Seq. No. 168086

Seq. ID LIB3234-053-P1-K1-A12

Method BLASTX NCBI GI g1345973 BLAST score 223 E value 2.0e-18



Match length 62 74 % identity NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No.

168087

LIB3234-053-P1-K1-A2 Seq. ID

Method BLASTX g1345973 NCBI GI BLAST score 436 2.0e-43 E value Match length 92 90 % identity

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No.

168088

Seq. ID

LIB3234-053-P1-K1-A3 BLASTX

Method NCBI GI

g4406784

BLAST score E value

84

Match length

1.0e-4492

% identity

96

NCBI Description

(AC006532) putative oligopeptide transport protein

[Arabidopsis thaliana]

Seq. No.

168089

Seq. ID

LIB3234-053-P1-K1-A4

Method NCBI GI BLASTN g3449334

BLAST score

E value

311 1.0e-175

Match length

344

% identity

97

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.

168090

Seq. ID

LIB3234-053-P1-K1-A6

Method NCBI GI BLASTX g2541876

BLAST score



```
9.0e-17
E value
Match length
                  81
% identity
                  44
NCBI Description
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
                  [Nicotiana tabacum]
Seq. No.
                  168091
                  LIB3234-053-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120667
BLAST score
                  302
                  9.0e-28
E value
                  75
Match length
                  79
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi 166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  168092
Seq. ID
                  LIB3234-053-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  q2058313
BLAST score
                  405
E value
                  1.0e-39
                  98
Match length
                  78
% identity
NCBI Description (X97433) cinnamoyl-CoA reductase [Eucalyptus qunnii]
Seq. No.
                  168093
Seq. ID
                  LIB3234-053-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q4096078
BLAST score
                  354
E value
                  0.0e+00
Match length
                  378
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168094
Seq. ID
                  LIB3234-053-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2244841
BLAST score
                  273
```

E value 4.0e-24 Match length 104 % identity 56

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

168095 Seq. No.

Seq. ID LIB3234-053-P1-K1-B2

Method BLASTX NCBI GI g1864017

% identity

99



```
BLAST score
                  548
                  2.0e-56
E value
Match length
                  104
% identity
                  100
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. No.
                  168096
                  LIB3234-053-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4678371
BLAST score
                  229
E value
                  1.0e-126
Match length
                  289
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
                  (ESSA project)
Seq. No.
                  168097
Seq. ID
                  LIB3234-053-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2244841
BLAST score
                  261
E value
                  6.0e-23
Match length
                  97
% identity
                  57
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168098
                  LIB3234-053-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  117
E value
                  3.0e-59
Match length
                  319
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  168099
                  LIB3234-053-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558592
BLAST score
                  271
E value
                  5.0e-24
Match length
                  112
% identity
NCBI Description
                 (AC006555) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168100
Seq. ID
                  LIB3234-053-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g3702724
BLAST score
                  377
E value
                  0.0e+00
Match length
                  392
```

22750

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



```
K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168101
Seq. ID
                  LIB3234-053-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q136739
BLAST score
                  254
                  8.0e-35
E value
                  116
Match length
                  69
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  168102
Seq. No.
                  LIB3234-053-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244870
BLAST score
                  101
                  2.0e-49
E value
                  304
Match length
                  89
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  168103
Seq. No.
                  LIB3234-053-P1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2160132
BLAST score
                  43
E value
                  3.0e-15
Match length
                  140
                  63
% identity
NCBI Description
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
                  168104
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2947062
BLAST score
                  148
E value
                  2.0e-09
Match length
                  101
% identity
                   42
NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]
```

Seq. No. 168105

Seq. ID LIB3234-053-P1-K1-C9

Method BLASTX
NCBI GI g3176685
BLAST score 338
E value 8.0e-32
Match length 64
% identity 98

NCBI Description (AC003671) Strong similarity to spermidine synthase 1,

gb_Y08252 and possibly closer similarity to spermidine synthase 2 gb_Y08253 from Datura stramonium. ESTs gb_N38155, gb_T41738, gb_AA597626, gb_AA712967 and gb_AA712346 come from this ge

Seq. No. 168106

Seq. ID LIB3234-053-P1-K1-D11

Method BLASTN
NCBI GI g2264302
BLAST score 89
E value 2.0e-42
Match length 244
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 168107

Seq. ID LIB3234-053-P1-K1-D2

Method BLASTX
NCBI GI g4678299
BLAST score 601
E value 1.0e-62
Match length 121
% identity 98

NCBI Description (AL049655) cysteine proteinase precursor-like protein

[Arabidopsis thaliana]

Seq. No. 168108

Seq. ID LIB3234-053-P1-K1-D3

Method BLASTX
NCBI GI g1709970
BLAST score 355
E value 9.0e-34
Match length 101
% identity 69

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 168109

Seq. ID LIB3234-053-P1-K1-D4

Method BLASTN
NCBI GI g3668073
BLAST score 210
E value 1.0e-115
Match length 218
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T4C15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168110

Seq. ID LIB3234-053-P1-K1-D6

Method BLASTX
NCBI GI g2245048
BLAST score 410
E value 3.0e-40
Match length 129
% identity 67

NCBI Description (Z97342) resistance gene homolog [Arabidopsis thaliana]



```
Seq. No.
                   168111
                   LIB3234-053-P1-K1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4335711
BLAST score
                   226
E value
                   1.0e-124
                   375
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168112
                   LIB3234-053-P1-K1-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4468103
BLAST score
                   362
                   0.0e+00
E value
Match length
                   383
                   98
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                   (ESSA project)
                   168113
Seq. No.
                   LIB3234-053-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1749546
BLAST score
                   220
E value
                   6.0e-18
Match length
                   123
                   46
% identity
NCBI Description
                   (D89169) similar to Saccharomyces cerevisiae SCD6 protein,
                   SWISS-PROT Accession Number P45978 [Schizosaccharomyces
                   pombe]
Seq. No.
                   168114
Seq. ID
                   LIB3234-053-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   q4538918
BLAST score
                   338
E value
                   0.0e+00
Match length
                   366
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18
                   (ESSA project)
                  <sup>~</sup>168115
Seq. No.
Seq. ID
                   LIB3234-053-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   q4519195
BLAST score
                   55
```

E value 4.0e-22 Match length 223 % identity 81

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MQC12, complete sequence



```
168116
Seq. No.
                  LIB3234-053-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1491615
BLAST score
                  511
                  5.0e-52
E value
                  127
Match length
                  75
% identity
                  (X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  168117
Seq. No.
                  LIB3234-053-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4758634
BLAST score
                  158
                  4.0e-14
E value
                  84
Match length
                  42
% identity
                  Sec24p, S. Cerevisiae, homolog of
NCBI Description
                  >gi 1723050 sp P53992 Y079 HUMAN HYPOTHETICAL PROTEIN
                  KIAA0079 (HA3543) >gi_559717_dbj_BAA07558_ (D38555) The
                  ha3543 gene product is related to S.cerevisiae protein
                  encoded in chromosome VIII. [Homo sapiens]
                  >gi_4741921_gb_AAD28756.1_ (AF130464) sec24D protein [Homo
                  sapiens]
                  168118
Seq. No.
                  LIB3234-053-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2702284
                  45
BLAST score
                  5.0e-24
E value
Match length
                  71
                  92
% identity
NCBI Description
                  (AC003033) Argonaute (AG01)-like protein [Arabidopsis
                  thaliana]
                  168119
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                  65
E value
                  3.0e-28
Match length
                  205
                  91
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168120
Seq. No.
                  LIB3234-053-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757411
```

Method BLASTN
NCBI GI g4757411
BLAST score 34
E value 1.0e-09
Match length 238
% identity 79



```
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXC7, complete sequence
                  168121
Seq. No.
                  LIB3234-053-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363488
                  394
BLAST score
                  2.0e-38
E value
                  78
Match length
                  99
% identity
                  IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
                  168122
Seq. No.
                  LIB3234-053-P1-K1-G11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4589435
BLAST score
                  366
                  0.0e+00
E value
                  378
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOE17, complete sequence
                  168123
Seq. No.
                  LIB3234-053-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3386593
                  72
BLAST score
                  2.0e-32
E value
                  213
Match length
                  85
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168124
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1076660
BLAST score
                  308
E value
                  3.0e-28
                  95
Match length
% identity
                  69
                  D13F(MYBST1) protein - potato >gi_786426_bbs_159122
NCBI Description
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
```

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.

Seq. ID LIB3234-053-P1-K1-G4

168125

Method BLASTX NCBI GI g1170503 BLAST score 333 E value 7.0e-40



Match length 90 % identity 93

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)

>gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1

[Arabidopsis thaliana]

Seq. No. 168126

Seq. ID LIB3234-053-P1-K1-G5

Method BLASTX
NCBI GI g2160158
BLAST score 365
E value 5.0e-35
Match length 115
% identity 64

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb_EF1G_XENLA). ESTs gb T20564,gb T45940,gb T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 168127

Seq. ID LIB3234-053-P1-K1-G6

Method BLASTN
NCBI GI 93869069
BLAST score 53
E value 2.0e-21
Match length 113

Match length 113 % identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 168128

Seq. ID LIB3234-053-P1-K1-G8

Method BLASTN
NCBI GI g3150396
BLAST score 358
E value 0.0e+00
Match length 362
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168129

Seq. ID LIB3234-053-P1-K1-G9

Method BLASTN
NCBI GI g2914688
BLAST score 351
E value 0.0e+00
Match length 371
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168130

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Seq. ID LIB3234-053-P1-K1-H10

Method BLASTX NCBI GI g2651314

BLAST score

E value

125

7.0e-64



```
BLAST score
                  361
                  2.0e-34
E value
                  106
Match length
                  69
% identity
                  (AC002336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                  thaliana]
                  168131
Seq. No.
                  LIB3234-053-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  420
                  2.0e-41
E value
Match length
                  83
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343 emb_CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_2505871_emb CAA72909 (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                  qb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
Seq. No.
                  168132
                  LIB3234-053-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4038037
BLAST score
                  145
E value
                  4.0e-09
Match length
                  130
% identity
NCBI Description (AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168133
Seq. ID
                  LIB3234-053-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q166570
BLAST score
                  241
E value
                  2.0e-20
Match length
                  105
% identity
NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                  168134
Seq. ID
                  LIB3234-053-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  g3659491
```



Match length 264 % identity 89

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 168135

Seq. ID LIB3234-053-P1-K1-H7

Method BLASTX
NCBI GI g3913425
BLAST score 632
E value 3.0e-66
Match length 127
% identity 96

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 168136

Seq. ID LIB3234-053-P1-K1-H8

Method BLASTX
NCBI GI g4263713
BLAST score 287
E value 9.0e-26
Match length 124
% identity 52

NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 168137

Seq. ID LIB3234-053-P1-K1-H9

Method BLASTN
NCBI GI g2262135
BLAST score 164
E value 4.0e-87
Match length 216
% identity 54

NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15

cM, complete sequence

Seq. No. 168138

Seq. ID LIB3234-054-P1-K1-A1

Method BLASTX
NCBI GI g4262232
BLAST score 390
E value 7.0e-38
Match length 111
% identity 75

NCBI Description (AC006200) putative ribosomal protein L7 [Arabidopsis

thaliana]

Seq. No. 168139

Seq. ID LIB3234-054-P1-K1-A10

Method BLASTX
NCBI GI g3859606
BLAST score 677
E value 1.0e-71
Match length 123

Match length 12 % identity 98



51

78

Match length

% identity

```
(AF104919) contains similarity to cysteine proteases (Pfam:
NCBI Description
                  PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                  168140
Seq. No.
                  LIB3234-054-P1-K1-A11
Seg. ID
Method
                  BLASTX
                  g2459417
NCBI GI
                  404
BLAST score
                  2.0e-39
E value
                  124
Match length
% identity
                  69
                  (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                  [Arabidopsis thaliana]
                  168141
Seq. No.
                  LIB3234-054-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g452470
                  93
BLAST score
                  5.0e-18
E value
                  64
Match length
% identity
                  91
NCBI Description (U05218) ATP sulfurylase [Arabidopsis thaliana]
                  168142
Seq. No.
                  LIB3234-054-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  g1170503
NCBI GI
BLAST score
                  433
                  6.0e-43
E value
                  83
Match length
                  100
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                  >gi_322503_pir__JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                   (X65052) eukaryotic translation in Itiation factor 4A-I
                   [Arabidopsis thaliana]
                  168143
Seq. No.
                  LIB3234-054-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g1531762
NCBI GI
BLAST score
                  195
E value
                  5.0e-15
Match length
                  51
% identity
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
                  168144
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q4468806
BLAST score
                  212
E value
                  5.0e-17
```



```
NCBI Description
                 (AL035601) cytochrome P450 monooxygenase-like protein
                  [Arabidopsis thaliana]
                  168145
Seq. No.
                  LIB3234-054-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869072
BLAST score
                  36
                  5.0e-11
E value
Match length
                  72
% identity
                  88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJB24, complete sequence [Arabidopsis thaliana]
                  168146
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q2894598
BLAST score
                  532
                  2.0e-54
E value
Match length
                  126
% identity
                  86
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  168147
Seq. ID
                  LIB3234-054-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  g1448916
BLAST score
                  266
E value
                  1.0e-148
Match length
                  352
% identity
                  94
NCBI Description Arabidopsis thaliana threonine synthase mRNA, 3' end of cds
                  168148
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  452
                  4.0e-45
E value
Match length
                  90
% identity
                  96
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  168149
Seq. ID
                  LIB3234-054-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4325343
BLAST score
                  606
E value
                  3.0e-63
Match length
                  122
% identity
```

22760

NCBI Description (AF128393) contains similarity to homeobox domains (Pfam:



PF00046, Score, 36.5, E=6.9e-08, N=1) [Arabidopsis thaliana]

Seq. No. 168150 Seq. ID LIB3234-054-P1-K1-B3 Method BLASTN NCBI GI q1707006 BLAST score 365 0.0e+00 E value Match length 369 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168151 Seq. ID LIB3234-054-P1-K1-B4 Method BLASTN NCBI GI q1353238 BLAST score 36 9.0e-11 E value Match length 64 89 % identity Arabidopsis thaliana Col-O putative RNA helicase A mRNA, NCBI Description complete cds Seq. No. 168152 Seq. ID LIB3234-054-P1-K1-B5 Method BLASTN NCBI GI a4063730 BLAST score 146 E value 2.0e-76 Match length 378 % identity 98 NCBI Description Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana] Seq. No. 168153 Seq. ID LIB3234-054-P1-K1-B6 Method BLASTN NCBI GI g4063730 BLAST score 121 E value 2.0e-61 Match length 304 92 % identity Arabidopsis thaliana BAC F21J6 from chromosome V, NCBI Description containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana] Seq. No. 168154 Seq. ID LIB3234-054-P1-K1-B7 BLASTN Method NCBI GI g2924651 BLAST score 218 E value 1.0e-119 Match length 309 % identity 97

22761

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 168155 LIB3234-054-P1-K1-B8 Seq. ID Method BLASTX NCBI GI q1351272 BLAST score 416 6.0e-41E value 99 Match length 83 % identity TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 NCBI Description (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi 742408 prf 2009415A triose phosphate isomerase [Arabidopsis thaliana] 168156 Seq. No. LIB3234-054-P1-K1-B9 Seq. ID Method BLASTX NCBI GI g21911 BLAST score 178 5.0e-13E value Match length 73 % identity 44 NCBI Description (X62625) vicilin [Theobroma cacao] 168157 Seq. No. Seq. ID LIB3234-054-P1-K1-C1 Method BLASTX NCBI GI g4512697 BLAST score 226 1.0e-18 E value Match length 84 56 % identity NCBI Description (AC006569) unknown protein [Arabidopsis thaliana] Seq. No. 168158 Seq. ID LIB3234-054-P1-K1-C10 Method BLASTN g511598 NCBI GI BLAST score 368 E value 0.0e + 00372 Match length % identity 28 Arabidopsis thaliana cell wall protein (APTR-1) gene, NCBI Description complete cds Seq. No. 168159 Seq. ID LIB3234-054-P1-K1-C11 Method BLASTX NCBI GI q2662343 BLAST score 508 E value 1.0e-51 Match length 106 % identity 92

Seq. No. 168160

NCBI Description

(D63581) EF-1 alpha [Oryza sativa]



LIB3234-054-P1-K1-C12 Seq. ID Method BLASTN NCBI GI q4581103 BLAST score 152 5.0e-80 E value 276 Match length 100 % identity Arabidopsis thaliana chromosome II BAC T24I21 genomic NCBI Description sequence, complete sequence 168161 Seq. No. LIB3234-054-P1-K1-C2 Seq. ID BLASTX Method NCBI GI g4263777 529 BLAST score 3.0e-54E value Match length 113 87 % identity (AC006068) putative serine carboxypeptidase II [Arabidopsis NCBI Description thaliana] >gi 4510391 gb AAD21479.1 (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana] Seq. No. 168162 LIB3234-054-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g1710780 BLAST score 411 E value 2.0e-40 110 Match length 73 % identity 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433 NCBI Description (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina] 168163 Seq. No. LIB3234-054-P1-K1-C4 Seq. ID Method BLASTN NCBI GI q511598 BLAST score 343 0.0e + 00E value 375 Match length % identity Arabidopsis thaliana cell wall protein (APTR-1) gene, NCBI Description complete cds 168164 Seq. No. Seq. ID LIB3234-054-P1-K1-C5 Method BLASTX NCBI GI q4406764

Method BLASTX
NCBI GI 94406764
BLAST score 306
E value 3.0e-37
Match length 86
% identity 58

NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis

thaliana]

Seq. No. 168165



```
LIB3234-054-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3985958
BLAST score
                  215
                  1.0e-117
E value
Match length
                  380
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168166
                  LIB3234-054-P1-K1-C7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3292807
BLAST score
                  345
                  0.0e+00
E value
Match length
                  377
                  97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                  (ESSAII project)
                  168167
Seq. No.
                  LIB3234-054-P1-K1-C8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3292807
BLAST score
                  294
E value
                  1.0e-164
Match length
                  374
                  94
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
                  (ESSAII project)
                  168168
Seq. No.
                  LIB3234-054-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135406
BLAST score
                  519
E value
                  5.0e-53
                  97
Match length
% identity
                  100
NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                  168169
Seq. ID
                  LIB3234-054-P1-K1-D1
```

Method BLASTX NCBI GI q4056502 BLAST score 516 E value 1.0e-52 Match length 102 % identity

NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 168170

Seq. ID LIB3234-054-P1-K1-D10



Method BLASTN g2696018 NCBI GI 337 BLAST score 0.0e+00E value Match length 369 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXC9, complete sequence [Arabidopsis thaliana]

168171 Seq. No.

LIB3234-054-P1-K1-D12 Seq. ID

Method BLASTN NCBI GI g2959729 BLAST score 308 E value 1.0e-173 312 Match length % identity 100

NCBI Description Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No. 168172

LIB3234-054-P1-K1-D2 Seq. ID

Method BLASTN NCBI GI g4115930 BLAST score 290 E value 1.0e-162 Match length 378 % identity 94

NCBI Description Arabidopsis thaliana BAC T4B21

168173 Seq. No.

LIB3234-054-P1-K1-D3 Seq. ID

Method BLASTX NCBI GI g3335169 BLAST score 534 E value 8.0e-55 Match length 103

% identity 97

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 168174

Seq. ID LIB3234-054-P1-K1-D4

Method BLASTN NCBI GI g3241920 BLAST score 228 E value 1.0e-125 Match length 374 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAE1, complete sequence [Arabidopsis thaliana]

Seq. No. 168175

Seq. ID LIB3234-054-P1-K1-D5

Method BLASTN NCBI GI g2947056 BLAST score 350



```
E value
                     0.0e + 00
Match length
                     374
% identity
                     87
                    Arabidopsis thaliana chromosome II BAC T20F6 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                     168176
Seq. No.
Seq. ID
                    LIB3234-054-P1-K1-D6
Method
                    BLASTX
NCBI GI
                     q1703108
BLAST score
                     543
E value
                     8.0e-56
Match length
                     100
                     100
% identity
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                     thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                     thaliana]
                     168177
Seq. No.
Seq. ID
                    LIB3234-054-P1-K1-D8
Method
                    BLASTX
NCBI GI
                     g1737492
BLAST score
                     281
E value
                     4.0e-25
Match length
                     91
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                     168178
Seq. ID
                    LIB3234-054-P1-K1-D9
Method
                    BLASTX
NCBI GI
                     q2924784
BLAST score
                    98
E value
                     1.0e-03
Match length
                    111
                     13
% identity
NCBI Description (AC002334) similar to jasmonate inducible protein
                     [Arabidopsis thaliana]
                     168179
Seq. No.
Seq. ID
                    LIB3234-054-P1-K1-E1
                    BLASTX
Method
NCBI GI
                     g3413716
BLAST score
                     364
E value
                     8.0e-35
                     80
Match length
```

% identity

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana] >qi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]

168180 Seq. No.

Seq. ID LIB3234-054-P1-K1-E10

Method BLASTX NCBI GI g1107501



BLAST score 410 3.0e-40E value Match length 116 72 % identity

(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) NCBI Description Match to gb X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb AA394824 come from

this gene. [Arabidopsis thaliana]

168181 Seq. No.

LIB3234-054-P1-K1-E11 Seq. ID

Method BLASTN NCBI GI g2914688 BLAST score 189 1.0e-102 E value 319 Match length 94 % identity

Arabidopsis thaliana chromosome II BAC F24L7 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

168182 Seq. No.

LIB3234-054-P1-K1-E2 Seq. ID

Method BLASTX NCBI GI g4678285 374 BLAST score E value 5.0e-36 Match length 122

% identity 58

(AL049660) putative protein [Arabidopsis thaliana] NCBI Description

168183 Seq. No.

LIB3234-054-P1-K1-E4 Seq. ID

BLASTX Method NCBI GI g1107501 BLAST score 408 E value 5.0e-40Match length 109 % identity 75

(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) NCBI Description

Match to gb X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 168184

Seq. ID LIB3234-054-P1-K1-E5

Method BLASTN NCBI GI q3695372 BLAST score 272 E value 1.0e-151 Match length 347 95 % identity

NCBI Description Arabidopsis thaliana BAC F1104

Seq. No. 168185

Seq. ID LIB3234-054-P1-K1-E6

Method BLASTN NCBI GI g3046847



```
BLAST score
                  124
                  2.0e-63
E value
                  327
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                  KI1J9, complete sequence [Arabidopsis thaliana]
                  168186
Seq. No.
                  LIB3234-054-P1-K1-E7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3928074
BLAST score
                  49
                  1.0e-18
E value
                  60
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T7F6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168187
Seq. No.
                  LIB3234-054-P1-K1-E9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4432811
BLAST score
                  349
                  0.0e+00
E value
                   361
Match length .
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16D14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168188
                  LIB3234-054-P1-K1-F1
Seq. ID
Method
                  BLASTX
                   g3128169
NCBI GI
                   95
BLAST score
E value
                  1.0e-17
Match length
                  91
% identity
                   54
                 (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168189
                  LIB3234-054-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3925363
BLAST score
                   148
                   2.0e-09
E value
Match length
                   120
% identity
NCBI Description
                  (AF067961) homeodomain protein [Malus domestica]
                   168190
Seq. No.
Seq. ID
                   LIB3234-054-P1-K1-F2
Method
                  BLASTN
NCBI GI
                   q1245181
BLAST score
                   359
E value
                   0.0e + 00
```

22768

374

99

Match length % identity



complete cds

```
168191
Seq. No.
                  LIB3234-054-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g1109697
NCBI GI
BLAST score
                  610
                  1.0e-63
E value
                  125
Match length
% identity
                  92
                 (X83380) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168192
                  LIB3234-054-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4063568
BLAST score
                  627
                  1.0e-65
E value
Match length
                  125
                  100
% identity
NCBI Description
                  (AF035916) ATP synthase beta subunit [Triplochlamys
                  multiflora]
                  168193
Seq. No.
                  LIB3234-054-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g3445209
NCBI GI
BLAST score
                  146
                  9.0e-10
E value
                  38
Match length
                  68
% identity
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana]
                  168194
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-F8
                  BLASTX
Method
NCBI GI
                  q3335169
BLAST score
                  583
E value
                  2.0e-60
Match length
                  112
% identity
                  98
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  168195
Seq. ID
                  LIB3234-054-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q131398
BLAST score
                  479
E value
                  2.0e-48
Match length
                  113
% identity
                  86
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi 72714_pir__F2MU10 photosystem II 10K protein precursor
```

NCBI Description Arabidopsis thaliana sterol delta-7 reductase (ST7R) mRNA,



- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

 Seq. No.
 168196

 Seq. ID
 LIB3234-054-P1-K1-G1

 Method
 BLASTN

 NCBI GI
 g4337186

 BLAST score
 212

 E value
 1.0e-116

Match length 376 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168197

Seq. ID LIB3234-054-P1-K1-G11

Method BLASTX
NCBI GI g132074
BLAST score 574
E value 2.0e-59
Match length 106
% identity 99

% identity 99 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 168198

Seq. ID LIB3234-054-P1-K1-G4

Method BLASTN
NCBI GI g2696018
BLAST score 346
E value 0.0e+00
Match length 358
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 168199

Seq. ID LIB3234-054-P1-K1-G5

Method BLASTX
NCBI GI g1335862
BLAST score 613
E value 5.0e-64
Match length 126
% identity 94

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 168200

Seq. ID LIB3234-054-P1-K1-G6

Method BLASTN NCBI GI g2618602



```
BLAST score
                   186
                   1.0e-100
E value
                   186
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   168201
Seq. No.
                   LIB3234-054-P1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g133729
BLAST score
                   317
                   2.0e-29
E value
Match length
                   80
                   79
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi 70941 pir R3NT11
                   ribosomal protein S11 - common tobacco chloroplast
                   >gi_11861_emb_CAA77377_ (Z00044) ribosomal protein S11
[Nicotiana tabacum] >gi_225229_prf__1211235BL ribosomal
                   protein S11 [Nicotiana tabacum]
Seq. No.
                   168202
                   LIB3234-054-P1-K1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2864607
BLAST score
                   247
E value
                   1.0e-137
Match length
                   297
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                    (ESSAII project)
                   168203
Seq. No.
                   LIB3234-054-P1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4589433
BLAST score
                    370
E value
                    0.0e + 00
                    378
Match length
                    99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNI5, complete sequence
Seq. No.
                    168204
                   LIB3234-054-P1-K1-H11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3193305
BLAST score
                   153
E value
                    1.0e-80
```

Match length 327 % identity 80

NCBI Description Arabidopsis thaliana BAC F3D13

Seq. No. 168205

Seq. ID LIB3234-054-P1-K1-H12

Method BLASTN NCBI GI g2924257



```
BLAST score
                  65
                  5.0e-28
E value
                  93
Match length
                  92
% identity
NCBI Description
                 Tobacco chloroplast genome DNA
Seq. No.
                  168206
                  LIB3234-054-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1279568
BLAST score
                  41
                  9.0e-14
E value
                  49
Match length
                  96
% identity
NCBI Description Nicotiana acuminata chloroplast JLB region, 1-250bp
                  168207
Seq. No.
                  LIB3234-054-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529680
BLAST score
                  496
                  3.0e-50
E value
Match length
                  114
% identity
                  49
                  (AC002535) putative protein disulfide-isomerase precursor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  168208
                  LIB3234-054-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g122781
BLAST score
                  202
E value
                  8.0e-16
Match length
                  52
                  69
% identity
                  POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)
NCBI Description
                  >gi_82210_pir__A05198 hypothetical protein 229 - common
                  tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044)
                  hypothetical protein [Nicotiana tabacum]
                  >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]
Seq. No.
                  168209
                  LIB3234-054-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351061
BLAST score
                  197
E value
                  1.0e-107
Match length
                  351
```

% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAF19, complete sequence [Arabidopsis thaliana]

Seq. No. 168210

Seq. ID LIB3234-054-P1-K1-H8

Method BLASTX NCBI GI g1628583 BLAST score 639



```
4.0e-67
E value
Match length
                   124
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  168211
                  LIB3234-054-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                   35
E value
                   4.0e-10
                   67
Match length
                  88
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSL1, complete sequence [Arabidopsis thaliana]
                   168212
Seq. No.
                  LIB3234-055-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2605714
BLAST score
                   489
E value
                   2.0e-49
Match length
                  115
% identity
                   83
NCBI Description
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
                  168213
Seq. No.
                  LIB3234-055-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2351062
BLAST score
                   383
                   0.0e+00
E value
                   383
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

Match length

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 168214 Seq. ID LIB3234-055-P1-K1-A12

Method BLASTN NCBI GI g4159712 BLAST score 156 E value 2.0e-82 291 Match length

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 168215

% identity

Seq. ID LIB3234-055-P1-K1-A2

96

Method BLASTX NCBI GI g3850816 BLAST score 378 E value 2.0e-36



Match length 79 % identity 85

NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza

sativa]

Seq. No. 168216

Seq. ID LIB3234-055-P1-K1-A3

Method BLASTN
NCBI GI g2760165
BLAST score 59
E value 2.0e-24
Match length 301
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 168217

Seq. ID LIB3234-055-P1-K1-A4

Method BLASTX
NCBI GI g4585989
BLAST score 175
E value 1.0e-12
Match length 85
% identity 48

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 168218

Seq. ID LIB3234-055-P1-K1-A6

Method BLASTX
NCBI GI g1345973
BLAST score 439
E value 1.0e-43
Match length 99
% identity 82

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 168219

Seq. ID LIB3234-055-P1-K1-A8

Method BLASTX
NCBI GI g4704766
BLAST score 66
E value 3.0e-26
Match length 124
% identity 46

NCBI Description (AF131223) protein disulfide isomerase homolog; PDI

[Datisca glomerata]

Seq. No. 168220

Seq. ID LIB3234-055-P1-K1-B1



Method BLASTN
NCBI GI g2842474
BLAST score 140
E value 3.0e-73
Match length 156
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 168221

Seq. ID LIB3234-055-P1-K1-B10

Method BLASTX
NCBI GI g112740
BLAST score 260
E value 1.0e-22
Match length 115
% identity 51

NCBI Description NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)

>gi 81691 pir A25997 napin precursor (napA) - rape

>gi 167153 (J02586) prepronapin [Brassica napus] >gi 167155

(J02798) napin [Brassica napus]

Seq. No. 168222

Seq. ID LIB3234-055-P1-K1-B12

Method BLASTX
NCBI GI g1711382
BLAST score 289
E value 5.0e-26
Match length 97
% identity 48

NCBI Description SET PROTEIN >gi 940889 (U30470) SET [Drosophila

melanogaster]

Seq. No. 168223

Seq. ID LIB3234-055-P1-K1-B2

Method BLASTX
NCBI GI g2129532
BLAST score 330
E value 8.0e-31
Match length 93
% identity 71

NCBI Description acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -

Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis

thaliana]

Seq. No. 168224

Seq. ID LIB3234-055-P1-K1-B3

Method BLASTX
NCBI GI g4006924
BLAST score 587
E value 6.0e-61
Match length 129
% identity 88

NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]



```
Seq. No.
                       168225
    Seq. ID
                      LIB3234-055-P1-K1-B4
Method
                      BLASTN
    NCBI GI
                       g4662609
    BLAST score
                      254
                       1.0e-141
    E value
                      287
    Match length
    % identity
                       97
    NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,
                       complete sequence
                       168226
    Seq. No.
    Seq. ID
                      LIB3234-055-P1-K1-B5
    Method
                      BLASTN
    NCBI GI
                       q4662609
    BLAST score
                       258
    E value
                       1.0e-143
                       287
    Match length
    % identity
                       98
                      Genomic sequence for Arabidopsis thaliana BAC F10A5,
    NCBI Description
                       complete sequence
                       168227
    Seq. No.
  Seq. ID
                      LIB3234-055-P1-K1-B6
    Method
                      BLASTX
    NCBI GI
                       g4734006
    BLAST score
                       152
    E value
                       6.0e-10
    Match length
                      62
    % identity
                       48
    NCBI Description (AC007178) hypothetical protein [Arabidopsis thaliana]
    Seq. No.
                       168228
    Seq. ID
                      LIB3234-055-P1-K1-B7
    Method
                      BLASTN
    NCBI GI
                       g2264306
    BLAST score
                      304
    E value
                       1.0e-170
    Match length
                       336
    % identity
                       98
    NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                      MBK5, complete sequence [Arabidopsis thaliana]
    Seq. No.
                       168229
    Seq. ID
                      LIB3234-055-P1-K1-B8
    Method
                      BLASTX
    NCBI GI
                      g3023848
```

BLAST score 612 E value 6.0e-64

Match length 126 59 % identity

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE NCBI Description

PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis

thaliana]

Seq. No. 168230

E value

7.0e-58



LIB3234-055-P1-K1-B9

Seq. ID

```
Method
                   BLASTX
NCBI GI
                   q498038
BLAST score
                   235
E value
                   5.0e-20
Match length
                   85
% identity
NCBI Description (L33792) lipid transfer protein [Senecio odorus]
Seq. No.
                   168231
Seq. ID
                   LIB3234-055-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q498038
BLAST score
                   504
E value
                   3.0e-51
Match length
                   127
% identity
                   76
NCBI Description (L33792) lipid transfer protein [Senecio odorus]
Seq. No.
                  168232
Seq. ID
                  LIB3234-055-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  q4309747
BLAST score
                   60
E value
                   3.0e-25
Match length
                  179
% identity
                   72
NCBI Description Arabidopsis thaliana chromosome II BAC T13E11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168233
Seq. ID
                  LIB3234-055-P1-K1-C12
Method
                  BLASTN
NCBI GI
                   g2244991
BLAST score
                  195
E value
                  1.0e-105
Match length
                  389
% identity
                   98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  168234
Seq. ID
                  LIB3234-055-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2058311
BLAST score
                  410
E value
                  3.0e-40
                  99
Match length
                  78
% identity
NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
Seq. No.
                  168235
Seq. ID
                  LIB3234-055-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g3449332
BLAST score
                  115
```



```
Match length
                   317
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSF19, complete sequence [Arabidopsis thaliana]
                  168236
Seq. No.
                  LIB3234-055-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3641835
                   289
BLAST score
E value
                  1.0e-162
Match length
                  346
% identity
                   96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
                   (ESSAII project)
                   168237
Seq. No.
Seq. ID
                  LIB3234-055-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4454032
                   343
BLAST score
E value
                   2.0e-32
Match length
                  111
                   62
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  168238
                  LIB3234-055-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3461814
BLAST score
                   687
E value
                   1.0e-72
Match length
                   128
% identity
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168239
                   LIB3234-055-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1526424
BLAST score
                   338
E value
                   6.0e-32
                  79
Match length
% identity
NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]
Seq. No.
                   168240
Seq. ID
                  LIB3234-055-P1-K1-C8
Method
                  BLASTX
NCBI GI
                   g1041704
BLAST score
                   206
E value
                   2.0e-16
```

78 Match length 56 % identity

NCBI Description (U30478) expansin At-EXP5 [Arabidopsis thaliana]

Seq. No. 168241

Match length

% identity

80



```
LIB3234-055-P1-K1-C9
Seq. ID
                  BLASTN
Method
NCBI GI
                 - g4309747
BLAST score
                   372
E value
                   0.0e+00
Match length
                   376
                   39
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T13E11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168242
Seq. ID
                  LIB3234-055-P1-K1-D10
Method
                  BLASTX
                  g3023848
NCBI GI
BLAST score
                  552
E value
                   6.0e-57
Match length
                  108
                   57
% identity
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thaliana]
                  168243
Seq. No.
Seq. ID
                  LIB3234-055-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4586241
BLAST score
                  155
                   9.0e-82
E value
Match length
                  218
% identity
                   92
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                   (ESSA project)
                   168244
Seq. No.
Seq. ID
                  LIB3234-055-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q4263771
BLAST score
                   283
E value
                   3.0e-25
Match length
                  73
% identity
                   68
NCBI Description
                  (AC006218) putative nonspecific lipid-transfer protein
                   precursor [Arabidopsis thaliana]
                   >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
                   nonspecific lipid-transfer protein precursor [Arabidopsis
                   thaliana]
Seq. No.
                  168245
Seq. ID
                  LIB3234-055-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3850816
BLAST score
                  415
E value
                   9.0e-41
```

22779

NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza

```
sativa]
Seq. No.
                  168246
Seq. ID
                  LIB3234-055-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g4589450
                                                           - ولايسا
BLAST score
                  174
E value
                   4.0e-93
Match length
                   370
% identity
                   96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T31K7, complete sequence
                  168247
Seq. No.
                  LIB3234-055-P1-K1-D7
Seq. ID
Method
                  BLASTN
                  g3047074
NCBI GI
BLAST score
                   300
E value
                  1.0e-168
Match length
                  370
% identity
                  94
NCBI Description Arabidopsis thaliana BAC F21E10
                  168248
Seq. No.
                  LIB3234-055-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  575
                  1.0e-59
E value
Match length
                  128
% identity
                   88
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  168249
Seq. ID
                  LIB3234-055-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  q4589439
BLAST score
                   237
```

E value 1.0e-131 Match length 305 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 168250

Seq. ID LIB3234-055-P1-K1-E12

Method BLASTX NCBI GI g267073 BLAST score 572 E value 3.0e-59 Match length 104 % identity 100

TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin NCBI Description

beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No.

Seq. ID

168256

LIB3234-055-P1-K1-F12



```
Seg. No.
                   168251
 Seq. ID
                   LIB3234-055-P1-K1-E2
 Method
                   BLASTN
 NCBI GI
                   g2160132
 BLAST score
                   374
 E value
                   0.0e + 00
 Match length
                   390
 % identity
                   99
 NCBI Description Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168252
 Seq. ID
                   LIB3234-055-P1-K1-E3
 Method
                   BLASTX
 NCBI GI
                   g3327204
 BLAST score
                   372
 E value
                   9.0e-36
 Match length
                   128
 % identity
                   57
 NCBI Description (AB014595) KIAA0695 protein [Homo sapiens]
 Seq. No.
                   168253
 Seq. ID
                   LIB3234-055-P1-K1-E4
 Method
                   BLASTX
 NCBI GI
                   q3461828
 BLAST score
                   186
. E value
                   6.0e-14
 Match length
                   119
 % identity
 NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   168254
 Seq. ID
                   LIB3234-055-P1-K1-F10
 Method
                   BLASTX
 NCBI GI
                   g3264778
 BLAST score
                   365
 E value
                   6.0e-35
 Match length
                   123
 % identity
                   66
 NCBI Description (AF072536) H-protein promoter binding factor-1 [Arabidopsis
                   thaliana]
                   168255
 Seq. No.
 Seq. ID
                   LIB3234-055-P1-K1-F11
 Method
                   BLASTX
 NCBI GI
                   g1628583
 BLAST score
                   646
 E value
                   7.0e-68
 Match length
                   127
 % identity
                   98
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
```



Method BLASTN
NCBI GI g3193311
BLAST score 392
E value 0.0e+00
Match length 392
% identity 100

NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 168257

Seq. ID LIB3234-055-P1-K1-F2

Method BLASTX
NCBI GI g1480347
BLAST score 207
E value 2.0e-16
Match length 109
% identity 48

NCBI Description (X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]

Seq. No. 168258

Seq. ID LIB3234-055-P1-K1-F5

Method BLASTX
NCBI GI g3193310
BLAST score 621
E value 6.0e-65
Match length 131
% identity 94

NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1

(GB:Y07563) [Arabidopsis thaliana]

Seq. No. 168259

Seq. ID LIB3234-055-P1-K1-F7

Method BLASTX
NCBI GI g3335169
BLAST score 671
E value 8.0e-71
Match length 125
% identity 100

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 168260

Seq. ID LIB3234-055-P1-K1-F8

Method BLASTX
NCBI GI g3660471
BLAST score 301
E value 2.0e-27
Match length 97
% identity 62

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 168261

Seq. ID LIB3234-055-P1-K1-G1

Method BLASTN NCBI GI g547390 BLAST score 333



E value 0.0e+00 Match length 341 % identity 99

NCBI Description Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No. 168262

Seq. ID LIB3234-055-P1-K1-G11

Method BLASTN
NCBI GI g2924731
BLAST score 330
E value 0.0e+00
Match length 381
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSI17, complete sequence [Arabidopsis thaliana]

Seq. No. 168263

Seq. ID LIB3234-055-P1-K1-G2

Method BLASTX
NCBI GI g1107501
BLAST score 378
E value 2.0e-36
Match length 119
% identity 66

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 168264

Seq. ID LIB3234-055-P1-K1-G3

Method BLASTX
NCBI GI g4204299
BLAST score 649
E value 3.0e-68
Match length 126
% identity 100

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 168265

Seq. ID LIB3234-055-P1-K1-G4

Method BLASTX
NCBI GI g2160151
BLAST score 555
E value 3.0e-57
Match length 112
% identity 99

NCBI Description (AC000375) Strong similarity to Brassica aspartic protease

(gb X77260). [Arabidopsis thaliana]

Seq. No. 168266

Seq. ID LIB3234-055-P1-K1-G5

Method BLASTX
NCBI GI g4583544
BLAST score 440
E value 1.0e-43



```
90
Match length
                   91
% identity
                   (Z95637) acyl-CoA:1-acylglycerol-3-phosphate
NCBI Description
                   acyltransferase [Brassica napus]
Seq. No.
                   168267
                   LIB3234-055-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3461828
BLAST score
                   154
E value
                   3.0e-10
                   88
Match length
% identity
                   40
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   168268
                   LIB3234-055-P1-K1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2760164
BLAST score
                   380
                   0.0e+00
E value
Match length
                   396
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168269
                   LIB3234-055-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2342723
BLAST score
                   179
E value
                   3.0e-13
                   104
Match length
% identity
                   36
NCBI Description
                  (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   168270
Seq. ID
                   LIB3234-055-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q3292836
BLAST score
                   455
E value
                   2.0e-45
Match length
                   94
                   99
% identity
NCBI Description
                   (AL031018) gamma-glutamylcysteine synthetase [Arabidopsis
                   thaliana] >gi_4262277_gb_AAD14544_ (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]
Seq. No.
                   168271
                   LIB3234-055-P1-K1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2564048
BLAST score
                   368
```

E value 0.0e+00Match length 380 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

% identity

NCBI Description



MKD15, complete sequence [Arabidopsis thaliana]

168272 Seq. No. LIB3234-055-P1-K1-H8 Seq. ID Method BLASTX NCBI GI g1864017 586 BLAST score 7.0e-61 E value 112 Match length 99 % identity (D63396) elongation factor-1 alpha [Nicotiana tabacum] NCBI Description 168273 Seq. No. LIB3234-056-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g114330 BLAST score 578 5.0e-60 E value 115 Match length 97 % identity PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) NCBI Description >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35) type 1, plasma membrane - Arabidopsis thaliana >gi 166746 (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis thaliana] Seq. No. 168274 LIB3234-056-P1-K1-A10 Seq. ID Method BLASTX g2289006 NCBI GI BLAST score 469 E value 4.0e-47Match length 106 88 % identity NCBI Description (AC002335) glutathione perosidase isolog [Arabidopsis thaliana] 168275 Seq. No. LIB3234-056-P1-K1-A12 Seq. ID Method BLASTN NCBI GI g2864607 BLAST score 166 E value 2.0e-88 Match length 326 100 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 NCBI Description (ESSAII project) Seq. No. 168276 Seq. ID LIB3234-056-P1-K1-A2 Method BLASTX NCBI GI q2160151 BLAST score 336 E value 6.0e-40 Match length 90

(AC000375) Strong similarity to Brassica aspartic protease



(gb_X77260). [Arabidopsis thaliana]

Seq. No. 168277

Seq. ID LIB3234-056-P1-K1-A3

Method BLASTN
NCBI GI g2760164
BLAST score 386
E value 0.0e+00
Match length 394
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18P6, complete sequence [Arabidopsis thaliana]

Seq. No. 168278

Seq. ID LIB3234-056-P1-K1-A6

Method BLASTN
NCBI GI 94757401
BLAST score 137
E value 5.0e-71
Match length 375
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 168279

Seq. ID LIB3234-056-P1-K1-A7

Method BLASTX
NCBI GI g1345973
BLAST score 570
E value 5.0e-59
Match length 110
% identity 93

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 168280

Seq. ID LIB3234-056-P1-K1-A8

Method BLASTN
NCBI GI g2760164
BLAST score 209
E value 1.0e-114
Match length 251
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18P6, complete sequence [Arabidopsis thaliana]

Seq. No. 168281

Seq. ID LIB3234-056-P1-K1-B1

Method BLASTX NCBI GI g2924784



```
BLAST score 98
E value 1.0e-03
Match length 114
% identity 13
```

NCBI Description (AC002334) similar to jasmonate inducible protein

[Arabidopsis thaliana]

Seq. No. 168282

Seq. ID LIB3234-056-P1-K1-B10

Method BLASTX
NCBI GI g3819099
BLAST score 268
E value 1.0e-23
Match length 129
% identity 46

NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No. 168283

Seq. ID LIB3234-056-P1-K1-B11

Method BLASTX
NCBI GI 94650842
BLAST score 636
E value 1.0e-66
Match length 126
% identity 96

NCBI Description (AB026185) elongation factor 2 [Lithospermum erythrorhizon]

Seq. No. 168284

Seq. ID LIB3234-056-P1-K1-B2

Method BLASTX
NCBI GI g133872
BLAST score 329
E value 1.0e-30
Match length 84
% identity 73

NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)

>gi_282838_pir__S26494 ribosomal protein S1, chloroplast spinach >gi_322404_pir__A44121 small subunit ribosomal
protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi_170143 (M82923) chloroplast ribosomal protein S1

[Spinacia oleracea]

Seq. No. 168285

Seq. ID LIB3234-056-P1-K1-B3

Method BLASTX
NCBI GI g2961390
BLAST score 188
E value 3.0e-14
Match length 47
% identity 79

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 168286

Seq. ID LIB3234-056-P1-K1-B4

Method BLASTN



```
NCBI GI
                  g4185128
BLAST score
                  162
                  5.0e-86
E value
                   311
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II P1 MSF3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168287
Seq. No.
                  LIB3234-056-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2398679
BLAST score
                   460
                   5.0e-46
E value
                  113
Match length
                   77
% identity
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                   synthase [Morinda citrifolia]
                  168288
Seq. No.
                  LIB3234-056-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2088638
BLAST score
                   170
                   9.0e-91
E value
Match length
                   246
                   92
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   168289
Seq. No.
                   LIB3234-056-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g70644
                   531
BLAST score
E value
                   2.0e-54
Match length
                   109
% identity
                   19
NCBI Description ubiquitin precursor - common sunflower (fragment)
                   168290
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   q2828182
BLAST score
                   362
E value
                   0.0e + 00
Match length
                   370
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168291
```

Seq. ID LIB3234-056-P1-K1-C11

Method BLASTN
NCBI GI g2914688
BLAST score 182
E value 5.0e-98



Match length 289 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168292

Seq. ID LIB3234-056-P1-K1-C12

Method BLASTN
NCBI GI g3406034
BLAST score 191
E value 1.0e-103
Match length 261
% identity 94

NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 168293

Seq. ID LIB3234-056-P1-K1-C2

Method BLASTX
NCBI GI g4507433
BLAST score 190
E value 2.0e-14
Match length 114
% identity 39

NCBI Description testis enhanced gene transcript

>gi_1729891_sp_P55061_TEGT_HUMAN TEGT PROTEIN (TESTIS ENHANCED GENE TRANSCRIPT) >gi 2136254 pir I38334 TEGT

(testis enhanced gene transcript) - human

>gi_458545_emb_CAA53472_ (X75861) TEGT [Homo sapiens]

Seq. No. 168294

Seq. ID LIB3234-056-P1-K1-C3

Method BLASTX
NCBI GI g1698690
BLAST score 623
E value 4.0e-65
Match length 131
% identity 90

NCBI Description (U67317) beta-ketoacyl-ACP synthase II [Cuphea wrightii]

Seq. No. 168295

Seq. ID LIB3234-056-P1-K1-C4

Method BLASTX
NCBI GI g166570
BLAST score 230
E value 4.0e-19
Match length 103
% identity 48

NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No. 168296

Seq. ID LIB3234-056-P1-K1-C5

Method BLASTX
NCBI GI g4454032
BLAST score 155
E value 1.0e-10
Match length 87



```
52
% identity
NCBI Description
                  (AL035394) putative protein [Arabidopsis thaliana]
                  168297
Seq. No.
                  LIB3234-056-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3927822
BLAST score
                  229
                  1.0e-126
E value
Match length
                  295
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168298
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-C9
Method
                  BLASTX
                  g2244979
NCBI GI
BLAST score
                  374
                  8.0e-49
E value
Match length
                  114
% identity
                  92
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168299
Seq. ID
                  LIB3234-056-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g2435510
BLAST score
                  299
                  1.0e-167
E value
Match length
                  388
                  93
% identity
NCBI Description Arabidopsis thaliana BAC TM017A05
Seq. No.
                  168300
Seq. ID
                  LIB3234-056-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  34
E value
                  1.0e-09
Match length
                  132
                  86
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                   (ESSA project)
Seq. No.
                  168301
Seq. ID
                  LIB3234-056-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3819099
BLAST score
                  265
E value
                  3.0e-23
Match length
                  121
% identity
                   46
```

Seq. No. 168302

22790

NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]



LIB3234-056-P1-K1-D3 Seq. ID ${\tt BLASTX}$ Method NCBI GI q3335169 BLAST score 692 E value 3.0e-73Match length 131 98 % identity (AF067857) embryo-specific protein 1 [Arabidopsis thaliana] NCBI Description >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] 168303 Seq. No. LIB3234-056-P1-K1-D5 Seq. ID Method BLASTN NCBI GI g4159708 BLAST score 370 E value 0.0e+00378 Match length 93 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence 168304 Seq. No. LIB3234-056-P1-K1-D6 Seq. ID Method BLASTN NCBI GI q4115912 BLAST score 45 E value 4.0e-16 Match length 148 % identity 45 NCBI Description Arabidopsis thaliana BAC F3H7 168305 Seq. No. LIB3234-056-P1-K1-D7 Seq. ID Method BLASTX NCBI GI q2501296 BLAST score 253 E value 9.0e-22 Match length 118 % identity 41 DNA GYRASE SUBUNIT B >qi 1652801 dbj BAA17720 (D90908) DNA NCBI Description gyrase B subunit [Synechocystis sp.] Seq. No. 168306 LIB3234-056-P1-K1-D8 Seq. ID Method BLASTX NCBI GI g3157937 BLAST score 562 E value 5.0e-58

Match length 117 88 % identity

NCBI Description (AC002131) Identical to aspartic proteinase cDNA qb U51036

from A. thaliana. ESTs gb N96313, gb T21893, gb R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591,

gb AA728734, gb

Seq. No.

Seq. ID

168312

LIB3234-056-P1-K1-E4



```
Seq. No.
                   168307
                   LIB3234-056-P1-K1-E1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4589439
BLAST score
                   186
E value
                   1.0e-100
                   270
Match length
                   94
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQM1, complete sequence
Seq. No.
                   168308
                   LIB3234-056-P1-K1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220644
BLAST score
                   48
E value
                   7.0e-18
Match length
                   261
                   86
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MXL8, complete sequence [Arabidopsis thaliana]
                   168309
Seq. No.
                   LIB3234-056-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1531762
BLAST score
                   170
E value
                   4.0e-12
Match length
                   47
                   74
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   168310
Seq. No.
                   LIB3234-056-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1654140
BLAST score
                   467
E value
                   7.0e-47
Match length
                   129
% identity
                   67
NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]
Seq. No.
                   168311
                   LIB3234-056-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q135467
BLAST score
                   590
E value
                   3.0e-61
Match length
                   107
                   100
% identity
NCBI Description
                   TUBULIN BETA-4 CHAIN >gi 2129546 pir S68122 beta-tubulin 4
                   - Arabidopsis thaliana >\overline{g}i 16664\overline{0} (M\overline{21}415) beta-tubulin
                   [Arabidopsis thaliana]
```

Seq. ID

Method

NCBI GI



```
Method
                  BLASTN
NCBI GI
                   q3763944
BLAST score
                   116
E value
                   2.0e-58
Match length
                   324
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
NCBI Description
                   (ESSAII project)
                   168313
Seq. No.
                  LIB3234-056-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g82263
BLAST score
                   280
                   6.0e-25
E value
Match length
                   62
                   81
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                   c1 precursor (clone pC(1)3II) - potato
                   168314
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g3869067
BLAST score
                   271
E value
                   1.0e-151
Match length
                   404
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168315
                  LIB3234-056-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204298
BLAST score
                   510
E value
                   5.0e-52
Match length
                   96
% identity
                   100
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   168316
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g3522936
BLAST score
                   575
E value
                   2.0e-59
Match length
                   118
% identity
NCBI Description
                   (AC004411) putative alcohol dehydrogenase [Arabidopsis
                   thaliana]
                   168317
Seq. No.
```

22793

LIB3234-056-P1-K1-F1

BLASTN

g2924257

```
BLAST score
                   52
E value
                   3.0e-20
Match length
                  179
% identity
                   93
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                   168318
Seq. ID
                  LIB3234-056-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g170354
BLAST score
                  542
E value
                   1.0e-55
Match length
                  111
% identity
                  20
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                  168319
Seq. ID
                  LIB3234-056-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q2829914
BLAST score
                  111
E value
                   9.0e-34
Match length
                  80
% identity
                  97
NCBI Description (AC002291) putative peroxidase [Arabidopsis thaliana]
                  168320
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1335862
BLAST score
                  610
E value
                  1.0e-63
Match length
                  124
% identity
                  96
NCBI Description (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                  168321
Seq. ID
                  LIB3234-056-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  261
E value
                  1.0e-145
Match length
                  325
                  94
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
                  168322
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  237
E value
                  7.0e-20
Match length
                  113
% identity
                  42
```

NCBI Description vicilin gene B [Saguinus oedipus]



```
Seq. No.
                  168323
                  LIB3234-056-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548847
BLAST score
                  387
                  2.0e-37
E value
Match length
                  77
                  99
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi_1086182_pir__S39501 ribosomal protein S12 -
                  curled-leaved tobacco >gi 225248 prf 1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
                  168324
Seq. No.
                  LIB3234-056-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4713943
BLAST score
                  55
E value
                  4.0e-22
Match length
                  156
% identity
                  90
NCBI Description Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
                  complete sequence
Seq. No.
                  168325
                  LIB3234-056-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4454447
                  89
BLAST score
                  5.0e-43
E value
Match length
                  93
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168326
Seq. ID
                  LIB3234-056-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q4455262
BLAST score
                  157
E value
                  5.0e-83
                  336
Match length
% identity
                  87
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
```

Seq. No. 168327

Seq. ID LIB3234-056-P1-K1-G11

Method BLASTN
NCBI GI g3402747
BLAST score 204
E value 1.0e-111
Match length 215
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22

(ESSAII project)



```
Seq. No.
                   168328
Seq. ID
                   LIB3234-056-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   q3402747
BLAST score
                   39
E value
                   1.0e-12
Match length
                   67
                   97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22
                   (ESSAII project)
                   168329
Seq. No.
                   LIB3234-056-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1107501
BLAST score
                   204
E value
                   2.0e-16
Match length
                   79
                   57
% identity
NCBI Description
                   (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                   Match to gb X91954 orf gene product from A. thaliana. ESTs
                   gb_Z17604, \overline{\text{gb}}_{\text{H}}76594, gb_AA597972 and gb_AA394824 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   168330
Seq. ID
                   LIB3234-056-P1-K1-G4
Method
                   BLASTN
                   g4206762
NCBI GI
BLAST score
                   124
E value
                   2.0e-63
Match length
                   234
% identity
NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker
                   protein homolog (CWLP) mRNA, complete cds
Seq. No.
                   168331
                   LIB3234-056-P1-K1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4678266
BLAST score
                   48
E value
                   4.0e-18
Match length
                   115
% identity
                   91
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
                   (ESSA project)
Seq. No.
                   168332
Seq. ID
                   LIB3234-056-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   q4468103
BLAST score
                   382
E value
                   0.0e+00
```

Match length 390 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)



```
Seq. No.
                   168333
Seq. ID
                  LIB3234-056-P1-K1-G8
Method
                  BLASTX
                  g4510397
NCBI GI
BLAST score
                  649
E value
                   3.0e-68
Match length
                  127
% identity
                   97
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  168334
Seq. ID
                  LIB3234-056-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2924514
BLAST score
                  422
E value
                  1.0e-41
Match length
                  82
% identity
                  98
NCBI Description (AL022023) protein kinase-like [Arabidopsis thaliana]
                  168335
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q4510397
BLAST score
                  702
E value
                  2.0e-74
Match length
                  132
% identity
                  99
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  168336
Seq. ID
                  LIB3234-056-P1-K1-H10
Method
                  BLASTN
                  g4455262
NCBI GI
BLAST score
                  375
E value
                  0.0e + 00
Match length
                  383
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
Seq. No.
                  168337
Seq. ID
                  LIB3234-056-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g3402745
BLAST score
                  116
E value
                  1.0e-58
                  204
Match length
% identity
                  89
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                  (ESSAII project)
Seq. No.
                  168338
```

Seq. ID LIB3234-056-P1-K1-H12

Method BLASTX NCBI GI g4415934 BLAST score 150

% identity

79



```
E value
                   7.0e-10
Match length
                   87
% identity
                   45
NCBI Description
                  (AC006418) putative auxin response factor 1 [Arabidopsis
                   thaliana]
Seq. No.
                   168339
Seq. ID
                   LIB3234-056-P1-K1-H2
Method
                  BLASTX
NCBI GI
                   q4558592
BLAST score
                   481
E value
                   2.0e-48
Match length
                   129
                   75
% identity
NCBI Description (AC006555) hypothetical protein [Arabidopsis thaliana]
                   168340
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4558592
BLAST score
                   74
E value
                   2.0e-22
Match length
                   122
% identity
NCBI Description (AC006555) hypothetical protein [Arabidopsis thaliana]
                   168341
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g481131
BLAST score
                   563
E value
                   4.0e-58
Match length
                   108
% identity
                   100
NCBI Description
                  sucrose transport protein SUC2 - Arabidopsis thaliana
                   >gi_407092_emb_CAA53150_ (X75382) sucrose-proton symporter
                   [Arabidopsis thaliana]
Seq. No.
                   168342
Seq. ID
                   LIB3234-056-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g2827529
BLAST score
                   347
E value
                   8.0e-33
Match length
                  114
% identity
                   69
NCBI Description (AL021633) putative protein [Arabidopsis thaliana]
Seq. No.
                   168343
Seq. ID
                  LIB3234-057-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  g1345973
BLAST score
                  398
E value
                  8.0e-39
Match length
                  94
```

22798

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No. 168344 Seq. ID LIB3234-057-P1-K1-A3 Method BLASTN NCBI GI q4469002 BLAST score 218 E value 1.0e-119 Match length 246 96 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 168345

Seq. ID LIB3234-057-P1-K1-A4

Method BLASTN
NCBI GI g2351068
BLAST score 368
E value 0.0e+00
Match length 372
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRH10, complete sequence [Arabidopsis thaliana]

Seq. No. 168346

Seq. ID LIB3234-057-P1-K1-A5

Method BLASTX
NCBI GI g2499973
BLAST score 385
E value 3.0e-37
Match length 95
% identity 83

NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)

>gi_1465366_emb_CAA66701_ (X98078) photosystem II

[Arabidopsis thaliana]

Seq. No. 168347

Seq. ID LIB3234-057-P1-K1-A7

Method BLASTX
NCBI GI g3822036
BLAST score 289
E value 5.0e-26
Match length 124
% identity 47

NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 168348

Seq. ID LIB3234-057-P1-K1-A8

Method BLASTX NCBI GI g4490333

Match length

% identity

125

75



```
BLAST score
                   401
                   3.0e-39
E value
                   92
Match length
% identity
                  86
NCBI Description
                  (AL035656) EF-Hand containing protein-like [Arabidopsis
                  thaliana]
                  168349
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g1592677
BLAST score
                  289
                  5.0e-26
E value
                  103
Match length
% identity
                  60
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                  168350
Seq. No.
                  LIB3234-057-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266989
BLAST score
                  475
E value
                  7.0e-48
Match length
                  125
                  75
% identity
NCBI Description
                  GTP-BINDING PROTEIN SAR1B >gi_322517_pir__$28603
                  GTP-binding protein - Arabidopsis thaliana >gi 166734
                   (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  168351
Seq. ID
                  LIB3234-057-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2842481
BLAST score
                  177
E value
                   6.0e-13
Match length
                  107
% identity
NCBI Description (AL021749) extensin-like protein [Arabidopsis thaliana]
Seq. No.
                  168352
Seq. ID
                  LIB3234-057-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  54
E value
                  2.0e-21
Match length
                  200
% identity
                  94
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  168353
Seq. ID
                  LIB3234-057-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2769642
BLAST score
                  514
E value
                  2.0e-52
```



NCBI Description (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon esculentum1 Seq. No. 168354 Seq. ID LIB3234-057-P1-K1-B3 Method BLASTX NCBI GI g3808062 BLAST score 143 E value 7.0e-09 Match length 61 % identity 44 NCBI Description (AB019195) PV100 [Cucurbita maxima] Seq. No. 168355 Seq. ID LIB3234-057-P1-K1-B4 Method BLASTN NCBI GI q2244747 BLAST score 344 E value 0.0e+00Match length 379 % identity 98 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No Seq. No. 168356 Seq. ID LIB3234-057-P1-K1-B6 Method BLASTX NCBI GI g1362003 BLAST score 635 E value 1.0e-66 Match length 125 % identity 98 NCBI Description protein phosphatase 2A B regulatory chain 55K - Arabidopsis thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of phosphatase $\overline{2}A$ [Arabidopsis thaliana] Seq. No. 168357 Seq. ID LIB3234-057-P1-K1-B7 Method BLASTN NCBI GI q4314374 BLAST score 229 E value 1.0e-126 Match length 323 % identity 25 NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168358 Seq. ID LIB3234-057-P1-K1-B9 Method BLASTX NCBI GI g3600054 BLAST score 478 E value 3.0e-48Match length 109 % identity 84

22801

NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                   168359
 Seq. ID
                   LIB3234-057-P1-K1-C10
 Method
                   BLASTX
 NCBI GI
                   g2511725
 BLAST score
                   649
 E value
                   3.0e-68
Match length
                   124
 % identity
                   100
NCBI Description (AF021937) catalase 1 [Arabidopsis thaliana]
Seq. No.
                   168360
 Seq. ID
                   LIB3234-057-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g3510347
BLAST score
                   288
E value
                   1.0e-161
Match length
                   378
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168361
Seq. ID
                   LIB3234-057-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g4539466
BLAST score
                   190
E value
                   2.0e-14
Match length
                   70
% identity
                   51
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                   168362
Seq. ID
                  LIB3234-057-P1-K1-C2
Method
                  BLASTN
NCBI GI
                   g3242700
BLAST score
                  293
E value
                   1.0e-164
Match length
                  377
% identity
                   95
NCBI Description Arabidopsis thaliana chromosome II BAC F26B6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168363
Seq. ID
                  LIB3234-057-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g4589950
BLAST score
                  179
E value
                  5.0e-96
Match length
                  355
% identity
                  94
NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic
                  sequence, complete sequence
Seq. No.
                  168364
Seq. ID
                  LIB3234-057-P1-K1-C5
Method
                  BLASTX
```

22802

q3236248

BLAST score 545 E value 5.0e-56 Match length 124 % identity 84

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 168365

Seq. ID LIB3234-057-P1-K1-C7

Method BLASTN
NCBI GI g2924257
BLAST score 30
E value 3.0e-07
Match length 148
% identity 91

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 168366

Seq. ID LIB3234-057-P1-K1-C8

Method BLASTX
NCBI GI g3913437
BLAST score 613
E value 5.0e-64
Match length 123
% identity 95

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 168367

Seq. ID LIB3234-057-P1-K1-C9

Method BLASTN
NCBI GI g3046855
BLAST score 48
E value 6.0e-18
Match length 271

% identity 83 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:

MSL1, complete sequence [Arabidopsis thaliana]

Seq. No. 168368

Seq. ID LIB3234-057-P1-K1-D10

Method BLASTX
NCBI GI g122781
BLAST score 267
E value 2.0e-23
Match length 70
% identity 71

NCBI Description POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)

>gi_82210_pir__A05198 hypothetical protein 229 - common tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044)

hypothetical protein [Nicotiana tabacum]

>gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]

Seq. No. 168369

Seq. ID LIB3234-057-P1-K1-D12

Method BLASTX

Seq. No.

Seq. ID

168374

LIB3234-057-P1-K1-D7

```
NCBI GI
                    g2129653
 BLAST score
                   286
 E value
                   1.0e-25
 Match length
                   125
 % identity
                   58
 NCBI Description
                   myosin heavy chain MYA2 - Arabidopsis thaliana
                   >gi_499047_emb_CAA84066_ (Z34293) myosin [Arabidopsis
                   thaliana]
 Seq. No.
                   168370
 Seq. ID
                   LIB3234-057-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g4321496
BLAST score
                   149
E value
                   9.0e-37
Match length
                   122
% identity
                   66
NCBI Description (AF049898) gibberellin 20-oxidase-1; 20ox-1 [Lycopersicon
                   esculentum]
Seq. No.
                   168371
Seq. ID
                   LIB3234-057-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q4582446
BLAST score
                   499
E value
                   1.0e-50
Match length
                   123
% identity
                   78
NCBI Description (AC007071) putative RING finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   168372
Seq. ID
                  LIB3234-057-P1-K1-D5
Method
                  BLASTX
NCBI GI
                   g116527
BLAST score
                   514
E value
                   2.0e-52
Match length
                  112
% identity
                  87
NCBI Description
                 PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)
                  >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum]
                  >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease
                  proteolytic subuni [Nicotiana tabacum]
Seq. No.
                  168373
Seq. ID
                  LIB3234-057-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4490333
BLAST score
                  82
E value
                  2.0e-49
Match length
                  124
% identity
                  85
NCBI Description
                  (AL035656) EF-Hand containing protein-like [Arabidopsis
                  thaliana]
```

```
Method
                   BLASTN
 NCBI GI
                   q2924257
 BLAST score
                   68
 E value
                   8.0e-30
Match length
                   214
 % identity
                   91
NCBI Description Tobacco chloroplast genome DNA
 Seq. No.
                   168375
Seq. ID
                   LIB3234-057-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g4204298
BLAST score
                   545
E value
                   5.0e-56
Match length
                   104
% identity
                   99
NCBI Description (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   168376
Seq. ID
                   LIB3234-057-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q2244835
BLAST score
                   300
E value
                   2.0e-30
Match length
                   71
% identity
                   100
NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
Seq. No.
                   168377
Seq. ID
                   LIB3234-057-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   g2494106
BLAST score
                   189
E value
                   1.0e-102
Match length
                   335
% identity
                   91
NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                  168378
Seq. ID
                  LIB3234-057-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  126
E value
                  2.0e-64
Match length
                  366
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                  MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168379
Seq. ID
                  LIB3234-057-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1170503
BLAST score
                  407
E value
                  7.0e-40
```

% identity

98

```
Match length
                    81
 % identity
                    96
NCBI Description
                    EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                    >gi_322503_pir__JC1452 translation initiation factor
                    eIF-4A1 - Arabidopsis thaliana >gi_16554 emb CAA46188
                    (X65052) eukaryotic translation in \overline{\text{i}} tiation factor 4A-\overline{1}
                    [Arabidopsis thaliana]
Seq. No.
                    168380
Seq. ID
                    LIB3234-057-P1-K1-E2
Method
                   BLASTX
NCBI GI
                    g2623303
BLAST score
                    118
E value
                    5.0e-06
Match length
                   119
% identity
NCBI Description (AC002409) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   168381
Seq. ID
                   LIB3234-057-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   548
E value
                   2.0e-56
Match length
                   106
% identity
                   98
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168382
Seq. ID
                   LIB3234-057-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g4519671
BLAST score
                   224
E value
                   2.0e-18
Match length
                   69
% identity
                   70
NCBI Description (AB017693) transfactor [Nicotiana tabacum]
Seq. No.
                   168383
Seq. ID
                   LIB3234-057-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g4757401
BLAST score
                   369
E value
                   0.0e+00
                   381
Match length
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGH6, complete sequence
Seq. No.
                   168384
Seq. ID
                   LIB3234-057-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g3075383
BLAST score
                   348
E value
                   0.0e+00
Match length
                   375
```

```
NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168385
 Seq. ID
                   LIB3234-057-P1-K1-E8
 Method
                   BLASTX
 NCBI GI
                   g2244749
 BLAST score
                   549
 E value
                   2.0e-56
 Match length
                   106
 % identity
                   98
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
 Seq. No.
                   168386
                   LIB3234-057-P1-K1-E9
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g1864017
BLAST score
                   547
E value
                   3.0e-56
Match length
                   109
% identity
                   96
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168387
Seq. ID
                   LIB3234-057-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g1931636
BLAST score
                   144
E value
                   3.0e-75
Match length
                   351
% identity
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.
                   168388
Seq. ID
                   LIB3234-057-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g1755162
BLAST score
                   625
E value
                   2.0e-65
Match length
                   122
% identity
                   97
NCBI Description (U75192) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  168389
Seq. ID
                  LIB3234-057-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2583106
BLAST score
                  259
E value
                  1.0e-144
Match length
                  356
% identity
                  93
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168390
Seq. ID
                  LIB3234-057-P1-K1-F3
Method
                  BLASTX
```

```
NCBI GI
                   g2129642
 BLAST score
                   600
 E value
                   2.0e-62
Match length
                   116
 % identity
NCBI Description
                   major latex protein type 3 - Arabidopsis thaliana
                   >gi 1107495 emb CAA63027 (X91961) major latex protein
                   type3 [Arabidopsis thaliana]
Seq. No.
                   168391
Seq. ID
                   LIB3234-057-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2642430
BLAST score
                   207
E value
                   2.0e-16
Match length
                   37
% identity
                   100
NCBI Description
                  (AC002391) putative AP2 domain containing protein
                   [Arabidopsis thaliana]
Seq. No.
                   168392
Seq. ID
                   LIB3234-057-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q112743
BLAST score
                   651
E value
                   2.0e-68
Match length
                   122
% identity
                   98
                   2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -
                   Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                   4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869
                   (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                   >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                   168393
Seq. ID
                  LIB3234-057-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  434
E value
                   5.0e-43
Match length
                  86
% identity
NCBI Description
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
                  thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  168394
Seq. ID
                  LIB3234-057-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  289
E value
                  5.0e-26
Match length
                  91
% identity
                  64
NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
```

Seq. No.

Seq. ID

168400

LIB3234-057-P1-K1-G5

```
(L40954) oleosin [Arabidopsis thaliana]
 Seq. No.
                   168395
 Seq. ID
                   LIB3234-057-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g4106930
BLAST score
                   69
E value
                   5.0e-20
Match length
                   80
% identity
                   66
NCBI Description (AF114794) succinate:cytochrome c oxidoreductase subunit 2
                   [Porphyra purpurea]
Seq. No.
                   168396
Seq. ID
                   LIB3234-057-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   g4691223
BLAST score
                   140
E value
                   8.0e-73
Match length
                   383
% identity
                   98
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
Seq. No.
                   168397
Seq. ID
                   LIB3234-057-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g2827529
BLAST score
                   280
E value
                   5.0e-25
Match length
                   80
% identity
                   78
NCBI Description (AL021633) putative protein [Arabidopsis thaliana]
Seq. No.
                   168398
Seq. ID
                  LIB3234-057-P1-K1-G2
Method
                  BLASTX
NCBI GI
                   g2832625
BLAST score
                  213
E value
                   4.0e-17
Match length
                  62
% identity
                   63
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  168399
Seq. ID
                  LIB3234-057-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g4432793
BLAST score
                  145
E value
                  8.0e-76
Match length
                  165
% identity
                  97
NCBI Description Arabidopsis thaliana chromosome II BAC T19K21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. ID

Method

```
Method
                    BLASTN
NCBI GI
                    q2739359
BLAST score
                    73
E value
                    8.0e-33
Match length
                    200
% identity
                    86
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T9J22 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168401
Seq. ID
                    LIB3234-057-P1-K1-G6
Method
                    BLASTX
NCBI GI
                    q4432845
BLAST score
                    145
E value
                    3.0e-09
Match length
                    63
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                    168402
Seq. ID
                   LIB3234-057-P1-K1-G8
Method
                   BLASTN
NCBI GI
                    q3985957
BLAST score
                    367
E value
                    0.0e + 00
Match length
                    371
% identity
                    100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168403
Seq. ID
                   LIB3234-057-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3023799
BLAST score
                   157
E value
                   1.0e-10
Match length
                   63
% identity
                   48
NCBI Description
                   DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_1118003 (U40768)
                   dihydroneopterin aldolase [Staphylococcus haemolyticus] >gi_1586495_prf__2204217C dihydroneopterin aldolase
                   [Staphylococcus haemolyticus]
Seq. No.
                   168404
Seq. ID
                   LIB3234-057-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   g2160132
BLAST score
                   92
E value
                   3.0e-44
Match length
                   231
% identity
                   86
NCBI Description
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168405
```

22810

LIB3234-057-P1-K1-H11

BLASTX

Match length

% identity

113

```
NCBI GI
                    q860891
BLAST score
                    456
E value
                    1.0e-45
Match length
                    92
% identity
                    95
NCBI Description
                    (X87636) PSII cytochome b559 alpha chain [Beta vulgaris]
                    >gi_860897_emb_CAA60972_ (X87637) PSII cytochrome b599
                    alpha chain [Beta vulgaris]
Seq. No.
                    168406
Seq. ID
                    LIB3234-057-P1-K1-H12
Method
                    BLASTN
NCBI GI
                    q2656032
BLAST score
                    192
E value
                    1.0e-104
Match length
                    318
% identity
                    100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
Seq. No.
                   168407
Seq. ID
                   LIB3234-057-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g1345973
BLAST score
                   421
E value
                   2.0e-41
Match length
                   95
% identity
NCBI Description
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   >gi_541882_pir_JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   168408
Seq. ID
                   LIB3234-057-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   g4220641
BLAST score
                   234
E value
                   1.0e-129
                   361
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168409
Seq. ID
                   LIB3234-057-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g544012
BLAST score
                   206
E value
                   3.0e-16
```

NCBI Description BASIC ENDOCHITINASE >gi 487030 pir S37341 chitinase (EC 3.2.1.14) chi14 - tomato (fragment) >gi_388509_emb_CAA78843_ (Z15138) chitinase [Lycopersicon esculentum] Seq. No. 168410 Seq. ID LIB3234-057-P1-K1-H5 Method BLASTX NCBI GI g116343 BLAST score 206 E value 3.0e-16 Match length 101 % identity 41 NCBI Description BASIC ENDOCHITINASE PRECURSOR Seq. No. 168411 Seq. ID LIB3234-057-P1-K1-H7 Method BLASTN NCBI GI g4199934 BLAST score 261 E value 1.0e-145 Match length 355 % identity 92 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana] Seq. No. 168412 Seq. ID LIB3234-057-P1-K1-H8 Method BLASTX NCBI GI q4588001 BLAST score 523 E value 2.0e-53 Match length 124 % identity 77 NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana] Seq. No. 168413 Seq. ID LIB3234-057-P1-K1-H9 Method BLASTX NCBI GI g2135333 BLAST score 268 E value 1.0e-23 Match length 108 % identity 48 NCBI Description Hep27 protein - human >gi_1079566 (U31875) Hep27 protein [Homo sapiens] Seq. No. 168414 Seq. ID LIB3234-058-P1-K1-A10 Method BLASTN NCBI GI g2264302 BLAST score 204 E value 1.0e-111 Match length 375 % identity 97 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 168415 Seq. ID LIB3234-058-P1-K1-A11 Method BLASTN NCBI GI g2924729 BLAST score 173 E value 2.0e-92 Match length 303 % identity 95 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana] Seq. No. 168416 Seq. ID LIB3234-058-P1-K1-A12 Method BLASTX NCBI GI g4204277 BLAST score 538 E value 3.0e-55 Match length 109 % identity 94 NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana] Seq. No. 168417 Seq. ID LIB3234-058-P1-K1-A2 Method BLASTX NCBI GI q135858 BLAST score 263 E value 5.0e-23 Match length 52 % identity 100 NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana] Seq. No. 168418 Seq. ID LIB3234-058-P1-K1-A3 Method BLASTN NCBI GI g3426033 BLAST score 251

E value 1.0e-139 Match length 375 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168419

Seq. ID LIB3234-058-P1-K1-A4

Method BLASTN NCBI GI g2191126 BLAST score 143 E value 8.0e-75Match length 179

Match length

% identity

101

88

```
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                   168420
Seq. ID
                   LIB3234-058-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   g4539415
BLAST score
                   374
E value
                   0.0e + 00
Match length
                   374
% identity
                   72
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                   project)
Seq. No.
                   168421
Seq. ID
                   LIB3234-058-P1-K1-A6
Method
                   BLASTN
NCBI GI
                   g3176694
BLAST score
                   376
E value
                   0.0e+00
Match length
                   380
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168422
Seq. ID
                   LIB3234-058-P1-K1-A7
Method
                   BLASTN
NCBI GI
                   g4027862
BLAST score
                   245
E value
                   1.0e-135
Match length
                   297
% identity
                   98
NCBI Description Arabidopsis thaliana chromosome 1 BAC T7A14 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                   168423
Seq. ID
                  LIB3234-058-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  388
E value
                   1.0e-37
Match length
                  111
% identity
                  71
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  168424
Seq. ID
                  LIB3234-058-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g2264307
BLAST score
                  49
E value
                  2.0e-18
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MED24, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    168425
 Seq. ID
                    LIB3234-058-P1-K1-B11
Method
                   BLASTX
NCBI GI
                    g1346523
BLAST score
                    386
E value
                    2.0e-37
Match length
                   78
 % identity
                    94
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                   ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                   >gi_1084428_pir__S49491 methionine adenosyltransferase (EC
                   2.5.1.6) - garden petunia >gi_559506 emb CAA57696 (X82214)
                   methionine adenosyltransferase [Petunia x hybrida]
Seq. No.
                   168426
Seq. ID
                   LIB3234-058-P1-K1-B12
Method
                   BLASTN
NCBI GI
                   g2827513
BLAST score
                   79
E value
                   2.0e-36
Match length
                   155
% identity
                   88
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
                   (ESSAII project)
Seq. No.
                   168427
Seq. ID
                   LIB3234-058-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g2244837
BLAST score
                   623
E value
                   3.0e-65
Match length
                   123
                   100
% identity
NCBI Description (Z97337) proteasome chain protein [Arabidopsis thaliana]
                   >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535)
                   20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
Seq. No.
                   168428
Seq. ID
                   LIB3234-058-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g2493696
BLAST score
                   322
E value
                   7.0e-30
Match length
                   86
% identity
                   67
NCBI Description HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204)
                  ORF185; hypothetical 21.4 kD protein [Brassica oleracea]
Seq. No.
                  168429
Seq. ID
                  LIB3234-058-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q4510392
BLAST score
                  350
```



```
E value
                    0.0e + 00
Match length
                    378
% identity
                    99
NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic
                    sequence, complete sequence
Seq. No.
                    168430
Seq. ID
                    LIB3234-058-P1-K1-B6
Method
                    BLASTN
NCBI GI
                    q4191760
BLAST score
                    261
E value
                    1.0e-145
Match length
                    285
% identity
                    54
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17F8,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                    168431
Seq. ID
                   LIB3234-058-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q120675
BLAST score
                   454
E value
                   2.0e-45
Match length
                   104
% identity
                   84
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi 21143 emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   168432
Seq. ID
                   LIB3234-058-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g1402904
BLAST score
                   515
E value
                   1.0e-52
Match length
                   99
% identity
                   97
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                   168433
Seq. ID
                   LIB3234-058-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4835234
BLAST score
                   407
E value
                   7.0e-40
Match length
                   82
% identity
NCBI Description
                  (AL049862) putative cold acclimation protein [Arabidopsis
                   thaliana]
```

Seq. No. 168434 Seq. ID LIB323

Seq. ID LIB3234-058-P1-K1-C12

Method BLASTX
NCBI GI g2459446
BLAST score 540

Match length

96

```
E value
                   2.0e-55
Match length
                   127
% identity
                   84
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   168435
Seq. ID
                   LIB3234-058-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3915847
BLAST score
                   379
E value
                   1.0e-36
Match length
                   83
% identity
                   89
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                   40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                   168436
Seq. ID
                   LIB3234-058-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g2828180
BLAST score
                   37
E value
                   2.0e-11
Match length
                   252
% identity
                   90
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168437
Seq. ID
                  LIB3234-058-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  142
E value
                   5.0e-74
Match length
                  325
% identity
                  85
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  168438
Seq. ID
                  LIB3234-058-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4455323
BLAST score
                  648
E value
                  4.0e-68
Match length
                  126
% identity
                  99
NCBI Description
                  (AL035525) aminopeptidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  168439
Seq. ID
                  LIB3234-058-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g16231
BLAST score
                  80
E value
                  1.0e-37
```

```
% identity
 NCBI Description
                   Arabidopsis CRA1 gene for 12S seed storage protein
                   >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage
                   protein CRA1 gene, exons 1-4
 Seq. No.
                   168440
 Seq. ID
                   LIB3234-058-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g4510397
BLAST score
                   634
E value
                   2.0e-66
Match length
                   139
% identity
                   89
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                   168441
Seq. ID
                   LIB3234-058-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g3250696
BLAST score
                   198
E value
                   2.0e-15
Match length
                   70
% identity
                   26
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                   168442
Seq. ID
                   LIB3234-058-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g3250696
BLAST score
                   226
E value
                   1.0e-18
Match length
                   92
% identity
                   27
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                   168443
Seq. ID
                   LIB3234-058-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q1694976
BLAST score
                   290
E value
                   3.0e-26
Match length
                  85
% identity
                  71
NCBI Description
                  (Y09482) HMG1 [Arabidopsis thaliana]
                  >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                  thalianal
Seq. No.
                  168444
Seq. ID
                  LIB3234-058-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g135858
BLAST score
                  501
E value
                  7.0e-51
Match length
                  120
% identity
                  82
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
```

Arabidopsis thaliana >gi_16182 emb CAA45114 (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf 1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

Seq. No.

168445

Seq. ID LIB3234-058-P1-K1-D4

Method BLASTX NCBI GI q119350 BLAST score 549 E value 2.0e-56 Match length 107 % identity 97

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase); identical to P25696

[Arabidopsis thaliana]

Seq. No. 168446

Seq. ID LIB3234-058-P1-K1-D5

Method BLASTX NCBI GI g120667 . BLAST score 471 E value 2.0e-47 Match length 105 % identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi_166706 (M64116) cystolic

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No. 168447

Seq. ID LIB3234-058-P1-K1-D6

Method BLASTN NCBI GI g3068702 BLAST score 95 E value 6.0e-46Match length 95 % identity 100

NCBI Description Arabidopsis thaliana putative transmembrane protein Glp

(AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No. 168448

Seq. ID LIB3234-058-P1-K1-D8

Method BLASTX NCBI GI g1352463 BLAST score 490

BLAST score

165

```
E value
                    1.0e-49
Match length
                    109
 % identity
                    88
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312
NCBI Description
                    (U04876) myo-inositol-1-phosphate synthase \overline{\mbox{(Arabidopsis)}}
                    thaliana]
Seq. No.
                    168449
                   LIB3234-058-P1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3985957
BLAST score
                    247
E value
                    1.0e-136
Match length
                   381
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168450
Seq. ID
                   LIB3234-058-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g1402904
BLAST score
                   463
E value
                   8.0e-67
Match length
                   127
% identity
                   96
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                   168451
Seq. ID
                   LIB3234-058-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   q4006885
BLAST score
                   308
E value
                   1.0e-173
Match length
                   383
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No
Seq. No.
                   168452
Seq. ID
                   LIB3234-058-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g3834314
BLAST score
                   580
E value
                   4.0e-60
Match length
                   123
% identity
                   91
NCBI Description
                   (AC005679) Similar to gene pi010 glycosyltransferase
                   gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs
                   gb T46079 and gb AA394466 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   168453
Seq. ID
                   LIB3234-058-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1695719
```

```
E value
                   1.0e-11
Match length
                   77
 % identity
                   57
NCBI Description (D89342) luminal binding protein [Arabidopsis thaliana]
Seq. No.
                   168454
Seq. ID
                   LIB3234-058-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g4158219
BLAST score
                   188
E value
                   3.0e-14
Match length
                   58
% identity
                   66
NCBI Description (Y18623) amylogenin [Oryza sativa]
Seq. No.
                  168455
Seq. ID
                  LIB3234-058-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  553
E value
                  6.0e-57
Match length
                  108
% identity
                  100
NCBI Description (AC003027) lcl prt_seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  168456
Seq. ID
                  LIB3234-058-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                  455
E value
                  2.0e-45
Match length
                  107
% identity
                  84
NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis
                  thalianal
Seq. No.
                  168457
Seq. ID
                  LIB3234-058-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g135858
BLAST score
                  276
E value
                  2.0e-24
Match length
                  54
% identity
                  100
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                  thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                  [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                  intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                  168458
Seq. ID
                  LIB3234-058-P1-K1-F1
Method
                  BLASTX
NCBI GI
```

22821

g1718097



BLAST score 352 E value 2.0e-33 Match length 101 % identity 61

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)

(41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir_A55016

lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar

ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No. 168459

Seq. ID LIB3234-058-P1-K1-F10

Method BLASTX
NCBI GI g1345973
BLAST score 668
E value 2.0e-70
Match length 116
% identity 100

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 168460

Seq. ID LIB3234-058-P1-K1-F11

Method BLASTN
NCBI GI g3869073
BLAST score 383
E value 0.0e+00
Match length 383
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKN22, complete sequence [Arabidopsis thaliana]

Seq. No. 168461

Seq. ID LIB3234-058-P1-K1-F3

Method BLASTX
NCBI GI g4559339
BLAST score 494
E value 4.0e-50
Match length 127
% identity 78

NCBI Description (AC007087) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 168462

Seq. ID LIB3234-058-P1-K1-F6

Method BLASTN
NCBI GI g1931636
BLAST score 365
E value 0.0e+00
Match length 389

```
% identity
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
                   168463
Seq. ID
                   LIB3234-058-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g4314369
BLAST score
                   511
E value
                   4.0e-52
Match length
                   113
% identity
                   94
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168464
Seq. ID
                   LIB3234-058-P1-K1-F8
Method
                   BLASTN
NCBI GI
                   g4512656
BLAST score
                   368
E value
                   0.0e+00
Match length
                   380
% identity
                   92
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic
                   sequence, complete sequence
Seq. No.
                   168465
Seq. ID
                   LIB3234-058-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3176708
BLAST score
                   410
E value
                   4.0e-40
Match length
                  80
% identity
                   97
NCBI Description
                  (AC002392) putative proline-rich protein APG [Arabidopsis
                  thaliana]
Seq. No.
                  168466
Seq. ID
                  LIB3234-058-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g4454585
BLAST score
                  133
E value
                  1.0e-68
Match length
                  377
% identity
                  91
NCBI Description Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5
                  cM, complete sequence
Seq. No.
                  168467
Seq. ID
                  LIB3234-058-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  g4063730
BLAST score
                  201
E value
                  1.0e-109
Match length
                  355
% identity
                  89
NCBI Description
                 Arabidopsis thaliana BAC F21J6 from chromosome V,
```

22823

sequence [Arabidopsis thaliana]

containing KNAT3 and mapping near 60.5 cM, complete

```
Seq. No.
                   168468
Seq. ID
                   LIB3234-058-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g4589964
BLAST score
                   613
E value
                   5.0e-64
Match length
                   127
% identity
NCBI Description (AC007169) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                   168469
Seq. ID
                   LIB3234-058-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   q4376087
BLAST score
                   266
E value
                   1.0e-148
Match length
                   383
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No
Seq. No.
                   168470
Seq. ID
                   LIB3234-058-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1809127
BLAST score
                   303
E value
                   1.0e-27
Match length
                   115
% identity
                   50
NCBI Description
                   (U77674) terminal flower 1 [Arabidopsis thaliana]
                   >gi_2208929_dbj_BAA20483_ (D86932) terminal flower1
                   [Arabidopsis thaliana] >gi_2208931_dbj_BAA20484 (D87130)
                   terminal flower1 [Arabidopsis thaliana]
                   >gi_2208933_dbj_BAA20485_ (D87519) terminal flower1
                   [Arabidopsis thaliana]
Seq. No.
                  168471
Seq. ID
                  LIB3234-058-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3548815
BLAST score
                  662
E value
                  9.0e-70
Match length
                  122
% identity
                  99
NCBI Description (AC005313) similar to axoneme-associated protein mst101
                  [Arabidopsis thaliana]
Seq. No.
                  168472
Seq. ID
                  LIB3234-058-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  653
E value
                  1.0e-68
Match length
                  130
% identity
                  100
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
```

thaliana]

```
Seq. No.
                   168473
 Seq. ID
                   LIB3234-058-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g2961390
BLAST score
                   651
E value
                   2.0e-68
Match length
                   121
% identity
                   100
NCBI Description
                   (AL022141) beta-galactosidase like protein [Arabidopsis
                   thaliana?
Seq. No.
                   168474
Seq. ID
                   LIB3234-058-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q541847
BLAST score
                   656
E value
                   4.0e-69
Match length
                   125
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                   168475
Seq. ID
                   LIB3234-058-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   q266989
BLAST score
                   459
E value
                   6.0e-46
Match length
                   109
% identity
                   83
NCBI Description
                   GTP-BINDING PROTEIN SAR1B >gi_322517 pir S28603
                   GTP-binding protein - Arabidopsis thaliana >gi 166734
                   (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                   168476
Seq. ID
                   LIB3234-058-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g2129651
BLAST score
                   196
E value
                   7.0e-41
Match length
                   92
% identity
                   100
NCBI Description
                  myosin heavy chain ATM2 - Arabidopsis thaliana (fragment)
                   >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis
                   thaliana]
Seq. No.
                   168477
Seq. ID
                  LIB3234-058-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  q4432793
BLAST score
                  108
E value
                   1.0e-53
Match length
                  270
% identity
                   46
NCBI Description Arabidopsis thaliana chromosome II BAC T19K21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   168478
Seq. ID
                   LIB3234-058-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   g4757398
BLAST score
                   39
E value
                   1.0e-12
Match length
                   63
% identity
                   90
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MED5, complete sequence
Seq. No.
                   168479
Seq. ID
                   LIB3234-058-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   q4159712
BLAST score
                   361
E value
                   0.0e+00
Match length
                   361
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MWI23, complete sequence
Seq. No.
                   168480
Seq. ID
                   LIB3234-058-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   q4204298
BLAST score
                   529
E value
                   4.0e-54
Match length
                  122
% identity
                   84
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  168481
Seq. ID
                  LIB3234-058-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  q4159707
BLAST score
                  179
E value
                  4.0e-96
Match length
                  331
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJK13, complete sequence
Seq. No.
                  168482
                  LIB3234-058-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135858
BLAST score
                  460
E value
                  3.0e-46
Match length
                  100
% identity
                  92
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
                  >gi_99760_pir _S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi_16182_emb_CAA45114 (X63551)
```

tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis

thaliana] >gi 166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. Seq. ID 168483

LIB3234-058-P1-K1-H8

Method BLASTN NCBI GI q4512656 BLAST score 159 E value 4.0e-84 Match length 290 % identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No. 168484

Seq. ID LIB3234-058-P1-K1-H9

Method BLASTX NCBI GI q3915961 BLAST score 376 E value 3.0e-36 Match length 95 % identity 73

HYPOTHETICAL 267 KD PROTEIN (ORF 2280) NCBI Description

>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] $>gi_2924285$ _emb_CAA77438_ (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 168485

Seq. ID LIB3234-059-P1-K1-A1

Method BLASTN NCBI GI g4159712 BLAST score 184 E value 4.0e-99 Match length 364 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 168486

LIB3234-059-P1-K1-A11 Seq. ID

Method BLASTN NCBI GI g2351061 BLAST score 214 E value 1.0e-117 Match length 371 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAF19, complete sequence [Arabidopsis thaliana]

Seq. No. 168487

Seq. ID LIB3234-059-P1-K1-A12

Method BLASTN NCBI GI g2477521 BLAST score 96 1.0e-46 E value Match length 304

```
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F22K2O genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168488
Seq. ID
                   LIB3234-059-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g3785977
BLAST score
                   597
E value
                   4.0e-62
Match length
                   125
% identity
                   93
NCBI Description
                  (AC005560) putative growth regulator protein [Arabidopsis
                   thaliana]
Seq. No.
                   168489
Seq. ID
                   LIB3234-059-P1-K1-A4
Method
                   BLASTN
NCBI GI
                   g2252823
BLAST score
                   366
E value
                   0.0e+00
Match length
                   382
% identity
                   99
NCBI Description Arabidopsis thaliana BAC IG005I10
Seq. No.
                   168490
Seq. ID
                   LIB3234-059-P1-K1-A5
Method
                  BLASTN
NCBI GI
                   g2351061
BLAST score
                   159
E value
                   4.0e-84
Match length
                  183
% identity
                   97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168491
Seq. ID
                  LIB3234-059-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2102691
BLAST score
                  235
E value
                  1.0e-19
Match length
                  90
% identity
NCBI Description (U64817) fructokinase [Lycopersicon esculentum]
Seq. No.
                  168492
Seq. ID
                  LIB3234-059-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g2961370
BLAST score
                  152
E value
                  3.0e-80
Match length
                  196
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13
```

(ESSAII project)

```
Seq. No.
                    168493
 Seq. ID
                    LIB3234-059-P1-K1-A9
 Method
                    BLASTX
 NCBI GI
                    g3201632
 BLAST score
                    287
E value
                    8.0e-26
Match length
                    98
 % identity
                    56
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                    168494
Seq. ID
                    LIB3234-059-P1-K1-B10
Method
                    BLASTX
NCBI GI
                    g4204298
BLAST score
                    519
E value
                    5.0e-53
Match length
                    127
% identity
                    79
NCBI Description (AC003027) lcl_prt_seq No definition line found
                    [Arabidopsis thaliana]
Seq. No.
                    168495
Seq. ID
                    LIB3234-059-P1-K1-B12
Method
                    BLASTX
NCBI GI
                    q3688189
BLAST score
                    151
E value
                    7.0e-10
Match length
                   33
% identity
                    91
NCBI Description (AL031804) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   168496
Seq. ID
                   LIB3234-059-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1351837
BLAST score
                   602
E value
                   1.0e-62
Match length
                   128
% identity
                   89
NCBI Description ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
                   BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II
                   beta-carboxyltransferase chain - rape chloroplast
                   >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase carboxyltransferase (beta subunit) [Brassica napus]
                   >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta
                   [Brassica napus]
Seq. No.
                   168497
Seq. ID
                   LIB3234-059-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   g2749918
BLAST score
                   313
E value
                   1.0e-176
Match length
                   370
% identity
                   95
                   Arabidopsis thaliana chromosome I BAC F316 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168498 Seq. ID LIB3234-059-P1-K1-B5 Method BLASTN NCBI GI g4531433 BLAST score 316 E value 1.0e-178 Match length 371 % identity NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence Seq. No. 168499 Seq. ID LIB3234-059-P1-K1-B6 Method BLASTX NCBI GI g1890352 BLAST score 434 E value 5.0e-43Match length 80 % identity NCBI Description (X91398) transcription factor L2 [Arabidopsis thaliana] Seq. No. 168500 Seq. ID LIB3234-059-P1-K1-B7 Method BLASTN NCBI GI q2584827 BLAST score 342 E value 0.0e + 00Match length 373 % identity 98 NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168501 Seq. ID LIB3234-059-P1-K1-B8 Method BLASTX NCBI GI q1345973 BLAST score 431 E value 1.0e-42 Match length 97 % identity 81 NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana] Seq. No. 168502 Seq. ID LIB3234-059-P1-K1-C10

Method BLASTN
NCBI GI g2264318
BLAST score 374
E value 0.0e+00

```
Match length
                    378
 % identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUP24, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168503
Seq. ID
                   LIB3234-059-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3080435
BLAST score
                   659
E value
                   2.0e-69
Match length
                   126
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                   168504
Seq. ID
                   LIB3234-059-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   q516389
BLAST score
                   44
E value
                   1.0e-15
Match length
                   112
% identity
                   86
NCBI Description M.jalapa 25S ribosomal RNA
Seq. No.
                   168505
Seq. ID
                   LIB3234-059-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   q4731050
BLAST score
                   47
E value
                   3.0e-17
Match length
                   59
% identity
                   95
NCBI Description
                   Drosophila melanogaster, chromosome 3L, region 79F1-80A2,
                   BAC clone BACR48E05, complete sequence
Seq. No.
                   168506
Seq. ID
                   LIB3234-059-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2160158
BLAST score
                   275
E value
                   2.0e-24
Match length
                   95
% identity
                   63
NCBI Description
                  (AC000132) Similar to elongation factor 1-gamma
                   (gb_EF1G_XENLA). ESTs gb_T20564, gb_T45940, gb T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   168507
Seq. ID
                   LIB3234-059-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   g2264318
BLAST score
                  299
E value
                  1.0e-168
Match length
                  306
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

Seq. No.

168508

```
Seq. ID
                   LIB3234-059-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   g3212102
BLAST score
                   305
E value
                   1.0e-171
Match length
                   350
% identity
NCBI Description
                   Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168509
Seq. ID
                   LIB3234-059-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g170354
BLAST score
                   540
E value
                   2.0e-55
Match length
                   114
% identity
NCBI Description
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                   168510
Seq. ID
                   LIB3234-059-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   q3449330
BLAST score
                   363
E value
                   0.0e + 00
Match length
                   383
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDJ14, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168511
Seq. ID
                  LIB3234-059-P1-K1-C8
Method
                  BLASTN
NCBI GI
                   g3449334
BLAST score
                   243
E value
                   1.0e-134
Match length
                  267
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168512
                  LIB3234-059-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q99688
BLAST score
                  628
E value
                  9.0e-66
Match length
                  126
% identity
                  96
NCBI Description
                  translation elongation factor eEF-1 alpha chain (gene A4) -
                  Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
```

MUP24, complete sequence [Arabidopsis thaliana]

BLAST score

385

```
Seq. No.
                   168513
 Seq. ID
                   LIB3234-059-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g4204277
BLAST score
                   619
E value
                   1.0e-64
Match length
                   117
% identity
                   98
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168514
Seq. ID
                   LIB3234-059-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g4432847
BLAST score
                   246
E value
                   1.0e-136
Match length
                   302
% identity
                   95
NCBI Description Arabidopsis thaliana chromosome II BAC F13B15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168515
Seq. ID
                   LIB3234-059-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g2828185
BLAST score
                   142
E value
                   5.0e-74
Match length
                   385
% identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUD21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168516
Seq. ID
                  LIB3234-059-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2781348
BLAST score
                  623
E value
                  3.0e-65
Match length
                  128
% identity
                  93
NCBI Description (AC003113) F2401.4 [Arabidopsis thaliana]
Seq. No.
                  168517
Seq. ID
                  LIB3234-059-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  47
E value
                  9.0e-18
Match length
                  125
% identity
                  36
NCBI Description vicilin gene B [Saguinus oedipus]
Seq. No.
                  168518
Seq. ID
                  LIB3234-059-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2583108
```

22833

Seq. No.

Seq. ID

168523

LIB3234-059-P1-K1-E2

E value 3.0e-37 Match length 81 % identity NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana] Seq. No. 168519 Seq. ID LIB3234-059-P1-K1-D7 Method BLASTN NCBI GI q16145 BLAST score 144 E value 3.0e-75Match length 275 % identity 99 NCBI Description A.thaliana mRNA for ABI3 protein Seq. No. 168520 Seq. ID LIB3234-059-P1-K1-D8 Method BLASTN NCBI GI g1279629 BLAST score 278 E value 1.0e-155 Match length 380 % identity 93 NCBI Description O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA Seq. No. 168521 Seq. ID LIB3234-059-P1-K1-D9 Method BLASTX NCBI GI g1345973 BLAST score 435 E value 4.0e-43Match length 98 % identity 82 NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM $>gi_541882_pir_JQ2335$ omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana $>gi_408483$ (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana] Seq. No. 168522 Seq. ID LIB3234-059-P1-K1-E1 Method BLASTX NCBI GI q4510373 BLAST score 176 E value 8.0e-13 Match length 59 % identity NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis thaliana]

```
Method
                   BLASTX
NCBI GI
                   g118926
BLAST score
                   353
E value
                   2.0e-33
Match length
                   121
 % identity
                   55
NCBI Description
                   DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
                   >gi_320600_pir__E45509 desiccation-related protein (clone
                   PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991)
                   dessication-related protein [Craterostigma plantagineum]
                   >gi_227781_prf__1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
Seq. No.
                   168524
Seq. ID
                   LIB3234-059-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g2118307
BLAST score
                   495
E value
                   3.0e-50
Match length
                   108
% identity
                   94
NCBI Description
                   cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
                   >gi_804950_emb_CAA58893_ (X84097) cysteine synthase
                   [Arabidopsis thaliana] >gi 1096196 prf _2111276A Ser(Ac)
                   thiol lyase [Arabidopsis thaliana]
Seq. No.
                   168525
Seq. ID
                   LIB3234-059-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3808062
BLAST score
                   149
E value
                   1.0e-09
Match length
                   62
% identity
                   45
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                   168526
Seq. ID
                  LIB3234-059-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g687844
BLAST score
                   136
E value
                   4.0e-08
Match length
                   91
% identity
NCBI Description
                  (U21320) contains TPR domain-like repeats [Caenorhabditis
                  elegans]
Seq. No.
                  168527
Seq. ID
                  LIB3234-059-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g585349
BLAST score
                  308
E value
                  3.0e-28
Match length
                  58
% identity
                  100
NCBI Description
                  CASEIN KINASE II, ALPHA CHAIN 1 (CK II)
                  >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-)
```

alpha-type chain (clone ATCKA1) - Arabidopsis thaliana >gi_391603_dbj_BAA01090_ (D10246) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No. 168528

Seq. ID LIB3234-059-P1-K1-E9

Method BLASTN
NCBI GI g4335711
BLAST score 36
E value 9.0e-11
Match length 88
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F9013 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168529

Seq. ID LIB3234-059-P1-K1-F1

Method BLASTN
NCBI GI g2244788
BLAST score 260
E value 1.0e-144
Match length 326
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 168530

Seq. ID LIB3234-059-P1-K1-F10

Method BLASTN
NCBI GI g1707006
BLAST score 67
E value 3.0e-29
Match length 187
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168531

Seq. ID LIB3234-059-P1-K1-F12

Method BLASTN
NCBI GI g3449326
BLAST score 349
E value 0.0e+00
Match length 369
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M22, complete sequence [Arabidopsis thaliana]

Seq. No. 168532

Seq. ID LIB3234-059-P1-K1-F2

Method BLASTX
NCBI GI g4589964
BLAST score 420
E value 2.0e-41
Match length 98
% identity 84

NCBI Description (AC007169) delta 9 desaturase [Arabidopsis thaliana]

```
Seq. No.
                   168533
 Seq. ID
                   LIB3234-059-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q4567246
BLAST score
                   449
E value
                   9.0e-45
Match length
                   98
% identity
                   87
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                   168534
Seq. No.
                   LIB3234-059-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263771
BLAST score
                   288
E value
                   6.0e-26
Match length
                   71
% identity
                   72
NCBI Description
                  (AC006218) putative nonspecific lipid-transfer protein
                   precursor [Arabidopsis thaliana]
                   >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
                   nonspecific lipid-transfer protein precursor [Arabidopsis
                   thaliana]
Seq. No.
                   168535
Seq. ID
                   LIB3234-059-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g135406
BLAST score
                   495
E value
                   3.0e-50
Match length
                   92
% identity
                   100
NCBI Description
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
                   alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                   168536
Seq. ID
                  LIB3234-059-P1-K1-F9
Method
                  BLASTX
NCBI GI
                   g4585997
BLAST score
                   637
E value
                  8.0e-67
Match length
                  125
% identity
                  97
NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168537
Seq. ID
                  LIB3234-059-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4204277
BLAST score
                  521
E value
                  2.0e-53
Match length
                  98
% identity
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 168538

Seq. ID LIB3234-059-P1-K1-G11

Method BLASTX
NCBI GI g2961375
BLAST score 109
E value 6.0e-05
Match length 126
% identity 73

NCBI Description (AL022141) NAM like protein [Arabidopsis thaliana]

Seq. No. 168539

Seq. ID LIB3234-059-P1-K1-G12

Method BLASTN
NCBI GI g2827644
BLAST score 199
E value 1.0e-108
Match length 363
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4

(ESSAII project)

Seq. No. 168540

Seq. ID LIB3234-059-P1-K1-G4

Method BLASTN
NCBI GI g2914688
BLAST score 276
E value 1.0e-154
Match length 341
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168541

Seq. ID LIB3234-059-P1-K1-G5

Method BLASTX
NCBI GI g4432860
BLAST score 267
E value 2.0e-23
Match length 126
% identity 21

NCBI Description (AC006300) putative glucose-induced repressor protein

[Arabidopsis thaliana]

Seq. No. 168542

Seq. ID LIB3234-059-P1-K1-G6

Method BLASTN
NCBI GI g2952432
BLAST score 102
E value 4.0e-50
Match length 144
% identity 99

NCBI Description Arabidopsis thaliana putative ubiquitin activating enzyme

E1 (ECR1) mRNA, complete cds

Seq. No. 168543

Seq. ID LIB3234-059-P1-K1-G7

% identity

49

```
Method
                   BLASTN
NCBI GI
                   a2760169
BLAST score
                   152
E value
                   6.0e-80
Match length
                   270
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFB13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168544
Seq. ID
                   LIB3234-059-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q266839
BLAST score
                   539
E value
                   2.0e-55
Match length
                   109
% identity
                   99
NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi 478764_pir__S29240
                   multicatalytic endopeptidase complex (EC 3.\overline{4.99.46}) alpha
                   chain - Arabidopsis thaliana >gi_16445_emb_CAA47298
                   (X66825) proteosome alpha subunit [Arabidopsis thaliana]
                   >gi_3421080 (AF043522) 20S proteasome subunit PAD1
                   [Arabidopsis thaliana] >gi_742351_prf__2009376B
                   proteasome: SUBUNIT = alpha [Arabidopsis thaliana]
Seq. No.
                   168545
Seq. ID
                   LIB3234-059-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g3702315
BLAST score
                  137
E value
                   5.0e-71
Match length
                  316
% identity
                   98
NCBI Description Arabidopsis thaliana chromosome II BAC T3F17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168546
Seq. ID
                  LIB3234-059-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  g3449317
BLAST score
                  49
E value
                  2.0e-18
Match length
                  150
% identity
                  89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKM21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168547
Seq. ID
                  LIB3234-059-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g166570
BLAST score
                  245
E value
                  7.0e-21
Match length
                  106
```

22839

NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No.

168553

```
Seq. No.
                   168548
Seq. ID
                   LIB3234-059-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q3894171
BLAST score
                   537
E value
                   4.0e-55
Match length
                   114
% identity
                   93
NCBI Description
                   (AC005312) putative glutathione s-transferase [Arabidopsis
                   thaliana]
Seq. No.
                   168549
Seq. ID
                   LIB3234-059-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q3157928
BLAST score
                   485
E value
                   5.0e-49
Match length
                   95
% identity
                   100
NCBI Description
                  (AC002131) Similar to fumarylacetoacetate hydrolase,
                   gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]
Seq. No.
                   168550
Seq. ID
                   LIB3234-059-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   q3659491
BLAST score
                   289
E value
                   1.0e-161
Match length
                   353
% identity
                   99
NCBI Description
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168551
Seq. ID
                  LIB3234-060-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g2288979
BLAST score
                   389
E value
                   0.0e+00
Match length
                  396
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168552
Seq. ID
                  LIB3234-060-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g3241927
BLAST score
                  362
E value
                  0.0e+00
Match length
                  395
% identity
                  61
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTE17, complete sequence [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3234-060-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g3985949
BLAST score
                   267
E value
                   1.0e-148
Match length
                   392
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168554
Seq. ID
                   LIB3234-060-P1-K1-A4
Method
                   BLASTN
NCBI GI
                   g4757406
BLAST score
                   379
E value
                   0.0e + 00
Match length
                   387
% identity
                   73
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MPF21, complete sequence
Seq. No.
                   168555
Seq. ID
                   LIB3234-060-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q1864017
BLAST score
                   481
E value
                   1.0e-48
Match length
                   92
% identity
                   100
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168556
Seq. ID
                   LIB3234-060-P1-K1-A6
Method
                  BLASTX
NCBI GI
                   q3953469
BLAST score
                   353
E value
                   2.0e-33
Match length
                  113
% identity
                   62
NCBI Description (AC002328) F20N2.14 [Arabidopsis thaliana]
Seq. No.
                   168557
Seq. ID
                  LIB3234-060-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  235
E value
                  1.0e-129
                  308
Match length
% identity
                  54
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                  (ESSA project)
```

Seq. No. 168558

Seq. ID LIB3234-060-P1-K1-B10

Method BLASTX NCBI GI g4678285 BLAST score 366

```
E value
                    5.0e-35
 Match length
                    130
 % identity
                    50
 NCBI Description (AL049660) putative protein [Arabidopsis thaliana]
 Seq. No.
                    168559
Seq. ID
                    LIB3234-060-P1-K1-B12
Method
                    BLASTN
NCBI GI
                    q2696018
BLAST score
                    211
E value
                    1.0e-115
Match length
                    394
% identity
                    98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168560
Seq. ID
                    LIB3234-060-P1-K1-B2
Method
                    BLASTN
NCBI GI
                    g166853
BLAST score
                    88
E value
                    2.0e-42
Match length
                    100
% identity
                    97
NCBI Description Arabidopsis thaliana RNA polymerase II fifth largest
                    subunit mRNA, complete cds
Seq. No.
                    168561
Seq. ID
                   LIB3234-060-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g1871185
BLAST score
                   192
E value
                   1.0e-14
Match length
                   100
% identity
                   38
NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]
Seq. No.
                   168562
Seq. ID
                   LIB3234-060-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g133960
BLAST score
                   235
E value
                   1.0e-19
Match length
                   68
% identity
                   72
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_70876_pir__R3NT4
                   ribosomal protein S4 - common tobacco chloroplast
                   >gi_11834_emb_CAA77354 (Z00044) ribosomal protein S4 [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal
                   protein S4 [Nicotiana tabacum]
Seq. No.
                   168563
Seq. ID
                   LIB3234-060-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g2262167
BLAST score
                   657
E value
                   4.0e-69
```

E value

8.0e-73

Match length 125 % identity 100 (AC002329) cytosolic ribosomal protein S4 [Arabidopsis NCBI Description thaliana] Seq. No. 168564 Seq. ID LIB3234-060-P1-K1-B8 Method BLASTX NCBI GI q135858 BLAST score 296 E value 8.0e-27 Match length 58 % identity 100 TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) NCBI Description >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis Thaliana] >gi 445128 prf 1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana] Seq. No. 168565 Seq. ID LIB3234-060-P1-K1-C1 Method BLASTX NCBI GI g3128176 BLAST score 221 E value 5.0e-18 Match length 104 % identity 35 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana] Seq. No. 168566 Seq. ID LIB3234-060-P1-K1-C10 Method BLASTX NCBI GI q1617268 BLAST score 573 E value 3.0e-59 Match length 130 % identity NCBI Description (Z72153) acyl CoA synthetase [Brassica napus] Seq. No. 168567 Seq. ID LIB3234-060-P1-K1-C11 Method BLASTX NCBI GI g1864017 BLAST score 376 E value 3.0e - 3692 Match length % identity NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum] Seq. No. 168568 Seq. ID LIB3234-060-P1-K1-C3 Method BLASTN NCBI GI g3548797 BLAST score 140

Match length 397 % identity 97 NCBI Description Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168569 Seq. ID LIB3234-060-P1-K1-C5 Method BLASTX NCBI GI g2494041 BLAST score 231 E value 3.0e-19 Match length 57 % identity 74 NCBI Description DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785 (D90917) diaminopimelate epimerase [Synechocystis sp.] Seq. No. 168570 Seq. ID LIB3234-060-P1-K1-C7 Method BLASTX NCBI GI q267069 BLAST score 536 E value 6.0e-55 Match length 99 % identity 100 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183 pir JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 168571 Seq. ID LIB3234-060-P1-K1-D1 Method BLASTX NCBI GI g3273743 BLAST score 552 E value 8.0e-57 Match length 105 % identity 100 NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi 3786019 (AC005499) unknown protein [Arabidopsis thaliana] Seq. No. 168572 Seq. ID LIB3234-060-P1-K1-D11 Method BLASTN

NCBI GI g4415905 BLAST score 361 E value 0.0e + 00Match length 393 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168573

Seq. ID LIB3234-060-P1-K1-D4

98

Method BLASTX NCBI GI g4234768 BLAST score 202

```
E value
                    2.0e-16
 Match length
                    37
 % identity
                    89
 NCBI Description (AF069468) sterol-C5-desaturase [Arabidopsis thaliana]
 Seq. No.
                    168574
 Seq. ID
                    LIB3234-060-P1-K1-D5
 Method
                   BLASTN
 NCBI GI
                    g2828182
 BLAST score
                    394
 E value
                    0.0e + 00
Match length
                   397
 % identity
                   83
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168575
Seq. ID
                   LIB3234-060-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q4432811
BLAST score
                   401
E value
                   0.0e + 00
Match length
                   401
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F16D14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168576
Seq. ID
                   LIB3234-060-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2129532
BLAST score
                   306
E value
                   5.0e-28
Match length
                   88
% identity
                   69
NCBI Description
                   acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
                   Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461)
                   acyl-[acyl-carrier protein] desaturase [Arabidopsis
                   thaliana]
Seq. No.
                   168577
Seq. ID
                   LIB3234-060-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g2160296
BLAST score
                   641
E value
                   3.0e-67
Match length
                   130
% identity
                   95
NCBI Description
                  (D61395) gamma-VPE [Arabidopsis thaliana]
Seq. No.
                   168578
Seq. ID
                   LIB3234-060-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q4582468
BLAST score
                   479
E value
                   2.0e-48
Match length
                   98
```

```
% identity
NCBI Description
                   (AC007071) putative 40S ribosomal protein; contains
                   C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   168579
Seq. ID
                   LIB3234-060-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   g2351062
BLAST score
                   286
E value
                   1.0e-160
Match length
                   378
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168580
Seq. ID
                   LIB3234-060-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g897638
BLAST score
                   244
E value
                   1.0e-20
Match length
                   50
% identity
                   92
NCBI Description
                  (M10124) unknown protein [Nicotiana tabacum]
                   >gi_224349_prf__1102209C ORF 3 [Nicotiana sp.]
Seq. No.
                   168581
Seq. ID
                   LIB3234-060-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q3157930
BLAST score
                   623
E value
                   4.0e-65
Match length
                   117
% identity
                   99
NCBI Description
                  (AC002131) Strong similarity to
                   amino-cyclopropane-carboxylic acid oxidase gb L27664 from
                   Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  168582
Seq. ID
                  LIB3234-060-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3193292
BLAST score
                  386
E value
                  2.0e-37
Match length
                  122
                  70
% identity
NCBI Description
                  (AF069298) similar to ATPases associated with various
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                  [Arabidopsis thaliana]
Seq. No.
                  168583
Seq. ID
                  LIB3234-060-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g3228389
BLAST score
                  321
E value
                  0.0e+00
```

```
Match length
                   353
% identity
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F17L21,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168584
Seq. ID
                  LIB3234-060-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g3241927
BLAST score
                   81
                  7.0e-38
E value
Match length
                   148
% identity
                   93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168585
Seq. ID
                  LIB3234-060-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g584882
BLAST score
                  763
E value
                  1.0e-81
Match length
                  132
                  100
% identity
NCBI Description
                  CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL
                  CYCLASE) >gi_452446 (U02555) cycloartenol synthase;
                   (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
Seq. No.
                  168586
Seq. ID
                  LIB3234-060-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  52
E value
                  3.0e-20
Match length
                  253
% identity
                  88
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  168587
Seq. ID
                  LIB3234-060-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g3241916
BLAST score
                  178
E value
                  2.0e-95
Match length
                  373
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168588
Seq. ID
                  LIB3234-060-P1-K1-F2
                  BLASTX
```

Method BLASTX
NCBI GI g2961390
BLAST score 555
E value 3.0e-57

Match length 125 % identity 86

NCBI GI

BLAST score

```
NCBI Description
                   (AL022141) beta-galactosidase like protein [Arabidopsis
                   thalianal
Seq. No.
                   168589
Seq. ID
                   LIB3234-060-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   g4262209
BLAST score
                   231
E value
                   1.0e-127
Match length
                   310
% identity
                   93
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T14A4 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168590
                   LIB3234-060-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351837
BLAST score
                   549
E value
                   1.0e-56
Match length
                   117
% identity
                   86
NCBI Description
                  ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
                   BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II
                   beta-carboxyltransferase chain - rape chloroplast
                   >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase
                   carboxyltransferase (beta subunit) [Brassica napus]
                   >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta
                   [Brassica napus]
Seq. No.
                   168591
Seq. ID
                  LIB3234-060-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g4584531
BLAST score
                   367
E value
                   0.0e + 00
Match length
                  387
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
                   (ESSA project)
Seq. No.
                  168592
Seq. ID
                  LIB3234-060-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4206762
BLAST score
                  239
E value
                  1.0e-132
Match length
                  304
                  96
% identity
NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  168593
Seq. ID
                  LIB3234-060-P1-K1-G1
Method
                  BLASTN
```

22848

g3399678



E value 1.0e-161 Match length 399 % identity 92

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 168594

Seq. ID LIB3234-060-P1-K1-G10

Method BLASTN
NCBI GI g2262155
BLAST score 355
E value 0.0e+00
Match length 391
% identity 98

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 168595

Seq. ID LIB3234-060-P1-K1-G11

Method BLASTX
NCBI GI g3915085
BLAST score 570
E value 6.0e-59
Match length 128
% identity 88

NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase

[Arabidopsis thaliana]

Seq. No. 168596

Seq. ID LIB3234-060-P1-K1-G12

Method BLASTN
NCBI GI g2244991
BLAST score 39
E value 1.0e-12

Match length 190 % identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 168597

Seq. ID LIB3234-060-P1-K1-G2

Method BLASTX
NCBI GI g3426060
BLAST score 46
E value 6.0e-10
Match length 72

% identity 65

NCBI Description (AJ007586) src2-like protein [Arabidopsis thaliana]

Seq. No. 168598

Seq. ID LIB3234-060-P1-K1-G3

Method BLASTX NCBI GI g3273743 BLAST score 616 E value 2.0e-64 Match length 118 % identity 99

NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis

thaliana] >gi_3786019 (AC005499) unknown protein

[Arabidopsis thaliana]

Seq. No. 168599

Seq. ID LIB3234-060-P1-K1-G4

Method BLASTN
NCBI GI g3779020
BLAST score 130
E value 7.0e-67
Match length 368
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC T4E14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168600

Seq. ID LIB3234-060-P1-K1-G5

Method BLASTX
NCBI GI g2924779
BLAST score 544
E value 7.0e-56
Match length 112
% identity 97

NCBI Description (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis

thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA

thiolase [Arabidopsis thaliana]

Seq. No. 168601

Seq. ID LIB3234-060-P1-K1-G6

Method BLASTX
NCBI GI g266839
BLAST score 586
E value 8.0e-61
Match length 118
% identity 99

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir_S29240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha

chain - Arabidopsis thaliana >gi 16445 emb CAA47298 (X66825) proteosome alpha subunit [Arabidopsis thaliana]

>gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
proteasome:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 168602

Seq. ID LIB3234-060-P1-K1-G7

Method BLASTN
NCBI GI g2564048
BLAST score 346
E value 0.0e+00
Match length 386
% identity 97

% identity

NCBI Description

90

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168603
Seq. ID
                   LIB3234-060-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g2494113
BLAST score
                   684
E value
                   2.0e-72
Match length
                   130
% identity
                   98
                   (AC002376) Strong similarity to Musa pectate lyase
NCBI Description
                   (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   168604
Seq. ID
                   LIB3234-060-P1-K1-H10
Method
                  BLASTX
NCBI GI
                   g2330730
BLAST score
                   163
E value
                   3.0e-11
Match length
                   45
% identity
NCBI Description (Z98532) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   168605
Seq. ID
                  LIB3234-060-P1-K1-H11
Method
                  BLASTN
NCBI GI
                   g4756963
BLAST score
                   354
E value
                   0.0e+00
Match length
                  378
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                  168606
Seq. ID
                  LIB3234-060-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g3702739
BLAST score
                  133
E value
                  9.0e-69
Match length
                  193
% identity
                  93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168607
Seq. ID
                  LIB3234-060-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  586
E value
                  8.0e-61
Match length
                  130
```

22851

HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302

heat shock cognate protein 70-1 - Arabidopsis thaliana

```
>gi_397482_emb_CAA52684 (X74604) heat shock protein 70
cognate [Arabidopsis thaliana]
168608
LIB3234-060-P1-K1-H5
```

Seq. ID Method BLASTX g4204298 NCBI GI BLAST score 331 E value 5.0e-31Match length 81 % identity 85

Seq. No.

(AC003027) lcl_prt_seq No definition line found NCBI Description

[Arabidopsis thaliana]

Seq. No. 168609

Seq. ID LIB3234-060-P1-K1-H6

Method BLASTX NCBI GI q2342727 BLAST score 401 E value 4.0e-39 Match length 103 75 % identity

NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 168610

Seq. ID LIB3234-060-P1-K1-H7

Method BLASTX NCBI GI g1402914 BLAST score 502 E value 5.0e-51Match length 99 100

% identity

NCBI Description (X98318) peroxidase [Arabidopsis thaliana]

Seq. No. 168611

Seq. ID LIB3234-060-P1-K1-H9

Method BLASTN NCBI GI g3894179 BLAST score 33 E value 6.0e-09 Match length 65 % identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F13H10 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168612

Seq. ID LIB3234-065-P1-K1-A11

72

Method BLASTN NCBI GI g4567193 BLAST score 43 E value 6.0e-15 Match length 173

Arabidopsis thaliana chromosome II BAC T26C19 genomic NCBI Description

sequence, complete sequence

Seq. No. 168613

% identity



```
Seq. ID
                  LIB3234-065-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4337178
BLAST score
                  463
E value
                  2.0e-46
                  92
Match length
                  97
% identity
NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]
Seq. No.
                  168614
Seq. ID
                  LIB3234-065-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g3449327
BLAST score
                  190
E value
                  1.0e-102
Match length
                  307
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168615
Seq. ID
                  LIB3234-065-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3107905
BLAST score
                  117
E value
                  8.0e-06
Match length
                  127
% identity
                  7
NCBI Description (D85101) leaf protein [Ipomoea nil]
Seq. No.
                  168616
                  LIB3234-065-P1-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046853
BLAST score
                  301
E value
                  1.0e-169
Match length
                  367
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168617
Seq. ID
                  LIB3234-065-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g2213606
BLAST score
                  159
E value
                  4.0e-84
Match length
                  288
% identity
                  88
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168618
```

Seq. ID LIB3234-065-P1-K1-A8

Method BLASTN NCBI GI g3449327 BLAST score 45

```
E value
                   3.0e-16
Match length
                   142
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168619
Seq. ID
                   LIB3234-065-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g1755162
BLAST score
                   303
E value
                   1.0e-27
Match length
                   91
% identity
                   59
NCBI Description (U75192) germin-like protein [Arabidopsis thaliana]
Seq. No.
                   168620
Seq. ID
                  LIB3234-065-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   g4531433
BLAST score
                   243
E value
                   1.0e-134
Match length
                   344
                   94
% identity
NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic
                  sequence, complete sequence
Seq. No.
                  168621
Seq. ID
                  LIB3234-065-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1669668
BLAST score
                   350
E value
                   3.0e-33
Match length
                  89
% identity
                  79
NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]
Seq. No.
                  168622
Seq. ID
                  LIB3234-065-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3176659
BLAST score
                  340
E value
                   6.0e-32
Match length
                  76
% identity
                  84
NCBI Description
                  (AC004393) Strong similarity to receptor kinase gb M80238
                  from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  168623
Seq. ID
                  LIB3234-065-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  133
E value
                  1.0e-68
Match length
                  387
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```



MDC11, complete sequence

Seq. No. 168624 LIB3234-065-P1-K1-B6 Seq. ID Method BLASTX NCBI GI q3450889 80 BLAST score E value 6.0e-41Match length 123 % identity 80 NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana] Seq. No. 168625 LIB3234-065-P1-K1-B9 Seq. ID Method BLASTN NCBI GI g3241917 BLAST score 108 E value 7.0e-54Match length 263 % identity 85 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana] Seq. No. 168626 Seq. ID LIB3234-065-P1-K1-C1 Method BLASTX NCBI GI g1255951 BLAST score 489 E value 2.0e-49 Match length 126 74 % identity NCBI Description (X96932) PS60 [Nicotiana tabacum] Seq. No. 168627 LIB3234-065-P1-K1-C11 Seq. ID Method BLASTX NCBI GI g3831443 BLAST score 310 E value 2.0e-28 Match length 60 100 % identity (AC005819) putative auxin-regulated protein [Arabidopsis NCBI Description thaliana] 168628 Seq. No. Seq. ID LIB3234-065-P1-K1-C2 Method BLASTX NCBI GI g2160133 BLAST score 265 E value 3.0e-23 Match length 94 % identity 63 NCBI Description (AC000375) Strong similarity to Arabidopsis

gb_X91953,F19K23.3,F19K23.15. ESTs

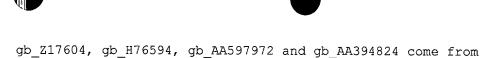
gb_T21984,gb ATTS0219,gb ATTS0207,gb T21984 come from this

gene. [Arabidopsis thaliana]

```
Seq. No.
                   168629
Seq. ID
                   LIB3234-065-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g127041
BLAST score
                   476
E value
                   6.0e-48
Match length
                   90
% identity
                   100
NCBI Description
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                   2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                   S-adenosylmethionine synthetase [Arabidopsis thaliana]
Seq. No.
                   168630
                  LIB3234-065-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4100059
BLAST score
                   43
E value
                   7.0e-15
Match length
                  110
% identity
                   86
NCBI Description
                  Arabidopsis thaliana AthlecRK4 pseudogene, complete
                   sequence, receptor lectin kinase 3 (AthlecRK3) gene,
                   complete cds, and AthlecRK2 pseudogene, complete sequence
Seq. No.
                  168631
Seq. ID
                  LIB3234-065-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4678946
BLAST score
                   532
E value
                  2.0e-54
Match length
                  104
% identity
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                  168632
Seq. ID
                  LIB3234-065-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  q4544381
BLAST score
                  323
E value
                  0.0e+00
Match length
                  384
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic
                  sequence, complete sequence
Seq. No.
                  168633
Seq. ID
                  LIB3234-065-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g114335
BLAST score
                  624
E value
                  3.0e-65
Match length
                  128
% identity
                  95
NCBI Description PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                  >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
```

```
(J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                   168634
Seq. ID
                   LIB3234-065-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g343514
BLAST score
                   67
E value
                   3.0e-29
Match length
                   91
% identity
                   93
NCBI Description Tobacco Thr-tRNA gene
Seq. No.
                   168635
Seq. ID
                   LIB3234-065-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   q4691223
BLAST score
                   149
E value
                   4.0e-78
Match length
                   382
% identity
                   95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
Seq. No.
                   168636
Seq. ID
                   LIB3234-065-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q114335
BLAST score
                   278
E value
                   6.0e-25
Match length
                   85
% identity
                   65
NCBI Description
                   PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                   >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                   type 2, plasma membrane - Arabidopsis thaliana >gi_166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                   168637
Seq. ID
                   LIB3234-065-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3421346
BLAST score
                   513
E value
                   3.0e-52
Match length
                   115
% identity
                   90
NCBI Description
                  (AJ007723) ribosomal protein S4 [Orobanche minor]
Seq. No.
                   168638
Seq. ID
                  LIB3234-065-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q1107501
BLAST score
                   402
E value
                   3.0e-39
Match length
                  117
% identity
                  70
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
```

type 2, plasma membrane - Arabidopsis thaliana >qi 166629



Seq. No. 168639

Seq. ID LIB3234-065-P1-K1-D7

Method BLASTX
NCBI GI g3004551
BLAST score 167
E value 1.0e-11
Match length 95
% identity 43

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

this gene. [Arabidopsis thaliana]

Seq. No. 168640

Seq. ID LIB3234-065-P1-K1-E1

Method BLASTX
NCBI GI g3183274
BLAST score 156
E value 2.0e-10
Match length 80
% identity 44

NCBI Description HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I

>gi_2239182_emb_CAB10102_ (Z97208) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 168641

Seq. ID LIB3234-065-P1-K1-E7

Method BLASTN
NCBI GI g1790921
BLAST score 369
E value 0.0e+00
Match length 377
% identity 99

NCBI Description Arabidopsis thaliana recA-like protein (AtDMC1) gene,

complete cds

Seq. No. 168642

Seq. ID LIB3234-065-P1-K1-E8

Method BLASTN
NCBI GI g1790921
BLAST score 281
E value 1.0e-157
Match length 342
% identity 98

NCBI Description Arabidopsis thaliana recA-like protein (AtDMC1) gene,

complete cds

Seq. No. 168643

Seq. ID LIB3234-065-P1-K1-F2

Method BLASTX
NCBI GI g119143
BLAST score 323
E value 3.0e-30
Match length 93
% identity 70

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1

```
alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
```

Seq. No. 168644 Seq. ID LIB3234-065-P1-K1-F4

Method BLASTX NCBI GI q3808062 BLAST score 155 E value 3.0e-10 Match length 64 % identity 45

NCBI Description (AB019195) PV100 [Cucurbita maxima]

Seq. No. 168645

Seq. ID LIB3234-065-P1-K1-F5

Method BLASTX NCBI GI q132074 BLAST score 604 E value 6.0e-63 Match length 111 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) $>gi_68063_pir_RKMUA1$ ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 168646

Seq. ID LIB3234-065-P1-K1-F8

Method BLASTX NCBI GI q3776559 BLAST score 294 E value 1.0e-26 Match length 124 % identity 48

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 168647

Seq. ID LIB3234-065-P1-K1-G1

Method BLASTX NCBI GI g4678368 BLAST score 492 E value 8.0e-50 Match length 94 % identity

NCBI Description (AJ132436) GA 2-oxidase [Arabidopsis thaliana]

Seq. No. 168648

Seq. ID LIB3234-065-P1-K1-G11

```
Method BLASTN
NCBI GI 94415928
BLAST score 161
E value 2.0e-85
Match length 235
% identity 96
NCBI Description Arabidon
```

NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168649

Seq. ID LIB3234-065-P1-K1-G12

Method BLASTN
NCBI GI g4115370
BLAST score 186
E value 1.0e-100
Match length 320
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168650

Seq. ID LIB3234-065-P1-K1-G3

Method BLASTX
NCBI GI g112681
BLAST score 432
E value 8.0e-43
Match length 93
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 168651

Seq. ID LIB3234-065-P1-K1-G5

Method BLASTX
NCBI GI g166570
BLAST score 171
E value 4.0e-12
Match length 103
% identity 38

NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No. 168652

Seq. ID LIB3234-065-P1-K1-G6

Method BLASTX
NCBI GI g135858
BLAST score 170
E value 1.0e-12
Match length 50
% identity 72

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein

Seq. No.

168658

[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 168653 Seq. ID LIB3234-065-P1-K1-H1 Method BLASTX NCBI GI g2088654 BLAST score 477 E value 5.0e-48 Match length 109 % identity 87 (AF002109) 60S acidic ribosomal protein P0 isolog NCBI Description [Arabidopsis thaliana] Seq. No. 168654 LIB3234-065-P1-K1-H10 Seq. ID Method BLASTX NCBI GI g3292817 BLAST score 158 E value 1.0e-10 Match length 53 % identity 64 NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana] 168655 Seq. No. Seq. ID LIB3234-065-P1-K1-H11 Method BLASTX NCBI GI g3236248 BLAST score 320 E value 6.0e - 30Match length 90 % identity 72 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana] Seq. No. 168656 Seq. ID LIB3234-065-P1-K1-H3 Method BLASTN NCBI GI q4467131 BLAST score 39 E value 1.0e-12 Match length 173 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project) Seq. No. 168657 Seq. ID LIB3234-070-P1-K1-A1 Method BLASTX NCBI GI g2160151 BLAST score 371 E value 1.0e-35 Match length 105 73 % identity (AC000375) Strong similarity to Brassica aspartic protease NCBI Description (gb_X77260). [Arabidopsis thaliana]

```
Seq. ID
                   LIB3234-070-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g3212869
BLAST score
                   208
E value
                   1.0e-16
Match length
                   49
% identity
                   73
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   168659
Seq. ID
                   LIB3234-070-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   q4753645
BLAST score
                   115
E value
                   2.0e-58
Match length
                   150
% identity
                   94
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
                   (ESSA project)
Seq. No.
                   168660
Seq. ID
                   LIB3234-070-P1-K1-A2
                   BLASTX
Method
NCBI GI
                   g629528
BLAST score
                   573
E value
                   3.0e-59
Match length
                   123
% identity
                   98
NCBI Description
                   hypothetical protein - Arabidopsis thaliana
                   >gi_1076335_pir__S51580 hypothetical protein 1 -
                   Arabidopsis thaliana >gi 499167 emb CAA56144 (X79707) ORF
                   [Arabidopsis thaliana]
Seq. No.
                   168661
Seq. ID
                   LIB3234-070-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q1531762
BLAST score
                   191
E value
                   2.0e-14
Match length
                   50
% identity
                   74
NCBI Description
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   168662
Seq. ID
                   LIB3234-070-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g4063552
BLAST score
                   608
E value
                   2.0e-63
Match length
                  123
% identity
                   98
NCBI Description
                  (AF035908) ATP synthase beta subunit [Muntingia calabura]
Seq. No.
                  168663
                  LIB3234-070-P1-K1-A6
Seq. ID
Method
                  BLASTN
```

BLAST score

E value

148

1.0e-77



```
NCBI GI
                   q4432829
BLAST score
                   334
                   0.0e+00
E value
Match length
                   373
% identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T1B3 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168664
                   LIB3234-070-P1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4314363
BLAST score
                   411
                   2.0e-40
E value
Match length
                   100
% identity
                   75
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168665
Seq. ID
                   LIB3234-070-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2244740
BLAST score
                   348
E value
                   5.0e-33
Match length
                   120
% identity
                   57
NCBI Description (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
                   168666
Seq. No.
Seq. ID
                   LIB3234-070-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1351272
BLAST score
                   391
E value
                   5.0e-38
Match length
                   99
% identity
                   78
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
Seq. No.
                   168667
Seq. ID
                   LIB3234-070-P1-K1-B2
Method
                   BLASTN
NCBI GI
                   g297420
BLAST score
                   94
E value
                   2.0e-45
Match length
                   201
                   92
% identity
NCBI Description Nicotiana sp. promoter DNA
                   168668
Seq. No.
Seq. ID
                   LIB3234-070-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g4512690
```

Match length 325 % identity 97 NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence Seq. No. 168669 LIB3234-070-P1-K1-B6 Seq. ID Method BLASTX NCBI GI g117822 BLAST score 594 E value 8.0e-62 Match length 126 % identity 90 NCBI Description CYTOCHROME B6 >gi_65635_pir__CBNT6 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast >gi_11858_emb_CAA77375 (Z00044) cytochrome b6 [Nicotiana tabacum] >gi_225226_prf__1211235BH cytochrome b6 [Nicotiana tabacum] Seq. No. 168670 LIB3234-070-P1-K1-C10 Seq. ID Method BLASTN NCBI GI q3047074 BLAST score 55 E value 4.0e-22 Match length 115 % identity 87 NCBI Description Arabidopsis thaliana BAC F21E10 Seq. No. 168671 Seq. ID LIB3234-070-P1-K1-C11 Method BLASTX NCBI GI q1706714 BLAST score 358 E value 4.0e-34 Match length 117 % identity NCBI Description ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) (ELECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS) >gi_1209054 (U32230) EtfS [Bradyrhizobium japonicum] Seq. No. 168672 Seq. ID LIB3234-070-P1-K1-C2 Method BLASTX NCBI GI g2827139 BLAST score 654 E value 7.0e-69

Match length 123 % identity 98

NCBI Description (AF027172) cellulose synthase catalytic subunit

> [Arabidopsis thaliana] >gi_4049343_emb_CAA22568 (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 168673

Seq. ID LIB3234-070-P1-K1-C3

```
Method
                   BLASTX
NCBI GI
                   g1655424
BLAST score
                   440
E value
                   1.0e-43
Match length
                   89
% identity
                   96
NCBI Description
                  (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]
                   >gi_3212878 (AC004005) GDP dissociation inhibitor
                   [Arabidopsis thaliana]
Seq. No.
                   168674
                   LIB3234-070-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911059
BLAST score
                   590
E value
                   2.0e-61
Match length
                   123
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  168675
Seq. ID
                  LIB3234-070-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g3193305
BLAST score
                   344
E value
                  0.0e+00
Match length
                  372
% identity
                   98
NCBI Description Arabidopsis thaliana BAC F3D13
Seq. No. Seq. ID
                  168676
                  LIB3234-070-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2829898
BLAST score
                  336
E value
                  1.0e-31
Match length
                  85
% identity
                  75
NCBI Description (AC002311) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168677
Seq. ID
                  LIB3234-070-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4557026
BLAST score
                  173
E value
                  2.0e-12
Match length
                  97
% identity
NCBI Description guanine nucleotide exchange factor p532 >gi 1477565
                  (U50078) p532 [Homo sapiens]
```

Seq. No. 168678

Seq. ID LIB3234-070-P1-K1-D12

Method BLASTX NCBI GI g2244749 BLAST score 464 E value 1.0e-46

NCBI Description

```
Match length
                   102
% identity
                   89
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                   168679
Seq. ID
                   LIB3234-070-P1-K1-D2
Method
                   BLASTN
NCBI GI
                   g4519191
BLAST score
                   34
E value
                   1.0e-09
Match length
                   70
% identity
                   87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9P8, complete sequence
Seq. No.
                   168680
Seq. ID
                   LIB3234-070-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   g3873174
BLAST score
                   351
E value
                   0.0e+00
Match length
                   375
                   98
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168681
Seq. ID
                   LIB3234-070-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g4757417
BLAST score
                   152
E value
                   5.0e-80
Match length
                   341
% identity
                   89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   T30G6, complete sequence
Seq. No.
                   168682
Seq. ID
                   LIB3234-070-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g3935151
BLAST score
                   582
E value
                   2.0e-60
Match length
                   110
% identity
                   98
NCBI Description
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                   168683
Seq. ID
                  LIB3234-070-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   q4204298
BLAST score
                   592
E value
                   1.0e-61
Match length
                  118
% identity
                   97
```

22866

[Arabidopsis thaliana]

(AC003027) lcl_prt_seq No definition line found

```
Seq. No.
                   168684
Seq. ID
                   LIB3234-070-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g3789925
BLAST score
                   54
E value
                   1.0e-22
Match length
                   120
% identity
                   50
NCBI Description
                  (AF086625) phosphoinositide-dependent protein kinase PDK1
                   [Mus musculus]
                   168685
Seq. No.
Seq. ID
                   LIB3234-070-P1-K1-E11
Method
                  BLASTX
NCBI GI
                   q4204263
BLAST score
                   309
E value
                   2.0e-28
Match length
                   98
                   65
% identity
NCBI Description
                  (AC005223) 40409 [Arabidopsis thaliana]
                   168686
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4056429
BLAST score
                   165
E value
                   9.0e-88
Match length
                  265
% identity
                   74
NCBI Description Arabidopsis thaliana chromosome 1 BAC F508 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168687
Seq. ID
                  LIB3234-070-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2507426
BLAST score
                  569
E value
                   7.0e-59
Match length
                  125
% identity
                  92
NCBI Description
                  ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR
                   (ALANINE--TRNA LIGASE) (ALARS) >gi 1673365 emb CAA80380
                   (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  168688
Seq. ID
                  LIB3234-070-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q3548797
BLAST score
                  234
E value
                  1.0e-129
Match length
                  375
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   168689
Seq. ID
                   LIB3234-070-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q4191814
BLAST score
                   169
E value
                   6.0e-12
Match length
                   117
                   35
% identity
NCBI Description (AB008680) alpha' subunit of beta-conglycinin [Glycine max]
Seq. No.
                   168690
Seq. ID
                   LIB3234-070-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q2492513
BLAST score
                   149
                   3.0e-34
E value
Match length
                   118
% identity
                   67
NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG 4
                   >gi_1652085_dbj_BAA17010_ (D90902) cell division protein
                   FtsH [Synechocystis sp.]
Seq. No.
                   168691
Seq. ID
                   LIB3234-070-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q2924784
BLAST score
                   98
E value
                   1.0e-03
Match length
                   103
% identity
                   13
NCBI Description
                  (AC002334) similar to jasmonate inducible protein
                   [Arabidopsis thaliana]
Seq. No.
                   168692
Seq. ID
                   LIB3234-070-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q2583120
BLAST score
                   616
E value
                   2.0e-64
Match length
                   123
% identity
                   99
NCBI Description
                   (AC002387) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   168693
Seq. ID
                  LIB3234-070-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3334123
BLAST score
                  387
```

E value 2.0e-37 Match length 99 % identity 83

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787

(AC002334) mitochondrial F1-ATPase, gamma subunit

[Arabidopsis thaliana]

Seq. No. 168694

Seq. ID LIB3234-070-P1-K1-F10

Method BLASTX
NCBI GI g3695023
BLAST score 305
E value 6.0e-28
Match length 122
% identity 52

NCBI Description (AF055850) unknown [Arabidopsis thaliana]

Seq. No. 168695

Seq. ID LIB3234-070-P1-K1-F3

Method BLASTX
NCBI GI g1864017
BLAST score 535
E value 7.0e-55
Match length 102
% identity 99

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 168696

Seq. ID LIB3234-070-P1-K1-F4

Method BLASTN
NCBI GI g3184270
BLAST score 189
E value 1.0e-102
Match length 295
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T8K22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168697

Seq. ID LIB3234-070-P1-K1-F5

Method BLASTX
NCBI GI g730645
BLAST score 469
E value 4.0e-47
Match length 107
% identity 89

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679 (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi 313188 emb CAA80681 (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi 1903366 gb AAB70449 (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788, gb ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 168698

Seq. ID LIB3234-070-P1-K1-F7

Method BLASTN
NCBI GI g2760171
BLAST score 345
E value 0.0e+00
Match length 369
% identity 98

% identity

98

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MPA24, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168699
                    LIB3234-070-P1-K1-F8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q132770
BLAST score
                    333
E value
                    3.0e-31
Match length
                    90
% identity
                    74
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L20 >gi_71275_pir__R5NT20
NCBI Description
                    ribosomal protein L20 - common tobacco chloroplast
                   >gi_11852_emb_CAA77372 (Z00044) ribosomal protein L20
[Nicotiana tabacum] >gi_225221_prf__1211235BC ribosomal
                   protein L20 [Nicotiana tabacum]
Seq. No.
                   168700
Seq. ID
                   LIB3234-070-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g2286069
BLAST score
                   411
E value
                   2.0e-40
Match length
                   123
% identity
                    67
NCBI Description
                  (U72155) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   168701
Seq. ID
                   LIB3234-070-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g4586256
BLAST score
                   574
E value
                   2.0e-59
Match length
                   121
% identity
                   94
                   (AL049640) probable photosystem I chain XI precursor
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   168702
Seq. ID
                   LIB3234-070-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g2980787
BLAST score
                   207
E value
                   1.0e-113
Match length
                   388
% identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
                   (ESSAII project)
Seq. No.
                   168703
Seq. ID
                   LIB3234-070-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g3335169
BLAST score
                   657
E value
                   3.0e-69
Match length
                   125
```

```
(AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  168704
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g3228389
BLAST score
                  356
E value
                  0.0e+00
Match length
                  380
% identity
                  98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168705
Seq. ID
                  LIB3234-070-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1170939
BLAST score
                  397
E value
                  1.0e-38
Match length
                  81
% identity
                  93
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867 (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
Seq. No.
                  168706
Seq. ID
                  LIB3234-070-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3819164
BLAST score
                  548
E value
                  2.0e-56
Match length
                  122
% identity
                  90
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  max]
                  168707
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4678299
BLAST score
                  54
E value
                  1.0e-53
Match length
                  112
% identity
                  98
NCBI Description
                  (AL049655) cysteine proteinase precursor-like protein
```

[Arabidopsis thaliana]

Seq. No. 168708

Seq. ID LIB3234-070-P1-K1-H3

Method BLASTX NCBI GI g4204308 BLAST score 356



E value 7.0e-34 Match length 68 % identity 91 NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana] Seq. No. 168709 Seq. ID LIB3234-070-P1-K1-H4 Method BLASTX NCBI GI g82051 BLAST score 317 3.0e-29 E value Match length 119 55 % identity NCBI Description lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota] Seq. No. 168710 Seq. ID LIB3234-070-P1-K1-H5 Method BLASTX NCBI GI q3024871 BLAST score 356 E value 7.0e - 34Match length 125 % identity 54 NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.] Seq. No. 168711 Seq. ID LIB3234-070-P1-K1-H6 Method BLASTX NCBI GI g3025470 BLAST score 341 E value 4.0e-32 Match length 127 % identity 49 NCBI Description (U76756) endo-beta-1,4-glucanase [Pinus radiata] Seq. No. 168712 Seq. ID LIB3234-070-P1-K1-H7 Method BLASTX NCBI GI g2980772 BLAST score 146 E value 3.0e-09 Match length 84 % identity NCBI Description (AL022198) putative protein [Arabidopsis thaliana] Seq. No. 168713

Seq. ID LIB3234-070-P1-K1-H8

Method BLASTN
NCBI GI g4079614
BLAST score 322
E value 0.0e+00

NCBI Description

```
370
Match length
% identity
                   96
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F21M11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168714
Seq. ID
                   LIB3234-071-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g336274
BLAST score
                   173
E value
                   2.0e-92
Match length
                   319
% identity
                   91
NCBI Description Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA,
                   tRNA-Arg, and tRNA-Asn genes
Seq. No.
                   168715
                  LIB3234-071-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789828
BLAST score
                   187
E value
                   4.0e-14
Match length
                   50
                   80
% identity
NCBI Description (AF061412) CAULIFLOWER [Arabidopsis thaliana]
Seq. No.
                  168716
                  LIB3234-071-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3688162
BLAST score
                  178
E value
                  1.0e-19
Match length
                   56
% identity
                   95
NCBI Description (AJ009672) centrin [Arabidopsis thaliana]
Seq. No.
                  168717
Seq. ID
                  LIB3234-071-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q3668073
BLAST score
                   313
E value
                  1.0e-176
Match length
                  357
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T4C15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168718
Seq. ID
                  LIB3234-071-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  q4589414
BLAST score
                  179
E value
                  4.0e-96
Match length
                  298
% identity
                  97
```

22873

K14B15, complete sequence

Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

```
Seq. No.
                  168719
Seq. ID
                  LIB3234-071-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g16181
BLAST score
                  81
E value
                  1.0e-37
Match length
                  305
% identity
                  85
NCBI Description
                  A.thaliana gene for tonoplast intrinsic protein
                  alpha-TIP(Ara) >gi_166622_gb_M84343_ATHATIP Arabidopsis
                  thaliana tonoplast intrinsic protein (alpha-TIP) gene,
                  complete cds
                  168720
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-A5
Method
                  BLASTX
                  g1621539
NCBI GI
BLAST score
                  285
E value
                  1.0e-25
Match length
                  106
                  62
% identity
NCBI Description
                  (U28415) annexin-like protein [Arabidopsis thaliana]
Seq. No.
                  168721
Seq. ID
                  LIB3234-071-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  195
E value
                  5.0e-15
Match length
                  101
% identity
                  40
NCBI Description vicilin gene B [Saguinus oedipus]
Seq. No.
                  168722
Seq. ID
                  LIB3234-071-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  q4589414
BLAST score
                  66
E value
                  8.0e-29
Match length
                  158
% identity
                  89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14B15, complete sequence
Seq. No.
                  168723
Seq. ID
                  LIB3234-071-P1-K1-B1
```

 Seq. No.
 168723

 Seq. ID
 LIB3234-071-P1-K1-B1

 Method
 BLASTN

 NCBI GI
 g4314374

 BLAST score
 288

E value 1.0e-161
Match length 292
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168724



```
Seq. ID
                  LIB3234-071-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q710625
BLAST score
                  246
E value
                  1.0e-136
Match length
                  281
% identity
                  96
NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds
Seq. No.
                  168725
```

Seq. ID LIB3234-071-P1-K1-B12 Method BLASTN

Method BLASTN
NCBI GI g4455262
BLAST score 303
E value 1.0e-170
Match length 360
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22

(ESSAII project)

Seq. No. 168726

Seq. ID LIB3234-071-P1-K1-B2

Method BLASTN
NCBI GI g4539378
BLAST score 132
E value 5.0e-68
Match length 328
% identity 77

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 168727

Seq. ID LIB3234-071-P1-K1-B3

Method BLASTX
NCBI GI g384341
BLAST score 184
E value 1.0e-13
Match length 97
% identity 39

NCBI Description major storage protein [Theobroma cacao]

Seq. No. 168728

Seq. ID LIB3234-071-P1-K1-B4

Method BLASTN
NCBI GI g3688161
BLAST score 105
E value 6.0e-52
Match length 124
% identity 100

NCBI Description Arabidopsis thaliana mRNA for centrin

Seq. No. 168729

Seq. ID LIB3234-071-P1-K1-B9

Method BLASTX
NCBI GI g3819164
BLAST score 392
E value 3.0e-38



Match length 94 % identity 83

NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine

max]

Seq. No. 168730

Seq. ID LIB3234-071-P1-K1-C1

Method BLASTN
NCBI GI g2760170
BLAST score 284
E value 1.0e-159
Match length 340
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 168731

Seq. ID LIB3234-071-P1-K1-C10

Method BLASTX
NCBI GI g1168256
BLAST score 119
E value 4.0e-58
Match length 120
% identity 97

NCBI Description ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR

(TRANSAMINASE A) >gi 693688 (U15026) aspartate

aminotransferase [Arabidopsis thaliana] >gi_3201622
(AC004669) aspartate aminotransferase [Arabidopsis

thaliana]

Seq. No. 168732

Seq. ID LIB3234-071-P1-K1-C3

Method BLASTX
NCBI GI g118926
BLAST score 161
E value 4.0e-11
Match length 69

% identity 46

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR

>gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 168733

Seq. ID LIB3234-071-P1-K1-C5

Method BLASTX
NCBI GI 94510397
BLAST score 613
E value 5.0e-64
Match length 122
% identity 96

NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No. 168734

Seq. ID LIB3234-071-P1-K1-C7

```
Method
                   BLASTX
NCBI GI
                   g3869253
BLAST score
                   229
                   4.0e-19
E value
Match length
                  104
% identity
                   51
NCBI Description
                  (U39288) ferredoxin-dependent glutamate synthase precursor
                   [Arabidopsis thaliana]
                  168735
Seq. No.
                  LIB3234-071-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334128
BLAST score
                  79
E value
                  2.0e-52
Match length
                  124
% identity
                  95
NCBI Description BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
                  PRECURSOR (BCCP) >gi 1066348 (U23155) acetyl-CoA
                   carboxylase biotin-containing subunit [Arabidopsis
                  thaliana]
Seq. No.
                  168736
Seq. ID
                  LIB3234-071-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g267073
BLAST score
                  634
E value
                  2.0e-66
Match length
                  125
% identity
                  97
NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  168737
Seq. ID
                  LIB3234-071-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q2494110
BLAST score
                  286
E value
                  1.0e-160
Match length
                  322
% identity
                  97
NCBI Description
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168738
Seq. ID
                  LIB3234-071-P1-K1-D4
                  BLASTN
                  g4757413
                  206
E value
                  1.0e-112
```

Method NCBI GI BLAST score

Match length 276 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXO21, complete sequence



Seq. No.

Seq. ID

168739

BLASTX

LIB3234-071-P1-K1-D5

```
Method
NCBI GI
                  g4581146
BLAST score
                  508
E value
                  1.0e-51
Match length
                  115
% identity
                  89
                  (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
                  168740
Seq. No.
                  LIB3234-071-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548847
BLAST score
                  379
E value
                  1.0e-36
                  75
Match length
                  99
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
                  >gi 1086182 pir S39501 ribosomal protein S12 -
                  curled-leaved tobacco >gi 225248 prf 1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
                  168741
Seq. No.
                  LIB3234-071-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642157
BLAST score
                  273
E value
                  4.0e-24
Match length
                  111
% identity
NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  168742
Seq. ID
                  LIB3234-071-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  559
E value
                  1.0e-57
Match length
                  122
% identity
                  87
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  168743
Seq. ID
                  LIB3234-071-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g514324
BLAST score
                  135
E value
                  3.0e-18
Match length
                  62
% identity
                  87
NCBI Description (L34773) RNA polymerase subunit [Arabidopsis thaliana]
                                      22878
```

>gi_2462755 (AC002292) RNA polymerase subunit (isoform B) [Arabidopsis thaliana] >gi_1586550_prf__2204246B RNA* polymerase [Arabidopsis thaliana]

Seq. No. 168744

Seq. ID LIB3234-071-P1-K1-E4

Method BLASTN
NCBI GI g3540210
BLAST score 166
E value 2.0e-88
Match length 317
% identity 89

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168745

Seq. ID LIB3234-071-P1-K1-E7

Method BLASTX
NCBI GI g2492514
BLAST score 361
E value 2.0e-34
Match length 92
% identity 77

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH

protease [Arabidopsis thaliana]

Seq. No. 168746

Seq. ID LIB3234-071-P1-K1-E9

Method BLASTN
NCBI GI g2828278
BLAST score 179
E value 4.0e-96
Match length 358
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 168747

Seq. ID LIB3234-071-P1-K1-F10

Method BLASTN
NCBI GI g2618604
BLAST score 363
E value 0.0e+00
Match length 383
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 168748

Seq. ID LIB3234-071-P1-K1-F12

Method BLASTX
NCBI GI g384341
BLAST score 173
E value 2.0e-12
Match length 101
% identity 38

Match length

NCBI Description

% identity

68

85



```
NCBI Description major storage protein [Theobroma cacao]
                  168749
Seq. No.
                  LIB3234-071-P1-K1-F3
Seq. ID
Method
                  BLASTN
                  g2351062
NCBI GI
BLAST score
                  343
E value
                  0.0e+00
Match length
                  375
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                  168750
Seq. No.
                  LIB3234-071-P1-K1-F4
Seq. ID
Method
                  BLASTN
                  g4757403
NCBI GI
BLAST score
                  37
E value
                  2.0e-11
Match length
                  69
                  89
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
Seq. No.
                  168751
                  LIB3234-071-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4406790
BLAST score
                  269
E value
                  1.0e-150
Match length
                  339
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC T1016 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168752
Seq. ID
                  LIB3234-071-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  q4678705
BLAST score
                  295
E value
                  1.0e-165
Match length
                  359
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                  (ESSA project)
Seq. No.
                  168753
Seq. ID
                  LIB3234-071-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q462147
BLAST score
                  65
E value
                  5.0e-22
```

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)

(PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase

GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

```
(EC 5.3.1.9) - Arabidopsis thaliana
>gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate
isomerase [Arabidopsis thaliana]
```

Seq. No. LIB3234-071-P1-K1-G12 Seq. ID Method BLASTX NCBI GI g2781354 BLAST score 554 E value 5.0e-57Match length 108 % identity 95

168754

NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana]

168755 Seq. No. LIB3234-071-P1-K1-G8 Seq. ID Method BLASTN

NCBI GI g3406034 BLAST score 46 E value 8.0e-17 Match length 175 % identity 88

NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 168756

Seq. ID LIB3234-071-P1-K1-H1

Method BLASTN NCBI GI , g3894179 BLAST score 81 E value 1.0e-37

Match length 201 % identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168757

Seq. ID LIB3234-071-P1-K1-H6

Method BLASTX NCBI GI g133750 BLAST score 547 E value 3.0e-56 Match length 108 97 % identity

CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 NCBI Description

> >gi_320170_pir__A26574 ribosomal protein S12 - soybean chloroplast >gi_11572_emb_CAA28661_ (X05013) rps12 [Glycine

max]

Seq. No. 168758

Seq. ID LIB3234-071-P1-K1-H8

Method BLASTN NCBI GI g4753195 BLAST score 298 E value 1.0e-167 Match length 372 % identity 88

```
Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
NCBI Description
                  cM, complete sequence
Seq. No.
                  168759
                  LIB3234-071-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924779
BLAST score
                  363
E value
                  6.0e-35
Match length
                  91
% identity
                  80
                  (ACO02334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                  thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi_2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
Seq. No.
                  168760
                  LIB3234-072-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4206762
BLAST score
                  215
E value
                  1.0e-117
Match length
                  282
% identity
                  93
NCBI Description
                  Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
                  168761
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  q2760164
BLAST score
                  364
E value
                  0.0e+00
Match length
                  380
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168762
Seq. ID
                  LIB3234-072-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3805849
BLAST score
                  625
E value
                  2.0e-65
Match length
                  125
% identity
                  98
NCBI Description
                  (AL031986) cytoplasmatic aconitate hydratase (citrate
                  hydro-lyase) (aconitase) (EC 4.2.1.3) [Arabidopsis thaliana]
```

Seq. No. Seq. ID LIB3234-072-P1-K1-A6

168763

Method BLASTN NCBI GI g4544435 BLAST score 34 E value 1.0e-09 Match length 64

NCBI Description



% identity 89 Arabidopsis thaliana chromosome II BAC F14M13 genomic NCBI Description sequence, complete sequence 168764 Seq. No. LIB3234-072-P1-K1-A9 Seq. ID Method BLASTX NCBI GI g2842490 BLAST score 608 E value 2.0e-63 Match length 117 % identity 97 (AL021749) heat-shock protein [Arabidopsis thaliana] NCBI Description Seq. No. 168765 LIB3234-072-P1-K1-B12 Seq. ID Method BLASTN NCBI GI q4206762 49 BLAST score 2.0e-18 E value Match length 88 % identity 89 NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds Seq. No. 168766 LIB3234-072-P1-K1-B3 Seq. ID Method BLASTN g4159704 NCBI GI 223 BLAST score E value 1.0e-122 Match length 361 97 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence Seq. No. 168767 Seq. ID LIB3234-072-P1-K1-B7 Method BLASTX NCBI GI g2244892 272 BLAST score E value 5.0e-24 Match length 68 76 % identity NCBI Description (Z97338) similarity to cycloartenol synthase [Arabidopsis thaliana] Seq. No. 168768 Seq. ID LIB3234-072-P1-K1-B8 Method BLASTX NCBI GI q1628583 BLAST score 226 E value 1.0e-21 Match length 105 % identity 63

22883

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S



168769

cruciferin seed storage protein [Arabidopsis thaliana]

LIB3234-072-P1-K1-C11 Seq. ID Method BLASTN NCBI GI q3659491 BLAST score 280 1.0e-156 E value Match length 343

98 % identity

Seq. No.

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

168770 Seq. No.

Seq. ID LIB3234-072-P1-K1-C12

Method BLASTX NCBI GI g1345973 BLAST score 421 E value 2.0e-41 Match length 95 81 % identity

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

> >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

168771 Seq. No.

Seq. ID LIB3234-072-P1-K1-C2

Method BLASTX NCBI GI g1345973 BLAST score 431 E value 1.0e-42Match length 97 81 % identity

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM NCBI Description

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 168772

Seq. ID LIB3234-072-P1-K1-C3

Method BLASTX NCBI GI q2500378 BLAST score 437 E value 2.0e-43 Match length 94 % identity 86

Seq. No.

Seq. ID

168778

LIB3234-072-P1-K1-D2



```
NCBI Description 60S RIBOSOMAL PROTEIN L37
                  168773
Seq. No.
                  LIB3234-072-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g2961542
NCBI GI
BLAST score
                  513
                  3.0e-52
E value
                  93
Match length
                  100
% identity
NCBI Description (AF050463) zinc finger transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  168774
                  LIB3234-072-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062165
BLAST score
                  74
                  8.4e-01
E value
Match length
                  111
                  32
% identity
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  168775
                  LIB3234-072-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785989
BLAST score
                  92
                  5.0e-63
E value
Match length
                  125
% identity
                  98
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                  168776
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  q4756963
BLAST score
                  227
E value
                  1.0e-125
Match length
                  368
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
                  168777
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  q1785729
BLAST score
                  35
E value
                  2.0e-10
Match length
                  141
% identity
NCBI Description A.thaliana mitochondrial genome, part B
```

% identity

NCBI Description

96



```
Method
                  BLASTX
NCBI GI
                  q2119846
                  555
BLAST score
E value
                  3.0e-57
Match length
                  115
                  91
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  168779
Seq. ID
                  LIB3234-072-P1-K1-D3
Method
                  BLASTN
                  g4115930
NCBI GI
BLAST score
                  346
E value
                  0.0e + 00
Match length
                  370
                  98
% identity
NCBI Description Arabidopsis thaliana BAC T4B21
Seq. No.
                  168780
                  LIB3234-072-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024871
BLAST score
                  244
E value
                  9.0e-21
Match length
                  101
% identity
                  49
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                  >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
                  sp.]
Seq. No.
                  168781
Seq. ID
                  LIB3234-072-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4325324
BLAST score
                  641
E value
                  3.0e-67
Match length
                  124
% identity
                  98
NCBI Description
                  (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                  thaliana]
Seq. No.
                  168782
Seq. ID
                  LIB3234-072-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g3738313
BLAST score
                  311
E value
                  1.0e-175
Match length
                  373
```

22886

Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

```
168783
Seq. No.
                  LIB3234-072-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263722
BLAST score
                  184
                  5.0e-29
E value
Match length
                  78
                  87
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168784
                  LIB3234-072-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935157
BLAST score
                  182
E value
                   2.0e-25
Match length
                  72
                  86
% identity
NCBI Description
                  (AC005106) T25N20.21 [Arabidopsis thaliana]
                  168785
Seq. No.
                  LIB3234-072-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2564048
BLAST score
                   233
E value
                  1.0e-128
Match length
                   325
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKD15, complete sequence [Arabidopsis thaliana]
                   168786
Seq. No.
Seq. ID
                   LIB3234-072-P1-K1-E3
Method
                  BLASTN
NCBI GI
                   q3892698
BLAST score
                   272
E value
                   1.0e-151
Match length
                   378
% identity
                   92
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2
                   (ESSAII project)
Seq. No.
                   168787
                   LIB3234-072-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911060
BLAST score
                   161
E value
                   5.0e-11
                  78
Match length
```

30 % identity

(AL021961) putative protein [Arabidopsis thaliana] NCBI Description

>gi_3297826_emb_CAA19884.1_ (AL031032) putative protein

[Arabidopsis thaliana]

Seq. No. 168788

Seq. ID LIB3234-072-P1-K1-F12



Method BLASTN
NCBI GI g4455168
BLAST score 104
E value 3.0e-51
Match length 312
% identity 88
NCBI Description Arabidop

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No. 168789

Seq. ID LIB3234-072-P1-K1-F2

Method BLASTN
NCBI GI 94519195
BLAST score 291
E value 1.0e-163
Match length 336
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MQC12, complete sequence

Seq. No. 168790

Seq. ID LIB3234-072-P1-K1-F3

Method BLASTX
NCBI GI g4154281
BLAST score 286
E value 1.0e-25
Match length 68
% identity 76

NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No. 168791

Seq. ID LIB3234-072-P1-K1-F4

Method BLASTX
NCBI GI g1791309
BLAST score 467
E value 6.0e-47
Match length 102
% identity 93

NCBI Description (U83500) cystathionine gamma-synthase [Arabidopsis

thaliana] >gi_2852454_dbj_BAA24699_ (AB010888)

cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 168792

Seq. ID LIB3234-072-P1-K1-F5

Method BLASTX
NCBI GI g1113941
BLAST score 274
E value 3.0e-24
Match length 89
% identity 60

NCBI Description (U40713) Pv42p [Phaseolus vulgaris]

Seq. No. 168793

Seq. ID LIB3234-072-P1-K1-F6

Method BLASTX NCBI GI g3334128

BLAST score 68



E value 1.0e-54
Match length 125
% identity 97
NCBI Description BIOTIN
PRECURS

CBI Description BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE

PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA carboxylase biotin-containing subunit [Arabidopsis

thaliana]

168794

Seq. No.

Seq. ID LIB3234-072-P1-K1-F7

Method BLASTX
NCBI GI g3096912
BLAST score 450
E value 6.0e-45
Match length 95
% identity 98

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3234-072-P1-K1-F9

168795

Method BLASTX
NCBI GI g3869088
BLAST score 430
E value 2.0e-42
Match length 103
% identity 81

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 168796

Seq. ID LIB3234-072-P1-K1-G1

Method BLASTX
NCBI GI g132074
BLAST score 577
E value 8.0e-60
Match length 106
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 168797

Seq. ID LIB3234-072-P1-K1-G10

Method BLASTX
NCBI GI g2829893
BLAST score 516
E value 1.0e-52
Match length 108
% identity 96

NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No. 168798

Seq. ID LIB3234-072-P1-K1-G12

Method BLASTX
NCBI GI g118926
BLAST score 252
E value 1.0e-21



```
97
Match length
                  54
% identity
NCBI Description
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
                  168799
Seq. No.
                  LIB3234-072-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132074
                  350
BLAST score
E value
                  3.0e-33
                  84
Match length
                  80
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  168800
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4154281
BLAST score
                  170
                  2.0e-12
E value
Match length
                  44
                  70
% identity
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
                  168801
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g2351065
BLAST score
                  300
E value
                  1.0e-168
Match length
                  352
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168802
                  LIB3234-072-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419757
                  522
BLAST score
E value
                  2.0e-53
```

Match length 125 83 % identity

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) precursor -

Arabidopsis thaliana

Seq. No. 168803

Seq. ID LIB3234-072-P1-K1-H1

Method BLASTX



```
NCBI GI
                   q1170606
BLAST score
                   271
E value
                   7.0e - 24
Match length
                  63
                  84
% identity
NCBI Description
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
                  >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
                  chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                  >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
                   In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
Seq. No.
                  168804
Seq. ID
                  LIB3234-072-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q4538990
BLAST score
                  246
E value
                  1.0e-136
                  345
Match length
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
                  (ESSA project)
Seq. No.
                  168805
Seq. ID
                  LIB3234-072-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4588779
BLAST score
                  264
E value
                   4.0e-23
Match length
                  75
                   67
% identity
NCBI Description (AF117267) UDP glucose: flavonoid 3-O-glucosyl transferase
                   [Malus domestica]
Seq. No.
                  168806
Seq. ID
                  LIB3234-072-P1-K1-H2
Method
                  BLASTN
NCBI GI '
                   q2828182
BLAST score
                  40
E value
                   3.0e-13
Match length
                   64
% identity
                   91
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOJ9, complete sequence [Arabidopsis thaliana]
                  168807
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3983125
BLAST score
                  492
E value
                  8.0e-50
```

Match length 125 78 % identity

NCBI Description (AF097648) phosphate/triose-phosphate translocator

precursor [Arabidopsis thaliana]

```
168808
Seq. No.
                  LIB3234-072-P1-K1-H4
Seq. ID
                  BLASTX
Method
                   g1871174
NCBI GI
                   504
BLAST score
                   3.0e-51
E value
                  122
Match length
                   74
% identity
                  (U90439) actin isolog [Arabidopsis thaliana]
NCBI Description
                  168809
Seq. No.
                  LIB3234-072-P1-K1-H5
Seq. ID
Method
                   BLASTX
                   g2649345
NCBI GI
                   369
BLAST score
E value
                   2.0e-35
                   120
Match length
                   58
% identity
                  (AE001019) tryptophan synthase, subunit beta (trpB-1)
NCBI Description
                   [Archaeoglobus fulgidus]
```

168810 Seq. No. LIB3234-072-P1-K1-H6 Seq. ID BLASTN Method NCBI GI g4753195 BLAST score 323

0.0e + 00E value 379 Match length 89 % identity

Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 NCBI Description

cM, complete sequence

168811 Seq. No.

LIB3234-072-P1-K1-H7 Seq. ID

Method BLASTX g1076423 NCBI GI 186 BLAST score 6.0e-35 E value Match length 104 79 % identity

transcription factor OBF5 - Arabidopsis thaliana (fragment) NCBI Description

>gi 414615 emb CAA49525 (X69900) ocs-element binding

factor 5 [Arabidopsis thaliana]

168812 Seq. No.

Seq. ID LIB3234-072-P1-K1-H8

Method BLASTX NCBI GI q4038491 BLAST score 177 E value 6.0e - 13Match length 122 % identity 36

(AJ131705) poly(ADP-ribose) polymerase [Arabidopsis NCBI Description

thaliana]

Seq. No. 168813



Seq. ID LIB3234-072-P1-K1-H9

Method BLASTN
NCBI GI g2342673
BLAST score 78
E value 8.0e-36
Match length 210
% identity 82

NCBI Description Sequence of BAC F7G19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 168814

Seq. ID LIB3234-074-P1-K1-A1

Method BLASTN
NCBI GI g2924257
BLAST score 31
E value 8.0e-09
Match length 31
% identity 50

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 168815

Seq. ID LIB3234-074-P1-K1-A10

Method BLASTN
NCBI GI g4589950
BLAST score 118
E value 4.0e-60
Match length 130
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic

sequence, complete sequence

Seq. No. 168816

Seq. ID LIB3234-074-P1-K1-A11

Method BLASTN
NCBI GI g4733980
BLAST score 38
E value 6.0e-12
Match length 198
% identity 80

NCBI Description Arabidopsis thaliana chromosome II BAC T27D6 genomic

sequence, complete sequence

Seq. No. 168817

Seq. ID LIB3234-074-P1-K1-A2

Method BLASTN
NCBI GI g4589438
BLAST score 373
E value 0.0e+00
Match length 385
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ2, complete sequence

Seq. No. 168818

Seq. ID LIB3234-074-P1-K1-A3

Method BLASTX NCBI GI g1276946



```
BLAST score
                  1.0e-22
E value
Match length
                  115
% identity
                  50
                  (U47078) globulin-like protein [Daucus carota] >gi_1458098
NCBI Description
                  (U62395) globulin-like protein [Daucus carota]
                  168819
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  340
                  6.0e-32
E value
                  73
Match length
                  90
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  168820
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3445209
BLAST score
                  406
                  9.0e-40
E value
Match length
                  101
% identity
                   71
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana]
                  168821
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  q2182286
BLAST score
                  167
E value
                   6.0e-89
Match length
                  342
% identity
                   98
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                  168822
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g1170939
BLAST score
                  514
E value
                  2.0e-52
```

Match length 104 94 % identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi 429108 emb CAA80867 (Z24743)

S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Match length

% identity

379 59

```
168823
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  158
                  1.0e-10
E value
Match length
                  64
                  47
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  168824
Seq. No.
                  LIB3234-074-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342727
BLAST score
                  522
E value
                  2.0e-53
Match length
                  126
                  80
% identity
NCBI Description
                 (AC002341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168825
Seq. ID
                  LIB3234-074-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  q3169169
BLAST score
                  59
                  2.0e-24
E value
Match length
                  132
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168826
                  LIB3234-074-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4586098
BLAST score
                  355
E value
                  0.0e+00
Match length
                  355
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                   (ESSA project)
Seq. No.
                  168827
Seq. ID
                  LIB3234-074-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g2828185
BLAST score
                  379
E value
                  0.0e + 00
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  168828
                  LIB3234-074-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125606
BLAST score
                  155
E value
                  2.0e-10
Match length
                  53
                  60
% identity
NCBI Description
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
                  tuberosum]
                  168829
Seq. No.
                  LIB3234-074-P1-K1-B9
Seq. ID
Method
                  BLASTN
                  g3169169
NCBI GI
BLAST score
                  63
                  7.0e-27
E value
                  160
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC F21P24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168830
                  LIB3234-074-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g511598
                  335
BLAST score
                  0.0e+00
E value
Match length
                   363
% identity
                  26
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
NCBI Description
                  complete cds
Seq. No.
                  168831
Seq. ID
                  LIB3234-074-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1350768
BLAST score
                   376
E value
                   3.0e - 36
Match length
                   90
% identity
                   83
NCBI Description 60S RIBOSOMAL PROTEIN L7A
                   168832
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-C12
Method
                  BLASTN
NCBI GI
                   g4263813
BLAST score
                   292
E value
                   1.0e-163
Match length
                   331
% identity
                   100
```

NCBI Description

Arabidopsis thaliana chromosome II BAC T13P21 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. ID
                  LIB3234-074-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1402914
                  447
BLAST score
                  1.0e-44
E value
                  93
Match length
% identity
                  96
                  (X98318) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168834
                  LIB3234-074-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  q1943751
NCBI GI
BLAST score
                  644
E value
                  1.0e-67
Match length
                  127
                  98
% identity
                  (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                  protein, complete sequence >gi 2078292 (U96455) ER-type
                  Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                  168835
Seq. No.
                  LIB3234-074-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g140285
BLAST score
                  203
                  5.0e-16
E value
Match length
                  46
% identity
                  85
                  HYPOTHETICAL 19 KD PROTEIN (ORF 168)
NCBI Description
                  >gi 2924263 emb CAA77415 (Z00044) Ycf3 protein [Nicotiana
                  tabacum]
                  168836
Seq. No.
                  LIB3234-074-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402914
BLAST score
                  588
E value
                  4.0e-61
                  117
Match length
                  99
% identity
NCBI Description (X98318) peroxidase [Arabidopsis thaliana]
                  168837
Seq. No.
                  LIB3234-074-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832611
BLAST score
                  320
                  1.0e-180
E value
Match length
                  380
                  96
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
                   (ESSAII project)
```

Seq. ID LIB3234-074-P1-K1-D10

Method BLASTN

```
g4220645
NCBI GI
BLAST score
                   349
                   0.0e + 00
E value
                   376
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYA6, complete sequence [Arabidopsis thaliana]
                   168839
Seq. No.
                   LIB3234-074-P1-K1-D11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220645
BLAST score
                   132
                   3.0e-68
E value
Match length
                   220
                   90
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYA6, complete sequence [Arabidopsis thaliana]
                   168840
Seq. No.
Seq. ID
                   LIB3234-074-P1-K1-D3
                   BLASTN
, Method
NCBI GI
                   g3046849
BLAST score
                   239
E value
                   1.0e-132
                   365
Match length
 % identity
                   92
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18L3, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168841
                   LIB3234-074-P1-K1-D4
 Seq. ID
Method
                   BLASTN
NCBI GI
                   q3046849
 BLAST score
                   124
E value
                    3.0e-63
Match length
                   205
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                   K18L3, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    168842
 Seq. ID
                   LIB3234-074-P1-K1-D6
Method
                   BLASTN
 NCBI GI
                   g1931636
 BLAST score
                   303
 E value
                    1.0e-170
 Match length
                   375
 % identity
                    95
 NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
```

Seq. ID LIB3234-074-P1-K1-D8

Method BLASTN
NCBI GI 94757417
BLAST score 374
E value 0.0e+00

```
378
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  T30G6, complete sequence
                  168844
Seq. No.
                  LIB3234-074-P1-K1-D9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4220645
BLAST score
                  345
                  0.0e+00
E value
                  372
Match length
% identity
                  98
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168845
                  LIB3234-074-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4587986
BLAST score
                  353
                  0.0e+00
E value
                  373
Match length
                  99
% identity
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
NCBI Description
                  sequence
                  168846
Seq. No.
                  LIB3234-074-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4558521
BLAST score
                   333
E value
                  0.0e+00
                  377
Match length
% identity
                   97
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
                   168847
Seq. No.
                  LIB3234-074-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832643
BLAST score
                  174
E value
                  1.0e-12
Match length
                  120
% identity
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168848
Seq. ID
                  LIB3234-074-P1-K1-E2
Method
                  BLASTN
NCBI GI
                   g3228389
BLAST score
                  310
E value
                  1.0e-174
                  354
Match length
```

22899

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

97

% identity



complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  168849
                  LIB3234-074-P1-K1-E3
Seq. ID
Method
                  BLASTN
                  g4539290
NCBI GI
BLAST score
                  327
                  0.0e+00
E value
Match length
                  384
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
NCBI Description
                  (ESSA project)
                  168850
Seq. No.
                  LIB3234-074-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4539290
BLAST score
                  197
E value
                  1.0e-107
Match length
                  237
% identity
                  96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
                  (ESSA project)
Seq. No.
                  168851
                  LIB3234-074-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046851
BLAST score
                  234
                  1.0e-129
E value
Match length
                  298
                  95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168852
                  LIB3234-074-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510397
BLAST score
                  602
E value
                  1.0e-62
Match length
                  113
% identity
                  99
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  168853
                  LIB3234-074-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q544122
BLAST score
                  668
E value
                  2.0e-70
Match length
                  127
                  99
% identity
NCBI Description APOCYTOCHROME F PRECURSOR >gi 629599 pir S45661
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
```

22900

cytochrome f precursor - turnip chloroplast
>gi_441282_emb_CAA54307_ (X77011) cytochrome f [Brassica

rapa]

Seq. No. 168854

Seq. ID LIB3234-074-P1-K1-F10

Method BLASTN
NCBI GI g4733991
BLAST score 53
E value 7.0e-21
Match length 85
% identity 46

NCBI Description Arabidopsis thaliana chromosome II BAC T4D8 genomic

sequence, complete sequence

Seq. No. 168855

Seq. ID LIB3234-074-P1-K1-F11

Method BLASTN
NCBI GI g3643588
BLAST score 233
E value 1.0e-128
Match length 288
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168856

Seq. ID LIB3234-074-P1-K1-F12

Method BLASTN
NCBI GI g3643588
BLAST score 153
E value 1.0e-80
Match length 169
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168857

Seq. ID LIB3234-074-P1-K1-F2

Method BLASTX
NCBI GI g1402878
BLAST score 352
E value 2.0e-33
Match length 125
% identity 56

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 168858

Seq. ID LIB3234-074-P1-K1-F3

Method BLASTN
NCBI GI g2459406
BLAST score 214
E value 1.0e-117
Match length 371
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168859

Seq. ID

168864

LIB3234-074-P1-K1-G3



```
LIB3234-074-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544432
BLAST score
                  293
E value
                  2.0e-26
Match length
                  62
                  85
% identity
NCBI Description
                  (AC006955) putative mannose-1-phosphate guanyltransferase
                   [Arabidopsis thaliana]
                  168860
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g3702724
BLAST score
                  102
E value
                   4.0e-50
Match length
                  153
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168861
                  LIB3234-074-P1-K1-G10
Seq. ID
Method
                  BLASTN
                  g1279569
NCBI GI
BLAST score
                  57
E value
                  3.0e-23
                  181
Match length
                  88
% identity
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
Seq. No.
                  168862
                  LIB3234-074-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3273742
BLAST score
                  192
E value
                   1.0e-104
Match length
                  269
                   97
% identity
                  Arabidopsis thaliana lipid transfer protein 2 precursor
NCBI Description
                   (LTP2) gene, complete cds
                   168863
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-G2
Method
                  BLASTX
NCBI GI
                   q548847
BLAST score
                  392
E value
                   4.0e-38
Match length
                  77
% identity
                  100
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
                   >gi_1086182_pir__S39501 ribosomal protein S12 -
                   curled-leaved tobacco >gi 225248 prf 1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
```



```
Method
                  BLASTX
                  g125606
NCBI GI
BLAST score
                  199
                  2.0e-15
E value
Match length
                  61
                  66
% identity
                 PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248
NCBI Description
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                  tuberosum]
                  168865
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g2660661
BLAST score
                  132
E value
                  2.0e-68
Match length
                  172
                  79
% identity
NCBI Description
                  Arabidopsis thaliana chromosome V BAC T19K24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168866
Seq. No.
                  LIB3234-074-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2660661
BLAST score
                  73
E value
                  7.0e - 33
Match length
                  198
% identity
                  93
NCBI Description
                  Arabidopsis thaliana chromosome V BAC T19K24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168867
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q1619602
BLAST score
                  280
E value
                  6.0e-25
Match length
                  90
% identity
                  59
NCBI Description
                 (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  168868
Seq. ID
                  LIB3234-074-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g166570
BLAST score
                  209
E value
                  9.0e-17
Match length
                  106
% identity
                  43
NCBI Description
                 (L04173) glycine rich protein [Arabidopsis thaliana]
```

Seq. ID LIB3234-074-P1-K1-G9

Method BLASTN NCBI GI g1279569

E value

Match length

2.0e-47

93

```
BLAST score
                  86
E value
                  1.0e-40
Match length
                  234
% identity
                  89
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
                  168870
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  q3885325
BLAST score
                  315
                  1.0e-177
E value
Match length
                  377
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T20P8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168871
                  LIB3234-074-P1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241923
BLAST score
                  274
E value
                  1.0e-153
Match length
                  290
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168872
Seq. ID
                  LIB3234-074-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3914899
BLAST score
                  195
E value
                  1.0e-15
Match length
                  45
% identity
                  78
                  40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
NCBI Description
                  protein S4 type I [Zea mays]
                  168873
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g4519190
BLAST score
                  289
E value
                  1.0e-161
                  364
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K6A12, complete sequence
Seq. No.
                  168874
Seq. ID
                  LIB3234-074-P1-K1-H4
                  BLASTX
Method
NCBI GI
                  g543841
BLAST score
                  472
```



% identity NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1 AC007236 2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana] Seq. No. 168875 Seq. ID LIB3234-074-P1-K1-H5 Method BLASTN NCBI GI g4544405 BLAST score 315 E value 1.0e-177 Match length 383

% identity 96
NCBI Description Arabidopsis thaliana chromosome II BAC F2818 genomic sequence, complete sequence

 Seq. No.
 168876

 Seq. ID
 LIB3234-074-P1-K1-H6

 Method
 BLASTX

 NCBI GI
 g2499973

 BLAST score
 418

 F value
 3.00-41

E value 3.0e-41
Match length 103
% identity 83

NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366 emb_CAA66701 (X98078) photosystem II

[Arabidopsis thaliana]

Seq. No. 168877

Seq. ID LIB3234-074-P1-K1-H7

Method BLASTX
NCBI GI g2262167
BLAST score 506
E value 2.0e-51
Match length 103
% identity 92

NCBI Description (AC002329) cytosolic ribosomal protein S4 [Arabidopsis

thaliana]

Seq. No. 168878

Seq. ID LIB3234-074-P1-K1-H9

Method BLASTN
NCBI GI g2494110
BLAST score 317
E value 1.0e-178
Match length 329
% identity 99

NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 168879

Seq. ID LIB3234-075-P1-K1-A1

Method BLASTN NCBI GI g2351061



BLAST score 83 E value 6.0e-39 Match length 121 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana] 168880 Seq. No. LIB3234-075-P1-K1-A10 Seq. ID Method BLASTX NCBI GI g2326363 428 BLAST score E value 2.0e-42 Match length 117 74 % identity NCBI Description (AJ001037) DNA-directed RNA polymerase [Arabidopsis thaliana] 168881 Seq. No. Seq. ID LIB3234-075-P1-K1-A12 BLASTN Method NCBI GI g12235 BLAST score 46 9.0e-17 E value Match length 74 91 % identity NCBI Description S.cereale chloroplast ribosomal protein S15 (rpS15) gene in inverted repeat I (IR-I), complete cds Seq. No. 168882 Seq. ID LIB3234-075-P1-K1-A2 Method BLASTX NCBI GI q2791606 BLAST score 228 E value 6.0e-19 Match length 68 % identity 54 NCBI Description (AL021287) gatB [Mycobacterium tuberculosis]

Seq. No.

Seq. ID LIB3234-075-P1-K1-A4

168883

Method BLASTX NCBI GI g4512627 BLAST score 180 E value 3.0e-40 Match length 101 % identity 92

NCBI Description (AC004793) Similar to gb Z29643 protein kinase C inhibitor

(PKCI) from Zea mays and a member of HIT family PF 01230.

[Arabidopsis thaliana]

Seq. No. 168884

Seq. ID LIB3234-075-P1-K1-A5

Method BLASTN NCBI GI g3128139 BLAST score 169 E value 4.0e-90



Match length 368 % identity 99 NCBI Description Ara

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No. 168885

Seq. ID LIB3234-075-P1-K1-A6

Method BLASTN
NCBI GI 94249393
BLAST score 365
E value 0.0e+00
Match length 369
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 168886

Seq. ID LIB3234-075-P1-K1-B10

Method BLASTX
NCBI GI g3335169
BLAST score 568
E value 8.0e-59
Match length 114
% identity 95

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 168887

Seq. ID LIB3234-075-P1-K1-B11

Method BLASTN
NCBI GI g4220635
BLAST score 324
E value 0.0e+00
Match length 360
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 168888

Seq. ID LIB3234-075-P1-K1-B12

Method BLASTN
NCBI GI g4220635
BLAST score 113
E value 8.0e-57
Match length 206
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 168889

Seq. ID LIB3234-075-P1-K1-B3

Method BLASTX
NCBI GI g4522003
BLAST score 566
E value 1.0e-58
Match length 120



90

(ESSAII project)

% identity

```
% identity
NCBI Description
                  (AC007069) putative protein kinase [Arabidopsis thaliana]
                  168890
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2605714
BLAST score
                  356
E value
                   6.0e - 34
Match length
                  108
% identity
                  71
NCBI Description
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
                  168891
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-B7
Method
                  BLASTX
                  g2129727
NCBI GI
BLAST score
                  316
E value
                  3.0e-29
                  96
Match length
                  74
% identity
NCBI Description
                  RNA-binding protein 37 - Arabidopsis thaliana >gi 1174153
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
                  168892
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  q4558586
BLAST score
                  255
E value
                  1.0e-141
Match length
                  360
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence,
                  complete sequence
Seq. No.
                  168893
Seq. ID
                  LIB3234-075-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  q12219
BLAST score
                  85
E value
                  5.0e-40
Match length
                  260
% identity
                  93
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.
                  168894
Seq. ID
                  LIB3234-075-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  34
E value
                  1.0e-09
Match length
                  58
```

22908

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009



```
Seq. No.
                   168895
Seq. ID
                   LIB3234-075-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q4490316
BLAST score
                   190
E value
                   3.0e-21
Match length
                   108
% identity
                   52
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                   168896
Seq. ID
                   LIB3234-075-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q226120
BLAST score
                   217
E value
                   1.0e-17
Match length
                   120
% identity
                   36
NCBI Description vicilin gene B [Saguinus oedipus]
Seq. No.
                   168897
Seq. ID
                   LIB3234-075-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g4510342
BLAST score
                   186
E value
                   5.0e-14
Match length
                   110
% identity
                   46
NCBI Description (AC006921) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   168898
Seq. ID
                   LIB3234-075-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g1944201
BLAST score
                   160
E value
                   6.0e-11
Match length
                   55
% identity
                   60
                   (AB002818) flavonoid 3-O-glucosyltransferase [Perilla
NCBI Description
                   frutescens]
Seq. No.
                   168899
Seq. ID
                   LIB3234-075-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g3024434
BLAST score
                   296
E value
                   7.0e-27
Match length
                   88
                   70
% identity
NCBI Description
                   26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                   PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_(D88663) Tat binding protein 1 [Brassica rapa]
```

Seq. ID LIB3234-075-P1-K1-D1

Method BLASTX



NCBI GI g3335171 BLAST score 547 E value 3.0e-56 Match length 116 % identity 90

NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No. 168901

Seq. ID LIB3234-075-P1-K1-D11

Method BLASTN
NCBI GI g2656026
BLAST score 346
E value 0.0e+00
Match length 362
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDF20

Seq. No. 168902

Seq. ID LIB3234-075-P1-K1-D12

Method BLASTX
NCBI GI g4006827
BLAST score 539
E value 2.0e-55
Match length 116
% identity 93

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 168903

Seq. ID LIB3234-075-P1-K1-D2

Method BLASTX
NCBI GI g2851581
BLAST score 517
E value 8.0e-53
Match length 106
% identity 96

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA CHAIN

>gi_2196464_emb_CAA74024_ (Y13690) DNA-dependent RNA

polymerase subunit beta [Arabidopsis thaliana]

Seq. No. 168904

Seq. ID LIB3234-075-P1-K1-D5

Method BLASTN
NCBI GI g4159701
BLAST score 42
E value 2.0e-14
Match length 124
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence

Seq. No. 168905

Seq. ID LIB3234-075-P1-K1-D6

Method BLASTX
NCBI GI g1864017
BLAST score 534
E value 8.0e-55



```
Match length
                   104
                   98
% identity
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
                  168906
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3335169
BLAST score
                   488
E value
                   2.0e-49
Match length
                   117
% identity
                   76
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                   168907
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4164473
BLAST score
                  175
                   1.0e-12
E value
Match length
                   40
% identity
                   78
                  (AF061157) negatively light-regulated protein [Vernicia
NCBI Description
                   fordiil
                   168908
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2129767
BLAST score
                   485
E value
                   4.0e-49
Match length
                   105
% identity
                   89
```

NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_

(D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 168909

Seq. ID LIB3234-075-P1-K1-E12

Method BLASTN
NCBI GI g3510341
BLAST score 228
E value 1.0e-125

E value 1.0e-125
Match length 362
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFC16, complete sequence [Arabidopsis thaliana]

Seq. No. 168910

Seq. ID LIB3234-075-P1-K1-E2

Method BLASTN
NCBI GI g4199934
BLAST score 124
E value 3.0e-63
Match length 156

```
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168911
                  LIB3234-075-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351066
BLAST score
                  37
E value
                  2.0e-11
Match length
                  138
% identity
                  88
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168912
Seq. ID
                  LIB3234-075-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3980388
BLAST score
                  288
                  6.0e-26
E value
Match length
                  61
% identity
                  95
NCBI Description
                  (AC004561) putative glutathione S-transferase [Arabidopsis
                  thaliana]
Seq. No.
                  168913
                  LIB3234-075-P1-K1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351066
BLAST score
                  254
E value
                  1.0e-141
Match length
                  315
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168914
Seq. ID
                  LIB3234-075-P1-K1-F1
                  BLASTN
Method
NCBI GI
                  g4159712
BLAST score
                  87
E value
                  2.0e-41
Match length
                  126
% identity
                  93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
```

Seq. ID LIB3234-075-P1-K1-F10

Method BLASTX
NCBI GI g132675
BLAST score 351
E value 2.0e-33
Match length 82
% identity 88

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi 71222 pir R5NT14



ribosomal protein L14 - common tobacco chloroplast >gi_11864_emb_CAA77379_ (Z00044) ribosomal protein L14 [Nicotiana tabacum] >gi_225233_prf__1211235BQ ribosomal protein L14 [Nicotiana tabacum]

Seq. No. 168916

Seq. ID LIB3234-075-P1-K1-F11

Method BLASTN
NCBI GI 94589411
BLAST score 55
E value 2.0e-22
Match length 63
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F5H8, complete sequence

Seq. No. 168917

Seq. ID LIB3234-075-P1-K1-F3

Method BLASTX
NCBI GI g4455159
BLAST score 301
E value 2.0e-27
Match length 118
% identity 61

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 168918

Seq. ID LIB3234-075-P1-K1-F5

Method BLASTX
NCBI GI g1695719
BLAST score 531
E value 2.0e-54
Match length 125
% identity 86

NCBI Description (D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No. 168919

Seq. ID LIB3234-075-P1-K1-F6

Method BLASTX
NCBI GI g3128172
BLAST score 491
E value 1.0e-49
Match length 108
% identity 92

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 168920

Seq. ID LIB3234-075-P1-K1-F7

Method BLASTN
NCBI GI g4159712
BLAST score 361
E value 0.0e+00
Match length 361
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence



```
Seq. No.
                   168921
Seq. ID
                  LIB3234-075-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q2924258
BLAST score
                   474
E value
                   9.0e-48
Match length
                  119
% identity
                  84
NCBI Description (Z00044) RNA polymerase beta" subunit [Nicotiana tabacum]
Seq. No.
                  168922
Seq. ID
                  LIB3234-075-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q3702724
BLAST score
                  334
E value
                  0.0e + 00
Match length
                   362
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168923
Seq. ID
                  LIB3234-075-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2062169
BLAST score
                  507
E value
                  1.0e-51
Match length
                  119
% identity
                  73
NCBI Description
                  (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
                  thaliana]
Seq. No.
                  168924
Seq. ID
                  LIB3234-075-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g3128136
BLAST score
                  349
E value
                  0.0e + 00
Match length
                  365
                   99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1F13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168925
Seq. ID
                  LIB3234-075-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1345967
BLAST score
                  68
E value
                  5.0e-29
Match length
                  93
                  72
% identity
```

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (VERSION 2) >gi_322649_pir__A44227 omega-3 fatty acid desaturase (EC 1.14.99.-) - rape >gi_167148 (L01418)

linoleic acid desaturase [Brassica napus]

Seq. No. 168926

Method

NCBI GI

BLASTX

g4835233



```
Seq. ID
                  LIB3234-076-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2246456
BLAST score
                  563
E value
                  3.0e-58
Match length
                  106
                  97
% identity
NCBI Description
                  (U71400) S-adenosyl-methionine-sterol-C-methyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  168927
Seq. ID
                  LIB3234-076-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q2244906
BLAST score
                  146
E value
                  1.0e-16
Match length
                  92
% identity
                  54
NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  168928
Seq. ID
                  LIB3234-076-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g2335191
BLAST score
                  36
                  9.0e-11
E value
                  36
Match length
% identity
                  100
NCBI Description Arabidopsis thaliana bHLH protein (Atmyc-146) gene,
                  complete cds
                  168929
Seq. No.
Seq. ID
                  LIB3234-076-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2244906
BLAST score
                  336
E value
                  1.0e-31
Match length
                  94
                  71
% identity
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  168930
Seq. ID
                  LIB3234-076-P1-K1-A4
                  BLASTX
Method
NCBI GI
                  g1839188
BLAST score
                  168
E value
                  7.0e-12
Match length
                  94
                  57
% identity
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
                  168931
Seq. No.
Seq. ID
                  LIB3234-076-P1-K1-A8
```



```
BLAST score
                   535
E value
                   6.0e-55
Match length
                   108
% identity
                   100
                   (AL049862) putative protein 1 photosystem II
NCBI Description
                   oxygen-evolving complex [Arabidopsis thaliana]
                   168932
Seq. No.
Seq. ID
                   LIB3234-076-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g541847
BLAST score
                   616
E value
                   2.0e-64
Match length
                   114
                   98
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
                   168933
Seq. No.
                   LIB3234-076-P1-K1-B12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2914688
BLAST score
                   184
E value
                   4.0e-99
Match length
                   360
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168934
Seq. ID
                   LIB3234-076-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   555
E value
                   3.0e-57
Match length
                   118
% identity
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   168935
                   LIB3234-076-P1-K1-B8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16428
BLAST score
                   180
E value
                   1.0e-96
                   368
Match length
```

98 % identity

NCBI Description A.thaliana posF21 gene

Seq. No. 168936

Seq. ID LIB3234-076-P1-K1-B9

Method BLASTN NCBI GI g3449332 BLAST score 343



E value 0.0e+00 Match length 355 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSF19, complete sequence [Arabidopsis thaliana]

Seq. No. 168937

Seq. ID LIB3234-076-P1-K1-C1

Method BLASTN
NCBI GI g2924257
BLAST score 61
E value 1.0e-25
Match length 85

% identity 93

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 168938

Seq. ID LIB3234-076-P1-K1-C10

Method BLASTX
NCBI GI g464987
BLAST score 524
E value 1.0e-53
Match length 96
% identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN -

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 168939

Seq. ID LIB3234-076-P1-K1-C11

Method BLASTN
NCBI GI g11576
BLAST score 132
E value 2.0e-68
Match length 164
% identity 95

NCBI Description Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,

NADH dehydrogenase and ORF

Seq. No. 168940

Seq. ID LIB3234-076-P1-K1-C12

Method BLASTX
NCBI GI g4587550
BLAST score 237
E value 6.0e-20
Match length 90
% identity 56

NCBI Description (AC006577) EST gb R64848 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 168941

Seq. ID LIB3234-076-P1-K1-C2

Method BLASTN



NCBI GI g3738313 BLAST score 50 4.0e-19 E value Match length 145 % identity 83 NCBI Description Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168942 LIB3234-076-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g2499945 BLAST score 523 E value 2.0e-53 Match length 105 100 % identity URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE NCBI Description PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir_ S46440 orotate phosphoribosyltransferase (EC $\overline{2}.4.2.10$) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana] Seq. No. 168943 Seq. ID LIB3234-076-P1-K1-C4 Method BLASTX NCBI GI q128877 BLAST score 343 E value 2.0e-32 Match length 100 73 % identity NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4L, CHLOROPLAST >gi_66167_pir__DENTNL NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - common tobacco chloroplast >gi_1223668_emb_CAA77396_ (Z00044) NADH dehydrogenase ND4L subunit [Nicotiana tabacum] >gi_225256_prf__1211235CQ NADH dehydrogenase 4L-like ORF 101 [Nicotiana tabacum] Seq. No. 168944 Seq. ID LIB3234-076-P1-K1-C6 Method BLASTN NCBI GI g2924257 BLAST score 37 E value 2.0e-11 Match length 89 % identity 91 NCBI Description Tobacco chloroplast genome DNA Seq. No. 168945 Seq. ID LIB3234-076-P1-K1-C7 Method BLASTN

Method BLASTN
NCBI GI g2252823
BLAST score 178
E value 8.0e-96
Match length 178
% identity 100

Match length

% identity

117 93



```
NCBI Description Arabidopsis thaliana BAC IG005I10
                    168946
Seq. No.
                    LIB3234-076-P1-K1-C8
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2252823
BLAST score
                    51
                    6.0e-20
E value
Match length
                    83
                    90
% identity
NCBI Description Arabidopsis thaliana BAC IG005I10
                    168947
Seq. No.
                    LIB3234-076-P1-K1-C9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1864017
BLAST score
                    548
E value
                    2.0e-56
                    104
Match length
                    100
% identity
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                    168948
Seq. No.
                    LIB3234-076-P1-K1-D1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q114532
BLAST score
                    548
E value
                    2.0e-56
Match length
                    122
% identity
                    89
NCBI Description ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
                    common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162)
                    alpha subunit of ATPase [Nicotiana tabacum]
                    >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha
                    [Nicotiana tabacum]
Seq. No.
                    168949
                    LIB3234-076-P1-K1-D3
Seq. ID
Method
                    BLASTN
NCBI GI
                    g3327867
BLAST score
                    367
E value
                    0.0e+00
Match length
                    367
% identity
                    100
NCBI Description
                    Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein
                    7, complete cds
                    168950
Seq. No.
Seq. ID
                    LIB3234-076-P1-K1-D5
Method
                    BLASTX
NCBI GI
                    g2288887
BLAST score
                    585
E value
                    8.0e-61
```

22919

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```
(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                   thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
                    >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                    [Arabidopsis thaliana]
                    168951
Seq. No.
Seq. ID
                   LIB3234-076-P1-K1-D7
Method
                   BLASTX
NCBI GI
                    g1592679
BLAST score
                    261
E value
                    9.0e-23
Match length
                    71
                    77
% identity
NCBI Description (X91915) LEA D113 homologue type1 [Arabidopsis thaliana]
Seq. No.
                    168952
Seq. ID
                   LIB3234-076-P1-K1-D8
Method
                   BLASTX
NCBI GI
                    q4090884
BLAST score
                    511
E value
                    4.0e-52
Match length
                    97
% identity
                    100
NCBI Description (AF025333) vesicle-associated membrane protein 7B;
                   synaptobrevin 7B [Arabidopsis thaliana]
                    168953
Seq. No.
                   LIB3234-076-P1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                    g4760411
BLAST score
                    340
E value
                    0.0e+00
Match length
                    365
% identity
                    98
NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
                   complete sequence
Seq. No.
                    168954
Seq. ID
                   LIB3234-076-P1-K1-E1
Method
                   BLASTX
NCBI GI
                    g1705463
BLAST score
                    471
E value
                    2.0e-47
Match length
                    104
% identity
                    86
NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi 2129547 pir S71201
                   biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806)
                    BIO2 protein [Arabidopsis thaliana] >gi 1769457 (L34413)
                   biotin synthase [Arabidopsis thaliana] >gi 2288983
                    (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                    >gi_1589016_prf__2209438A biotin synthase [Arabidopsis
```

Seq. ID LIB3234-076-P1-K1-E10

thaliana]

Method BLASTN
NCBI GI g2828185
BLAST score 262
E value 1.0e-145
Match length 353
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUD21, complete sequence [Arabidopsis thaliana]

Seq. No. 168956

Seq. ID LIB3234-076-P1-K1-E11

Method BLASTN
NCBI GI g2924257
BLAST score 70
E value 4.0e-31
Match length 134
% identity 89

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 168957

Seq. ID LIB3234-076-P1-K1-E2

Method BLASTX
NCBI GI g4559372
BLAST score 241
E value 2.0e-20
Match length 61
% identity 77

NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]

>gi 4646235 gb AAD26898.1 AC007266 6 (AC007266) putative

CONSTANS protein [Arabidopsis thaliana]

Seq. No. 168958

Seq. ID LIB3234-076-P1-K1-E3

Method BLASTX
NCBI GI g1169515
BLAST score 220
E value 3.0e-18
Match length 70
% identity 70

NCBI Description EM-LIKE PROTEIN GEA1 >gi_2119768_pir__S34819 embryonic

abundant protein Eml - Arabidopsis thaliana

>gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1

protein [Arabidopsis thaliana]

Seq. No. 168959

Seq. ID LIB3234-076-P1-K1-E6

Method BLASTX
NCBI GI 94558547
BLAST score 281
E value 4.0e-25
Match length 121
% identity 57

NCBI Description (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 168960

Seq. ID

Method

168965

BLASTX

LIB3234-076-P1-K1-F2



Seq. ID LIB3234-076-P1-K1-E7 Method BLASTX NCBI GI q3176874 BLAST score 406 E value 8.0e-40Match length 116 63 % identity NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis thaliana] Seq. No. 168961 Seq. ID LIB3234-076-P1-K1-E8 Method BLASTN NCBI GI a3789706 BLAST score 163 1.0e-86 E value Match length 325 % identity Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, NCBI Description complete sequence [Arabidopsis thaliana] 168962 Seq. No. Seq. ID LIB3234-076-P1-K1-E9 Method BLASTX NCBI GI q1628583 BLAST score 625 2.0e-65 E value Match length 120 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 168963 Seq. ID LIB3234-076-P1-K1-F1 Method BLASTN NCBI GI g2264309 BLAST score 360 E value 0.0e + 00Match length 360 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MJJ3, complete sequence [Arabidopsis thaliana] Seq. No. 168964 Seq. ID LIB3234-076-P1-K1-F12 Method BLASTX NCBI GI g2924258 BLAST score 563 E value 3.0e-58Match length 120 93 % identity (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum] NCBI Description



NCBI GI g3892057 BLAST score 585 E value 9.0e-61 Match length 122 % identity 49

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 168966

Seq. ID LIB3234-076-P1-K1-F4

Method BLASTX NCBI GI q120675 BLAST score 458 E value 7.0e-46Match length 105 % identity 84

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis

alba]

Seq. No. 168967

Seq. ID LIB3234-076-P1-K1-F5

Method BLASTN NCBI GI q3860242 BLAST score 298 E value 1.0e-167 Match length 374 % identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC T13M11 genomic

sequence, complete sequence

168968 Seq. No.

Seq. ID LIB3234-076-P1-K1-F7

Method BLASTX NCBI GI q4455336 BLAST score 422 E value 1.0e-41 Match length 77 100 % identity

NCBI Description (AL035525) pectinesterase-like protein [Arabidopsis

thaliana]

Seq. No. 168969

Seq. ID LIB3234-076-P1-K1-F8

Method BLASTN NCBI GI g4455321 BLAST score 45 E value 3.0e-16 Match length 85 89 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10

(ESSAII project)

Seq. No. 168970

LIB3234-076-P1-K1-G10 Seq. ID

Method BLASTN



NCBI GI q3298532 BLAST score 340 E value 0.0e + 00Match length 360 % identity 99 Arabidopsis thaliana chromosome II BAC T26B15 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168971 Seq. ID LIB3234-076-P1-K1-G11 Method BLASTX NCBI GI g2980771 BLAST score 435 E value 3.0e-43Match length 101 86 % identity (AL022198) chloroplast omega-6 fatty acid desaturase (fad6) NCBI Description [Arabidopsis thaliana] Seq. No. 168972 Seq. ID LIB3234-076-P1-K1-G2 Method BLASTN NCBI GI q4468103 BLAST score 333 E value 0.0e + 00Match length 362 98 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project) Seq. No. 168973 Seq. ID LIB3234-076-P1-K1-G4 Method BLASTN NCBI GI g3298532 BLAST score 48 5.0e-18 E value 86 Match length 94 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana] 168974 Seq. No. Seq. ID LIB3234-076-P1-K1-G5 BLASTX Method NCBI GI g2244750 494 BLAST score 4.0e-50 E value

Match length 110 % identity 87

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 168975

Seq. ID LIB3234-076-P1-K1-G6

Method BLASTX NCBI GI g1169601



```
BLAST score
                    389
E value
                    9.0e-38
Match length
                    98
                    80
% identity
                    OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                    >gi 493068 (U09503) chloroplast omega-6 fatty acid
                    desaturase [Arabidopsis thaliana]
                    168976
Seq. No.
Seq. ID
                    LIB3234-076-P1-K1-H1
Method
                    BLASTX
NCBI GI
                    g3355308
BLAST score
                    258
E value
                    2.0e-22
                    50
Match length
                    100
% identity
                   (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
NCBI Description
                    168977
Seq. No.
                    LIB3234-076-P1-K1-H10
Seq. ID
                    BLASTN
Method
NCBI GI
                    g2262135
BLAST score
                    117
                    3.0e-59
E value
Match length
                    216
% identity
                    93
NCBI Description
                    Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                    cM, complete sequence
                    168978
Seq. No.
Seq. ID
                    LIB3234-076-P1-K1-H12
Method
                    BLASTX
NCBI GI
                    q3367596
BLAST score
                    188
                    4.0e-23
E value
Match length
                    83
% identity
                    68
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
                    168979
Seq. No.
Seq. ID
                    LIB3234-076-P1-K1-H3
Method
                    BLASTX
NCBI GI
                    g1345973
BLAST score
                    677
E value
                    1.0e-71
Match length
                    122
% identity
                    100
                    OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
NCBI Description
                    omega-3 fatty acid desaturase [Arabidopsis thaliana]
```

>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]



168980 Seq. No. Seq. ID LIB3234-076-P1-K1-H4 Method BLASTN NCBI GI q2760169 BLAST score 151 1.0e-79 E value 167 Match length 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana] Seq. No. 168981 LIB3234-076-P1-K1-H5 Seq. ID Method BLASTN NCBI GI g2262135 BLAST score 151 E value 1.0e-79 Match length 214 93 % identity NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence Seq. No. 168982 Seq. ID LIB3234-076-P1-K1-H9 Method BLASTX NCBI GI a99837 BLAST score 195 4.0e-15 E value Match length 97 48 % identity NCBI Description 2S storage protein - wild cabbage >gi_17878_emb_CAA46783_ (X65970) 2S storage protein [Brassica oleracea] >gi_17880_emb_CAA46172_ (X65038) 2S storage protein [Brassica oleracea] Seq. No. 168983 Seq. ID LIB3234-077-P1-K1-A1 Method BLASTX NCBI GI g120667 BLAST score 181 E value 8.0e-14 55 Match length % identity 69 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 168984

Seq. ID LIB3234-077-P1-K1-A10

Method BLASTX
NCBI GI g3249096
BLAST score 471
E value 2.0e-47



Match length 108 % identity 90

NCBI Description (AC003114) Match to mRNA for importin alpha-like protein 4

(impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene.

[Arabidopsis thaliana]

Seq. No. 168985

Seq. ID LIB3234-077-P1-K1-A11

Method BLASTX
NCBI GI g4679028
BLAST score 58
E value 7.0e-26
Match length 130
% identity 47

NCBI Description (AF077207) HSPC021 [Homo sapiens]

Seq. No. 168986

Seq. ID LIB3234-077-P1-K1-A12

Method BLASTX
NCBI GI g4490737
BLAST score 333
E value 4.0e-31
Match length 127
% identity 56

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 168987

Seq. ID LIB3234-077-P1-K1-A2

Method BLASTX
NCBI GI g3980396
BLAST score 501
E value 7.0e-51
Match length 95
% identity 99

NCBI Description (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis

thaliana]

Seq. No. 168988

Seq. ID LIB3234-077-P1-K1-A3

Method BLASTX
NCBI GI g231442
BLAST score 63
E value 4.0e-37
Match length 126
% identity 59

NCBI Description HYPOTHETICAL 260 KD PROTEIN (ORF 2216) >gi 336938 (M81884)

ORF2216 [Epifagus virginiana] >gi 336942 (M81884) ORF2216

[Epifagus virginiana]

Seq. No. 168989

Seq. ID LIB3234-077-P1-K1-A4

Method BLASTX
NCBI GI g2829918
BLAST score 601
E value 1.0e-62
Match length 120

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% identity (AC002291) similar to "tub" protein gp U82468_2072162 NCBI Description [Arabidopsis thaliana] 168990 Seq. No. Seq. ID LIB3234-077-P1-K1-A8 Method BLASTX NCBI GI q3915961 BLAST score 592 E value 1.0e-61 Match length 124 % identity 90 HYPOTHETICAL 267 KD PROTEIN (ORF 2280) NCBI Description $\verb| >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] > gi_2924285_emb_CAA77438_ (Z00044) hypothetical | | |$ protein [Nicotiana tabacum] Seq. No. 168991 LIB3234-077-P1-K1-A9 Seq. ID Method BLASTX NCBI GI q3915961 BLAST score 400 E value 4.0e-39 Match length 106 75 % identity NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum] Seq. No. 168992 LIB3234-077-P1-K1-B1 Seq. ID Method BLASTN NCBI GI g3885325 BLAST score 324 E value 0.0e+00Match length 336 % identity 99 Arabidopsis thaliana chromosome II BAC T20P8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168993 LIB3234-077-P1-K1-B12 Seq. ID Method BLASTX NCBI GI g1486472 BLAST score 406 E value 1.0e-39 94 Match length % identity (X99853) oxoglutarate malate translocator [Solanum NCBI Description tuberosum]

Seq. No. 168994

Seq. ID LIB3234-077-P1-K1-B2

Method BLASTX NCBI GI g4678311 BLAST score 470

Match length

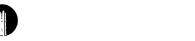
% identity

131

87



```
3.0e-47
E value
Match length
                  90
% identity
                  99
                  (AL049655) aquaporin/MIP-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168995
Seq. ID
                  LIB3234-077-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q3808062
BLAST score
                  155
                  2.0e-10
E value
Match length
                  64
                  45
% identity
NCBI Description (AB019195) PV100 [Cucurbita maxima]
                  168996
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  275
E value
                  1.0e-153
Match length
                  279
% identity
                  100
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168997
                  LIB3234-077-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757403
BLAST score
                  252
                  1.0e-139
E value
Match length
                  382
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
                  168998
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3445209
BLAST score
                  526
E value
                  8.0e-54
Match length
                  129
                  71
% identity
NCBI Description (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
                  168999
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-C2
                  BLASTX
Method
NCBI GI
                  g3953466
BLAST score
                  585
E value
                  1.0e-60
```



NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana] 169000 Seq. No. LIB3234-077-P1-K1-C5 Seq. ID Method BLASTN NCBI GI q2760165 BLAST score 144 3.0e-75 E value Match length 335 95 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana] 169001 Seq. No. Seq. ID LIB3234-077-P1-K1-C6 BLASTX Method NCBI GI q4587529 BLAST score 369 8.0e-36 E value Match length 78 90 % identity (AC007060) Strong similarity to F19I3.2 gi 3033375 putative NCBI Description berberine bridge enzyme from Arabidopsis thaliana BAC gb AC004238. EST gb_H76902 comes from this gene Seq. No. 169002 Seq. ID LIB3234-077-P1-K1-C7 Method BLASTX NCBI GI g544424 BLAST score 267 E value 2.0e-23 Match length 86 62 % identity GLYCINE-RICH RNA-BINDING PROTEIN 7 >qi 419755 pir S30147 NCBI Description glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi 4567224 gb AAD23639.1 AC007119 5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana] 169003 Seq. No. Seq. ID LIB3234-077-P1-K1-C8 Method BLASTX

Method BLASTX
NCBI GI g3395432
BLAST score 260
E value 1.0e-22
Match length 89
% identity 56

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 169004

Seq. ID LIB3234-077-P1-K1-C9

Method BLASTN
NCBI GI g2656026
BLAST score 250
E value 1.0e-138

NCBI GI

E value

BLAST score

g2832611

0.0e+00

379



```
Match length
                   293
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDF20
                   169005
Seq. No.
                   LIB3234-077-P1-K1-D1
Seq. ID
Method
                   BLASTX
                   g4204277
NCBI GI
BLAST score
                   654
                   8.0e-69
E value
Match length
                   121
                   100
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169006
Seq. No.
                   LIB3234-077-P1-K1-D10
Seq. ID
                   BLASTX
Method
                   g544424
NCBI GI
                   160
BLAST score
                   2.0e-20
E value
                   74
Match length
                   77
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi 4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   169007
                   LIB3234-077-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006881
BLAST score
                   447
E value
                   2.0e-44
Match length
                   115
                   80
% identity
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169008
                   LIB3234-077-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006881
BLAST score
                   361
E value
                   2.0e-34
Match length
                   109
                   72
% identity
NCBI Description (299707) putative protein [Arabidopsis thaliana]
Seq. No.
                   169009
                   LIB3234-077-P1-K1-D6
Seq. ID
                   BLASTN
Method
```

% identity

100



```
Match length
                  391
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
                   (ESSAII project)
                  169010
Seq. No.
                  LIB3234-077-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3461834
BLAST score
                  268
E value
                  1.0e-149
Match length
                  358
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T914 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  169011
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4309732
BLAST score
                  156
                  2.0e-10
E value
Match length
                  110
% identity
                  42
                 (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169012
Seq. ID
                  LIB3234-077-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g12279
BLAST score
                  35
E value
                   4.0e-10
                  43
Match length
% identity
                  95
NCBI Description
                  Spinach chloroplast genes for the D2 and 44 kd reaction
                   centre, chlorophyll a-binding protein and for tRNA-Ser
                   (UGA)
                  169013
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g4063536
BLAST score
                  604
E value
                  5.0e-63
Match length
                  120
% identity
                   97
NCBI Description (AF035900) ATP synthase beta subunit [Capparis spinosa]
                  169014
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-E2
                  BLASTN
Method
NCBI GI
                  g4586098
BLAST score
                  224
E value
                  1.0e-123
Match length
                  349
```

22932

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13



(ESSA project)

```
169015
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3128188
BLAST score
                  550
E value
                  1.0e-56
Match length
                  109
% identity
                  94
NCBI Description
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  169016
                  LIB3234-077-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  378
E value
                  0.0e + 00
                  394
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                  (ESSA project)
                  169017
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-E8
Method
                  BLASTN
                  g4510338
NCBI GI
BLAST score
                  391
                  0.0e + 00
E value
Match length
                  395
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic
                  sequence, complete sequence
                  169018
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3080442
BLAST score
                   705
E value
                  8.0e-75
Match length
                  128
% identity
                   98
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                   169019
Seq. ID
                  LIB3234-077-P1-K1-F10
Method
                  BLASTX
NCBI GI
                   g2342690
BLAST score
                  243
E value
                   1.0e-20
                  91
Match length
% identity
                   37
                   (AC000106) Similar to Homo copine I (gb U83246).
NCBI Description
                   [Arabidopsis thaliana]
                   169020
Seq. No.
                  LIB3234-077-P1-K1-F11
Seq. ID
```



Method BLASTX
NCBI GI g135858
BLAST score 292
E value 2.0e-26
Match length 57
% identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast

intrinsic protein alpha [Arabidopsis Thaliana]

Seq. No. 169021

Seq. ID LIB3234-077-P1-K1-F12

Method BLASTN
NCBI GI g4582411
BLAST score 110
E value 7.0e-55
Match length 130
% identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,

complete sequence

Seq. No. 169022

Seq. ID LIB3234-077-P1-K1-F2

Method BLASTN
NCBI GI g2828180
BLAST score 234
E value 1.0e-129
Match length 392
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDK4, complete sequence [Arabidopsis thaliana]

Seq. No. 169023

Seq. ID LIB3234-077-P1-K1-F4

Method BLASTN
NCBI GI 94589437
BLAST score 38
E value 3.0e-12
Match length 182
% identity 80

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 169024

Seq. ID LIB3234-077-P1-K1-F6

Method BLASTN
NCBI GI g16181
BLAST score 120
E value 4.0e-61
Match length 128
% identity 98

NCBI Description A.thaliana gene for tonoplast intrinsic protein

alpha-TIP(Ara) >gi_166622 gb M84343 ATHATIP Arabidopsis

```
thaliana tonoplast intrinsic protein (alpha-TIP) gene,
                  complete cds
                  169025
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1110531
BLAST score
                  171
E value
                  3.0e-12
Match length
                  124
% identity
                  37
NCBI Description (U40570) autoantigen Ku86 [Mesocricetus auratus]
Seq. No.
                  169026
Seq. ID
                  LIB3234-077-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2252841
BLAST score
                  492
E value
                  8.0e-50
Match length
                  125
% identity
                  75
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  169027
Seq. ID
                  LIB3234-077-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  72
E value
                  8.0e-24
Match length
                  106
% identity
                  64
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  169028
Seq. ID
                  LIB3234-077-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  383
E value
                  5.0e-37
                  91
Match length
                  79
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  169029
Seq. ID
                 - LIB3234-077-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2129577
BLAST score
                  429
E value
                  2.0e-42
Match length
                  83
```

Seq. No. 169030

99

% identity

22935

(U22340) DnaJ homolog [Arabidopsis thaliana]

NCBI Description DnaJ homolog protein - Arabidopsis thaliana >gi 727357

Seq. ID

Method



```
LIB3234-077-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924505
BLAST score
                  301
E value
                  1.0e-169
Match length
                  393
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
                  (ESSAII project)
Seq. No.
                  169031
Seq. ID
                  LIB3234-077-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  q4455339
BLAST score
                  125
E value
                  7.0e-64
Match length
                  199
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
NCBI Description
                  (ESSAII project)
                  169032
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q4115921
BLAST score
                  413
E value
                  1.0e-40
Match length
                  121
% identity
                  62
NCBI Description
                  (AF118222) F3H7.4 gene product [Arabidopsis thaliana]
                  >gi 4539434 emb CAB40022.1 (AL049523) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  169033
Seq. ID
                  LIB3234-077-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2970654
BLAST score
                  239
E value
                  4.0e-20
Match length
                  95
                  57
% identity
NCBI Description
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
                  unguiculata]
Seq. No.
                  169034
Seq. ID
                  LIB3234-077-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4337195
BLAST score
                  159
E value
                  9.0e-11
Match length
                  44
                  75
% identity
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169035
```

BLASTX

LIB3234-077-P1-K1-H11



NCBI GI q3915866 BLAST score 187 E value 5.0e-14 Match length 58 % identity 76

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

169036 Seq. No.

Seq. ID LIB3234-077-P1-K1-H3

Method BLASTN NCBI GI a3860242 BLAST score 330 E value 0.0e + 00Match length 389 96 % identity

Arabidopsis thaliana chromosome I BAC T13M11 genomic NCBI Description

sequence, complete sequence

Seq. No. 169037

Seq. ID LIB3234-077-P1-K1-H4

Method BLASTX NCBI GI q2160146 BLAST score 417 E value 5.0e-41Match length 99 85 % identity

(AC000375) Strong similarity to Arabidopsis NCBI Description

gb X91953, F21M12.3, F21M12.1. EST gb H36326 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 169038

Seq. ID LIB3234-077-P1-K1-H7

Method BLASTX NCBI GI g4581166 BLAST score 144 4.0e-09 E value Match length 55

% identity

NCBI Description (AC006220) hypothetical protein [Arabidopsis thaliana]

Seq. No. 169039

Seq. ID LIB3234-077-P1-K1-H8

Method BLASTX NCBI GI q1628583 BLAST score 355 E value 5.0e-34 Match length 88 % identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 169040

Seq. ID LIB3234-078-P1-K1-A11

Method BLASTN



NCBI GI g2980787 BLAST score 216 E value 1.0e-118 Match length 350 50 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project) Seq. No. 169041 Seq. ID LIB3234-078-P1-K1-A12 Method BLASTX NCBI GI q4581120 BLAST score 437 E value 2.0e-43Match length 78 100 % identity NCBI Description (AC005825) hypothetical protein [Arabidopsis thaliana] Seq. No. 169042 Seq. ID LIB3234-078-P1-K1-A3 Method BLASTX NCBI GI g267073 BLAST score 271 E value 5.0e-26 Match length 100 % identity 65 NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701) beta-3 tubulin [Arabidopsis thaliana] Seq. No. 169043 Seq. ID LIB3234-078-P1-K1-A4 Method BLASTN NCBI GI q3789706 BLAST score 179 E value 3.0e-96 Match length 294 % identity 96 NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 169044 Seq. ID LIB3234-078-P1-K1-A5 BLASTX g4008006

Method NCBI GI BLAST score 493 E value 5.0e-50 Match length 121 79

(AF084034) receptor-like protein kinase [Arabidopsis NCBI Description

thaliana]

169045 Seq. No.

% identity

Seq. ID LIB3234-078-P1-K1-A6

Method BLASTN NCBI GI g3763944



BLAST score 64 E value 1.0e-27 Match length 144 % identity 90

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No. 169046

Seq. ID LIB3234-078-P1-K1-A7

Method BLASTX
NCBI GI g1345973
BLAST score 229
E value 2.0e-19
Match length 46
% identity 93

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 169047

Seq. ID LIB3234-078-P1-K1-A9

Method BLASTN
NCBI GI g16375
BLAST score 34
E value 4.0e-10
Match length 106
% identity 83

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

protein

Seq. No. 169048

Seq. ID LIB3234-078-P1-K1-B1

Method BLASTX
NCBI GI g115783
BLAST score 490
E value 1.0e-49
Match length 104
% identity 88

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 169049

Seq. ID LIB3234-078-P1-K1-B10

Method BLASTX
NCBI GI g2832707
BLAST score 427
E value 3.0e-42
Match length 88
% identity 99



```
(ALO21713) translation initiation factor eIF-2 gamma
NCBI Description
                  chain-like protein [Arabidopsis thaliana]
                  169050
Seq. No.
                  LIB3234-078-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337188
BLAST score
                  284
E value
                  2.0e-25
Match length
                  82
% identity
                  76
                 (AC006403) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169051
                  LIB3234-078-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4415928
BLAST score
                  335
E value
                  0.0e+00
Match length
                  400
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  169052
Seq. No.
                  LIB3234-078-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2264302
BLAST score
                  387
E value
                  0.0e+00
Match length
                  387
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169053
Seq. ID
                  LIB3234-078-P1-K1-B6
Method
                  BLASTX
                  q1350680
NCBI GI
BLAST score
                  527
E value
                  6.0e-54
Match length
                  109
                  94
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
Seq. No.
                  169054
Seq. ID
                  LIB3234-078-P1-K1-B7
                  BLASTN
Method
                  g16375
NCBI GI
BLAST score
                  74
                  9.0e-34
E value
```

Seq. No. 169055

182 85

protein

Match length

% identity

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

Seq. No.

Seq. ID

169060

LIB3234-078-P1-K1-C3



```
LIB3234-078-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q123541
BLAST score
                   400
E value
                   5.0e-39
Match length
                   76
                   99
% identity
                   17.4 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.4)
NCBI Description
                   >gi_81639_pir__JQ0351 heat shock protein 17 - Arabidopsis
                   thaliana >gi_16340_emb_CAA35182_ (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]
                   169056
Seq. No.
                   LIB3234-078-P1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q16339
                   151
BLAST score
                   1.0e-79
E value
                   207
Match length
                   94
% identity
NCBI Description Arabidopsis HSP17.4 gene for 17.4kDa heat shock protein
                   169057
Seq. No.
Seq. ID
                   LIB3234-078-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g4589432
                   264
BLAST score
                   1.0e-147
E value
Match length
                   366
                   93
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MMJ24, complete sequence
                   169058
Seq. No.
Seq. ID
                   LIB3234-078-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   q2656030
BLAST score
                   380
E value
                   0.0e + 00
Match length
                   380
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUL8
                   169059
Seq. No.
Seq. ID
                   LIB3234-078-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   g4220468
BLAST score
                   330
E value
                   0.0e + 00
Match length
                   374
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T8011 genomic
```

22941

sequence, complete sequence [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g2245126

1.0e-135

245



```
Method
                  BLASTN
NCBI GI
                  q4589428
BLAST score
                  226
E value
                  1.0e-124
Match length
                  351
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
                  169061
Seq. No.
                  LIB3234-078-P1-K1-C4
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4589428
BLAST score
                   91
E value
                   9.0e-44
Match length
                  227
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
Seq. No.
                   169062
Seq. ID
                  LIB3234-078-P1-K1-C7
Method
                  BLASTX
NCBI GI
                   q1009712
BLAST score
                   351
E value
                   2.0e-33
Match length
                   100
% identity
                  (U27698) calreticulin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169063
                  LIB3234-078-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4314363
BLAST score
                   659
E value
                   2.0e-69
Match length
                   130
                   99
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169064
                   LIB3234-078-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3450842
BLAST score
                   436
E value
                   3.0e-43
Match length
                   94
                   82
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   169065
Seq. No.
                   LIB3234-078-P1-K1-D1
Seq. ID
Method
                   BLASTN
```



```
Match length
                     353
                     100
% identity
NCBI Description
                     Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                     fragment No
                     169066
Seq. No.
                     LIB3234-078-P1-K1-D10
Seq. ID
                     BLASTN
Method
                     g2245031
NCBI GI
BLAST score
                     243
                     1.0e-134
E value
Match length
                     378
                     96
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                     fragment No
                     169067
Seq. No.
                     LIB3234-078-P1-K1-D12
Seq. ID
Method
                     BLASTX
NCBI GI
                     g520478
BLAST score
                     444
                     3.0e-44
E value
                     89
Match length
                     100
% identity
                     (U09137) pyruvate dehydrogenase El beta subunit
NCBI Description
                      [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                     dehydrogenase [Arabidopsis thaliana]
Seq. No.
                     169068
                     LIB3234-078-P1-K1-D3
Seq. ID
Method
                     BLASTX
NCBI GI
                     g113026
BLAST score
                     518
                     7.0e-53
E value
Match length
                     113
% identity
                     88
                     ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                     >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D
                     S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
                     isocitrate lyase [Brassica napus]
Seq. No.
                     169069
Seq. ID
                     LIB3234-078-P1-K1-D4
Method
                     BLASTX
NCBI GI
                     g1402904
BLAST score
                     486
```

E value 3.0e-49Match length 96

NCBI Description (X98313) peroxidase [Arabidopsis thaliana]

169070 Seq. No.

% identity

Seq. ID LIB3234-078-P1-K1-D5

97

BLASTN Method

Seq. No.

Seq. ID

Method

169075

BLASTX

LIB3234-078-P1-K1-E12



```
g2894557
NCBI GI
BLAST score
                   392
E value
                   0.0e + 00
Match length
                   392
% identity
                   100
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T805
NCBI Description
                    (ESSAII project)
Seq. No.
                   169071
Seq. ID
                   LIB3234-078-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g1361982
BLAST score
                   546
E value
                    4.0e-56
Match length
                   103
% identity
                   100
                   4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
NCBI Description
                    thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase
                    [Arabidopsis thaliana]
                   169072
Seq. No.
                   LIB3234-078-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                    q400923
BLAST score
                    451
E value
                    5.0e-45
Match length
                    89
                    98
% identity
                   RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650)
NCBI Description
                   RAS-related GTP-binding protein [Pisum sativum]
                    169073
Seq. No.
Seq. ID
                   LIB3234-078-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g2738248
BLAST score
                    587
E value
                    6.0e-61
Match length
                    118
% identity
                    92
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                    [Arabidopsis thaliana]
                    169074
Seq. No.
Seq. ID
                    LIB3234-078-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    g99735
BLAST score
                    603
                    7.0e-63
E value
                    114
Match length
                    100
% identity
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                    Arabidopsis thaliana (fragment)
```

BLAST score

E value

457

1.0e-45



```
NCBI GI
                  g2065173
BLAST score
                  150
                  5.0e-15
E value
                  85
Match length
                  52
% identity
NCBI Description (Y11174) similarities with RP1 and EB1 [Homo sapiens]
Seq. No.
                  169076
                  LIB3234-078-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2828180
BLAST score
                  162
                  6.0e-86
E value
Match length
                  265
                  95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169077
Seq. ID
                  LIB3234-078-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  g4756963
                  347
BLAST score
                  0.0e + 00
E value
Match length
                  372
                  98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
Seq. No.
                  169078
                  LIB3234-078-P1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4589964
                  287
BLAST score
                  5.0e-26
E value
Match length
                  84
                  73
% identity
NCBI Description (AC007169) delta 9 desaturase [Arabidopsis thaliana]
                  169079
Seq. No.
Seq. ID
                  LIB3234-078-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g3335169
BLAST score
                  619
                  1.0e-64
E value
                  117
Match length
                  100
% identity
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  169080
Seq. No.
                  LIB3234-078-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266693
```



123 Match length % identity OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis NCBI Description thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana] 169081 Seq. No. Seq. ID LIB3234-078-P1-K1-F11 Method BLASTX NCBI GI q99735 BLAST score 563 E value 4.0e-58 Match length 114 94 % identity NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -Arabidopsis thaliana (fragment) 169082 Seq. No. LIB3234-078-P1-K1-F12 Seq. ID Method BLASTN NCBI GI g4544365 BLAST score 322 E value 0.0e + 00Match length - 384 96 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F26H6 genomic sequence, complete sequence Seq. No. 169083 Seq. ID LIB3234-078-P1-K1-F2 Method BLASTX NCBI GI q3023848 BLAST score 533 E value 1.0e-54 Match length 113 % identity 34 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE NCBI Description PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >qi 2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana] Seq. No. 169084 Seq. ID LIB3234-078-P1-K1-F4 Method BLASTX NCBI GI g4218002 BLAST score 459 6.0e-46E value Match length 93 100 % identity (AC006135) putative UTP-glucose glucosyltransferase NCBI Description

[Arabidopsis thaliana]

Seq. No. 169085

Seq. ID LIB3234-078-P1-K1-F5

Method BLASTN NCBI GI g3420042



BLAST score 371 E value 0.0e+00 Match length 391 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169086

Seq. ID LIB3234-078-P1-K1-F6

Method BLASTN
NCBI GI g2924651
BLAST score 208
E value 1.0e-113
Match length 216
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 169087

Seq. ID LIB3234-078-P1-K1-F7

Method BLASTN
NCBI GI g2924651
BLAST score 171
E value 2.0e-91
Match length 185
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 169088

Seq. ID LIB3234-078-P1-K1-F8

Method BLASTX
NCBI GI g2262167
BLAST score 598
E value 3.0e-62
Match length 114
% identity 100

NCBI Description (AC002329) cytosolic ribosomal protein S4 [Arabidopsis

thaliana]

Seq. No. 169089

Seq. ID LIB3234-078-P1-K1-F9

Method BLASTX
NCBI GI g2058311
BLAST score 405
E value 1.0e-39
Match length 98
% identity 78

NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No. 169090

Seq. ID LIB3234-078-P1-K1-G11

Method BLASTX
NCBI GI g126079
BLAST score 163
E value 3.0e-11
Match length 125

NCBI Description



```
% identity
NCBI Description
                    LATE EMBRYOGENESIS ABUNDANT PROTEIN 76 (LEA 76)
                    >gi_81683_pir__S04130 embryonic abundant protein (clone pLEA76) - rape >gi_17829_emb_CAA33406_ (X15348) LEA76 peptide (AA 1-280) [Brassica napus]
                    >gi 226789_prf__1605299A Lea76 gene [Brassica napus]
Seq. No.
                    169091
Seq. ID
                    LIB3234-078-P1-K1-G12
Method
                    BLASTX
NCBI GI
                    q1161171
BLAST score
                    156
E value
                    2.0e-10
Match length
                    121
% identity
                    18
NCBI Description
                   (L42465) late embryogenesis abundant protein [Picea glauca]
                    169092
Seq. No.
Seq. ID
                    LIB3234-078-P1-K1-G2
Method
                    BLASTX
NCBI GI
                    q3025470
BLAST score
                    376
E value
                    3.0e - 36
Match length
                    126
% identity
                    54
NCBI Description
                   (U76756) endo-beta-1,4-qlucanase [Pinus radiata]
Seq. No.
                    169093
Seq. ID
                    LIB3234-078-P1-K1-G4
Method
                    BLASTX
NCBI GI
                    g927575
BLAST score
                    63
E value
                    1.0e-11
Match length
                    78
% identity
                    55
NCBI Description (U12926) alpha galactosidase [Glycine max]
Seq. No.
                    169094
Seq. ID
                    LIB3234-078-P1-K1-G5
Method
                    BLASTX
NCBI GI
                    g1864017
BLAST score
                    559
E value
                    1.0e-57
Match length
                    106
% identity
                    100
NCBI Description
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                    169095
Seq. ID
                    LIB3234-078-P1-K1-G6
                    BLASTX
Method
NCBI GI
                    g2645971
BLAST score
                    509
E value
                    8.0e-52
Match length
                    110
% identity
                    83
```

22948

[Arabidopsis thaliana]

(AF034255) reversibly glycosylated polypeptide-3



Seq. No. 169096

Seq. ID LIB3234-078-P1-K1-G8

Method BLASTX
NCBI GI g112682
BLAST score 571
E value 4.0e-59
Match length 122
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 169097

Seq. ID LIB3234-078-P1-K1-G9

Method BLASTN
NCBI GI g3128142
BLAST score 311
E value 1.0e-175
Match length 356
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No. 169098

Seq. ID LIB3234-078-P1-K1-H1

Method BLASTX
NCBI GI g2244905
BLAST score 517
E value 9.0e-53
Match length 128
% identity 77

NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 169099

Seq. ID LIB3234-078-P1-K1-H10

Method BLASTN
NCBI GI g1707006
BLAST score 183
E value 1.0e-98
Match length 256
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169100

Seq. ID LIB3234-078-P1-K1-H11

Method BLASTN
NCBI GI g3659491
BLAST score 93
E value 2.0e-45
Match length 101
% identity 99

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome

E value Match length

% identity



1, complete sequence [Arabidopsis thaliana]

Seq. No. 169101 Seq. ID LIB3234-078-P1-K1-H2 Method BLASTX NCBI GI q2244905 BLAST score 382 E value 5.0e-37 Match length 110 % identity 68 NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana] Seq. No. 169102 Seq. ID LIB3234-078-P1-K1-H5 Method BLASTN NCBI GI g1707006 BLAST score 143 E value 9.0e-75 Match length 235 % identity 94 NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 169103 Seq. ID LIB3234-078-P1-K1-H6 Method BLASTX NCBI GI q633890 BLAST score 250 E value 2.0e-21 Match length 88 % identity 62 NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare] Seq. No. 169104 Seq. ID LIB3234-079-P1-K1-A11 Method BLASTX NCBI GI q3334123 BLAST score 645 E value 9.0e-68 Match length 132 99 % identity NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655480_dbj_BAA13599 (D88374) gamma subunit of
mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana] Seq. No. 169105 Seq. ID LIB3234-079-P1-K1-A12 Method BLASTX NCBI GI g2129753 BLAST score 662

22950

1.0e-69

132

```
threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
Seq. No.
                  169106
                  LIB3234-079-P1-K1-A2
Seq. ID
Method
                  BLASTN
                  g2182286
NCBI GI
BLAST score
                  66
E value
                  2.0e-29
Match length
                  74
% identity
                  97
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  169107
Seq. No.
Seq. ID
                  LIB3234-079-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4544385
BLAST score
                  252
E value
                  1.0e-21
Match length
                  79
                  70
% identity
NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  169108
Seq. ID
                  LIB3234-079-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g119143
BLAST score
                  691
E value
                  4.0e-73
Match length
                  131
                  100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
```

alpha chain - Arabidopsis thaliana >gi_295788 emb_CAA34453_(X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_(X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_(X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 169109

Seq. ID LIB3234-079-P1-K1-A8

Method BLASTX
NCBI GI g3831451
BLAST score 669
E value 2.0e-70
Match length 135
% identity 99

NCBI Description (AC005700) putative O-GlcNAc transferase [Arabidopsis

thaliana]

Seq. No. 169110

Seq. ID LIB3234-079-P1-K1-B10

NCBI GI

E value

BLAST score

g4519187

1.0e-101



```
Method
                  BLASTX
                  q3935149
NCBI GI
BLAST score
                  221
                  3.0e-18
E value
                  77
Match length
% identity
                  57
                  (AC005106) T25N20.13 [Arabidopsis thaliana]
NCBI Description
                  169111
Seq. No.
                  LIB3234-079-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244991
                  247
BLAST score
                  1.0e-136
E value
Match length
                  339
                   94
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   169112
Seq. No.
                  LIB3234-079-P1-K1-B12
Seq. ID
                   BLASTN
Method
                   q4263373
NCBI GI
                   59
BLAST score
                   2.0e-24
E value
                   142
Match length
                   87
% identity
                  Arabidopsis thaliana BAC T15G18 from chromosome IV, near 25
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
                   169113
Seq. No.
                   LIB3234-079-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   g2341042
NCBI GI
                   454
BLAST score
                   2.0e-45
E value
Match length
                   107
% identity
                   79
                  (AC000104) F19P19.26 [Arabidopsis thaliana]
NCBI Description
                   169114
Seq. No.
Seq. ID
                   LIB3234-079-P1-K1-B3
Method
                   BLASTN
                   g4757411
NCBI GI
                   259
BLAST score
                   1.0e-144
E value
                   354
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MXC7, complete sequence
                   169115
Seq. No.
                   LIB3234-079-P1-K1-B4
Seq. ID
                   BLASTN
Method
```

E value



```
258
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K1G2, complete sequence
                  169116
Seq. No.
                  LIB3234-079-P1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2499298
BLAST score
                  321
                   4.0e-30
E value
                   65
Match length
                  100
% identity
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST
NCBI Description
                  >gi 1619279 emb CAA67670_ (X99278) ndhG [Arabidopsis
                  thaliana]
                   169117
Seq. No.
                  LIB3234-079-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2129789
                   472
BLAST score
                   2.0e-47
E value
                   119
Match length
                   80
% identity
NCBI Description
                  biotin carboxyl carrier protein precursor (clone BP4) -
                   rape >gi 1070006_emb_CAA62264_ (X90730) Biotin carboxyl
                   carrier protein [Brassica napus] >gi_1589043_prf__2210244D
                   Ac-CoA carboxylase: ISOTYPE=bp4 [Brassica napus]
Seq. No.
                   169118
                   LIB3234-079-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581166
BLAST score
                   308
E value
                   3.0e-28
                   76
Match length
% identity
                   82
                  (AC006220) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169119
                   LIB3234-079-P1-K1-C10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4159704
                   21
BLAST score
E value
                   5.4e-02
Match length
                   212
% identity
                   83
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MCB17, complete sequence
Seq. No.
                   169120
Seq. ID
                   LIB3234-079-P1-K1-C11
                   BLASTN
Method
NCBI GI
                   g3056579
BLAST score
                   196
```

22953

1.0e-106



```
277
Match length
                   58
% identity
                   Arabidopsis thaliana BAC T1F9 chromosome 1, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   169121
Seq. No.
                   LIB3234-079-P1-K1-C12
Seq. ID
                   BLASTN
Method
                   g3212846
NCBI GI
                   385
BLAST score
                   0.0e + 00
E value
                   401
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169122
Seq. No.
                   LIB3234-079-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g266693
NCBI GI
                   235
BLAST score
                   7.0e-20
E value
                   93
Match length
                   59
% identity
                   OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
NCBI Description
                                                      (X62353) oleosin
                   thaliana >gi_16405_emb_CAA44225_
                   [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                   169123
Seq. No.
                   LIB3234-079-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1345973
BLAST score
                   363
                   1.0e-34
E value
Match length
                   90
% identity
                   77
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                    [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   169124
                   LIB3234-079-P1-K1-C6
Seq. ID
                   BLASTN
Method
                   g2264307
NCBI GI
```

BLAST score 313

1.0e-176 E value 393 Match length 95 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MED24, complete sequence [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g881615

2.0e-69

660



```
169125
Seq. No.
                   LIB3234-079-P1-K1-C8
Seq. ID
                   BLASTX
Method
                   g2499298
NCBI GI
                   321
BLAST score
                   4.0e-30
E value
                   65
Match length
                   100
% identity
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST
NCBI Description
                   >gi 1619279 emb CAA67670 (X99278) ndhG [Arabidopsis
                   thaliana]
                   169126
Seq. No.
                   LIB3234-079-P1-K1-D1
Seq. ID
Method
                   BLASTX
                   q135858
NCBI GI
BLAST score
                   505
                   2.0e-51
E value
                   124
Match length
                   81
% identity
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi 99760 pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                   tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                    [Arabidopsis Thaliana] >gi_445128_prf__1908432A tonoplast
                    intrinsic protein alpha [Arabidopsis Thaliana]
                    169127
Seq. No.
                   LIB3234-079-P1-K1-D10
Seq. ID
                   BLASTN
Method
                    g2924257
NCBI GI
                    41
BLAST score
                    1.0e-13
E value
                    124
Match length
                    89
% identity
NCBI Description Tobacco chloroplast genome DNA
                    169128
Seq. No.
                    LIB3234-079-P1-K1-D12
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2129642
                    284
BLAST score
                    7.0e-26
E value
                    48
Match length
                    98
% identity
                    major latex protein type 3 - Arabidopsis thaliana
NCBI Description
                    >gi_1107495_emb CAA63027 (X91961) major latex protein
                    type3 [Arabidopsis thaliana]
                    169129
 Seq. No.
                    LIB3234-079-P1-K1-D2
 Seq. ID
                    BLASTX
Method
```

Match length

% identity

89

76



```
130
Match length
% identity
                  (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
NCBI Description
                  >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
                  169130
Seq. No.
                  LIB3234-079-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169476
BLAST score
                  613
E value
                  5.0e-64
                  117
Match length
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  169131
Seq. No.
Seq. ID
                  LIB3234-079-P1-K1-D6
                  BLASTX
Method
NCBI GI
                  q2190016
BLAST score
                  312
E value
                  1.0e-28
                  128
Match length
% identity
                   45
NCBI Description (AB004269) alliinase [Allium tuberosum]
                   169132
Seq. No.
                  LIB3234-079-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3047060
BLAST score
                   62
                   3.0e-26
E value
Match length
                   66
% identity
                   98
NCBI Description Arabidopsis thaliana BAC F7N22
                   169133
Seq. No.
                   LIB3234-079-P1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4678266
                   297
BLAST score
                   1.0e-166
E value
Match length
                   341
% identity
                   97
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
NCBI Description
                   (ESSA project)
                   169134
Seq. No.
                   LIB3234-079-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2369714
BLAST score
                   336
E value
                   1.0e-31
```

Match length

110



```
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                   169135
Seq. No.
                   LIB3234-079-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g2662343
NCBI GI
                   332
BLAST score
                   5.0e - 31
E value
Match length
                   85
                   79
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   169136
Seq. No.
                   LIB3234-079-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g112681
NCBI GI
                    297
BLAST score
                    3.0e-27
E value
                    72
Match length
                    81
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                    cruciferin precursor (CRA1) - Arabidopsis thaliana
                    >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                    thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                    storage protein [Arabidopsis thaliana]
                    169137
Seq. No.
                    LIB3234-079-P1-K1-E4
Seq. ID
Method
                    BLASTX
                    q3915961
NCBI GI
                    501
BLAST score
                    7.0e-51
E value
                    128
Match length
                    77
% identity
                    HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                    >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                    protein [Nicotiana tabacum]
                    169138
 Seq. No.
                    LIB3234-079-P1-K1-E6
Seq. ID
                    BLASTN
Method
                    g166569
NCBI GI
                    278
 BLAST score
                    1.0e-155
 E value
                    369
Match length
                    99
 % identity
NCBI Description Arabidopsis thaliana glycine rich protein (RAB18) gene,
                    complete cds
                    169139
 Seq. No.
                    LIB3234-079-P1-K1-E9
 Seq. ID
 Method
                    BLASTX
                    g2129659
 NCBI GI
                    328
 BLAST score
                    1.0e-30
 E value
```



```
% identity
                  65
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
NCBI Description
                   (L40954) oleosin [Arabidopsis thaliana]
                  169140
Seq. No.
                  LIB3234-079-P1-K1-F1
Seq. ID
                  BLASTX
Method
                  g1486472
NCBI GI
                  225
BLAST score
                   1.0e-18
E value
                   56
Match length
                   79
% identity
                   (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                   tuberosum]
                   169141
Seq. No.
                   LIB3234-079-P1-K1-F2
Seq. ID
                   BLASTN
Method
                   q3046856
NCBI GI
BLAST score
                   273
                   1.0e-152
E value
                   297
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXI22, complete sequence [Arabidopsis thaliana]
                   169142
Seq. No.
                   LIB3234-079-P1-K1-F3
Seq. ID
Method
                   BLASTN
                   q2351072
NCBI GI
                   247
BLAST score
                   1.0e-137
E value
                   263
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYC6, complete sequence [Arabidopsis thaliana]
                   169143
Seq. No.
                   LIB3234-079-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g4510397
NCBI GI
                   691
BLAST score
                   4.0e-73
 E value
                   131
Match length
                   99
 % identity
                   (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
 NCBI Description
                   169144
 Seq. No.
                   LIB3234-079-P1-K1-F5
 Seq. ID
                   BLASTN
 Method
                   q4510392
 NCBI GI
                   38
 BLAST score
                   3.0e-12
 E value
                   129
 Match length
                   87
 % identity
                   Arabidopsis thaliana chromosome II BAC T17D12 genomic
 NCBI Description
```

22958

sequence, complete sequence



```
169145
Seq. No.
                  LIB3234-079-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  g3660469
NCBI GI
                  548
BLAST score
                  2.0e-56
E value
                  111
Match length
                  98
% identity
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                  thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                  succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                  169146
Seq. No.
                  LIB3234-079-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  q3096910
NCBI GI
                  529
BLAST score
                   3.0e-54
E value
                  112
Match length
                   88
% identity
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  169147
Seq. No.
                  LIB3234-079-P1-K1-F8
Seq. ID
Method
                  BLASTX
                   q529353
NCBI GI
                   270
BLAST score
E value
                   7.0e-24
                   97
Match length
                   48
% identity
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
                   169148
Seq. No.
Seq. ID
                   LIB3234-079-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q1345973
                   344
BLAST score
                   2.0e-32
E value
Match length
                   66
% identity
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi 1197795_dbj BAA05514 (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
                   169149
 Seq. No.
                   LIB3234-079-P1-K1-G10
Seq. ID
                   BLASTN
 Method
```

22959

g4510360

343

NCBI GI BLAST score



E value 0.0e+00
Match length 355
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 169150

Seq. ID LIB3234-079-P1-K1-G11

Method BLASTN
NCBI GI g4510360
BLAST score 201
E value 1.0e-109
Match length 268
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 169151

Seq. ID LIB3234-079-P1-K1-G12

Method BLASTX
NCBI GI g119350
BLAST score 533
E value 1.0e-54
Match length 104
% identity 100

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696

[Arabidopsis thaliana]

Seq. No. 169152

Seq. ID LIB3234-079-P1-K1-G3

Method BLASTX
NCBI GI g4204277
BLAST score 643
E value 2.0e-67
Match length 119
% identity 100

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 169153

Seq. ID LIB3234-079-P1-K1-G4

Method BLASTN
NCBI GI g2924733
BLAST score 35
E value 1.0e-10
Match length 111
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 169154

Seq. ID LIB3234-079-P1-K1-G5



BLASTX

g4115935

Method

NCBI GI

```
BLAST score
                   398
E value
                   8.0e-39
Match length
                   80
                   97
% identity
                  (AF118223) contains similarity to Helicobacter pylori
NCBI Description
                   peptide methionine sulfoxide reductase (msrA) (GB:AE000542)
                   [Arabidopsis thaliana]
Seq. No.
                   169155
                   LIB3234-079-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   511
                   3.0e-52
E value
Match length
                   98
                   100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   169156
                   LIB3234-079-P1-K1-G8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3337347
BLAST score
                   87
                   2.0e-41
E value
                   114
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F13P17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169157
Seq. ID
                   LIB3234-079-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q2132930
BLAST score
                   301
E value
                   2.0e-27
Match length
                   131
% identity
                   45
NCBI Description probable membrane protein YOR262w - yeast (Saccharomyces
                   cerevisiae) >gi_1420591_emb_CAA99484_ (Z75170) ORF YOR262w
                   [Saccharomyces cerevisiae]
                   169158
Seg. No.
                   LIB3234-079-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829896
BLAST score
                   123
E value
                   2.0e-13
                   75
Match length
% identity
                   59
                  (AC002311) highly similar to auxin-regulated protein GH3,
NCBI Description
                   gp X60033 18591 [Arabidopsis thaliana]
Seq. No.
                   169159
```



LIB3234-079-P1-K1-H2 Seq. ID BLASTN Method q4756963 NCBI GI BLAST score 349 0.0e + 00E value 379 Match length 97 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 NCBI Description (ESSA project) 169160 Seq. No. Seq. ID LIB3234-079-P1-K1-H3 BLASTX Method NCBI GI q4406780 678 BLAST score 1.0e-71 E value 128 Match length % identity (AC006532) putative multispanning membrane protein NCBI Description [Arabidopsis thaliana] 169161 Seq. No. LIB3234-079-P1-K1-H4 Seq. ID BLASTX Method q4567311 NCBI GI 246 BLAST score 6.0e-21 E value 58 Match length 76 % identity (AC005956) putative protein kinase [Arabidopsis thaliana] NCBI Description 169162 Seq. No. LIB3234-079-P1-K1-H5 Seq. ID BLASTN Method g2264320 NCBI GI 236 BLAST score 1.0e-130 E value 333 Match length 97 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MXI10, complete sequence [Arabidopsis thaliana] 169163 Seq. No. LIB3234-079-P1-K1-H6 Seq. ID Method BLASTX g4544445 NCBI GI 220 BLAST score 6.0e-18 E value 102 Match length 49 % identity (AC006592) putative pyrophosphate--fructose 6-phosphate NCBI Description 1-phosphotransferase [Arabidopsis thaliana] 169164 Seq. No. LIB3234-079-P1-K1-H7 Seq. ID

22962

BLASTX

q4582430

Method

NCBI GI

NCBI GI

BLAST score



```
614
BLAST score
                  3.0e-64
E value
                  118
Match length
% identity
                   (AC007196) nonsense-mediated mRNA decay protein
NCBI Description
                   [Arabidopsis thaliana]
                  169165
Seq. No.
                  LIB3234-079-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  q1076331
NCBI GI
                   225
BLAST score
                  1.0e-18
E value
                   44
Match length
                   100
% identity
                  histidine transport protein - Arabidopsis thaliana
NCBI Description
                   >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
                   1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His
                   transporter [Arabidopsis thaliana]
                   169166
Seq. No.
                   LIB3234-080-P1-K1-A10
Seq. ID
                   BLASTN
Method
                   g4220628
NCBI GI
BLAST score
                   132
                   5.0e-68
E value
                   337
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24C1, complete sequence [Arabidopsis thaliana]
                   169167
Seq. No.
                   LIB3234-080-P1-K1-A11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3445196
                   176
BLAST score
                   3.0e - 94
E value
                   280
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC T20K9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169168
Seq. No.
                   LIB3234-080-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   g4038040
NCBI GI
                   301
 BLAST score
                   2.0e-27
 E value
Match length
                   77
                   79
 % identity
                   (AC005936) proteinase inhibitor II [Arabidopsis thaliana]
 NCBI Description
                   169169
 Seq. No.
                   LIB3234-080-P1-K1-A3
 Seq. ID
                   BLASTX
 Method
```

22963

g1345973



E value 2.0e-16
Match length 63
% identity 67

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 169170

Seq. ID LIB3234-080-P1-K1-A5

Method BLASTX
NCBI GI g1350965
BLAST score 532
E value 2.0e-54
Match length 103
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12)

Seq. No. 169171

Seq. ID LIB3234-080-P1-K1-A6

Method BLASTX
NCBI GI g1345973
BLAST score 380
E value 1.0e-36
Match length 92
% identity 77

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No. 169172

Seq. ID LIB3234-080-P1-K1-A8

Method BLASTX
NCBI GI g1345973
BLAST score 417
E value 5.0e-41
Match length 94
% identity 81
NCBI Description OMEGA-3

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid



desaturase [Arabidopsis thaliana]

```
Seq. No.
                  169173
                  LIB3234-080-P1-K1-A9
Seq. ID
                  BLASTN
Method
                  g2564047
NCBI GI
BLAST score
                   109
                   3.0e-54
E value
                   343
Match length
                   96
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJB21, complete sequence [Arabidopsis thaliana]
                   169174
Seq. No.
                   LIB3234-080-P1-K1-B1
Seq. ID
Method
                   BLASTN
                   g2564047
NCBI GI
                   75
BLAST score
                   5.0e - 34
E value
                   276
Match length
                   94
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJB21, complete sequence [Arabidopsis thaliana]
                   169175
Seq. No.
                   LIB3234-080-P1-K1-B10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3292807
BLAST score
                   309
                   1.0e-173
E value
                   338
Match length
                   97
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                   (ESSAII project)
                   169176
Seq. No.
                   LIB3234-080-P1-K1-B11
Seq. ID
Method
                   BLASTX
                   q4204299
NCBI GI
                   564
BLAST score
                   3.0e-58
E value
                   110
Match length
                   100
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   169177
Seq. No.
                   LIB3234-080-P1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3540196
                   582
BLAST score
                   2.0e-60
E value
                   115
Match length
 % identity
                   100
                   (AC004260) Putative amp-binding protein [Arabidopsis
NCBI Description
                   thaliana]
```

% identity



```
169178
Seq. No.
                  LIB3234-080-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g120667
BLAST score
                  410
                   3.0e-40
E value
Match length
                  103
% identity
                   77
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                   thaliana >gi 166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                   dehydrogenase [Arabidopsis thaliana]
                   169179
Seq. No.
                   LIB3234-080-P1-K1-B3
Seq. ID
Method
                   BLASTN
                   q3445196
NCBI GI
BLAST score
                   187
                   1.0e-101
E value
Match length
                   291
% identity
                   99
                   Arabidopsis thaliana chromosome II BAC T20K9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169180
Seq. No.
                   LIB3234-080-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   g4539343
NCBI GI
                   45
BLAST score
                   2.0e-14
E value
                   96
Match length
                   50
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   169181
Seq. No.
                   LIB3234-080-P1-K1-B7
Seq. ID
                   BLASTN
Method
                   g2564047
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
                   128
Match length
                   96
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJB21, complete sequence [Arabidopsis thaliana]
                   169182
 Seq. No.
                   LIB3234-080-P1-K1-B8
 Seq. ID
                   BLASTN
Method
                   q4490291
NCBI GI
                   275
BLAST score
                   1.0e-153
E value
                   291
Match length
```

22966

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5



(ESSA project)

```
Seq. No.
                  169183
                  LIB3234-080-P1-K1-B9
Sea. ID
Methad
                  BLASTN
                  g3445196
NCBI GI
BLAST score
                  37
E value
                  2.0e-11
Match length
                  57
                  91
% identity
                  Arabidopsis thaliana chromosome II BAC T20K9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana].
                  169184
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-C10
                  BLASTN
Method
NCBI GI
                  q4741961
BLAST score
                  332
E value
                  0.0e + 00
                  360
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds
Seq. No.
                  169185
                  LIB3234-080-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g137580
BLAST score
                   188
E value
                   3.0e-14
Match length
                   118
                   34
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
NCBI Description
                   >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone
                   C72) - upland cotton >gi 167375 (M16891) vicilin precursor
                   [Gossypium hirsutum]
                   169186
Seq. No.
                   LIB3234-080-P1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1871173
                   366
BLAST score
                   0.0e + 00
E value
                   374
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC T06D20 genomic
NCBI Description
                   sequence, complete sequence
                   169187
Seq. No.
                   LIB3234-080-P1-K1-C4
Seq. ID
Method
                   BLASTN
                   g4572664
NCBI GI
BLAST score
                   226
E value
                   1.0e-124
Match length
                   358
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F25P17 genomic
```

sequence, complete sequence



```
169188
Seq. No.
                   LIB3234-080-P1-K1-C5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4572664
BLAST score
                   172
                   6.0e-92
E value
Match length
                   310
                   96
% identity
                  Arabidopsis thaliana chromosome II BAC F25P17 genomic
NCBI Description
                   sequence, complete sequence
                   169189
Seq. No.
Seq. ID
                   LIB3234-080-P1-K1-C6
                   BLASTX
Method
                   g2052379
NCBI GI
BLAST score
                   673
                   5.0e-71
E value
Match length
                   126
% identity
                   100
                  (U66343) calreticulin [Arabidopsis thaliana]
NCBI Description
                   169190
Seq. No.
                   LIB3234-080-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   q128838
NCBI GI
                   485
BLAST score
                   4.0e-49
E value
Match length
                   117
% identity
                   75
                   NADH-PLASTOQUINONE OXIDOREDUCTASE 49 KD SUBUNIT,
NCBI Description
                   CHLOROPLAST (ORF 393) >gi 82215_pir__A05216 NADH
                   dehydrogenase (ubiquinone) (EC \overline{1.6.5.3}) chain 393 - common
                   tobacco chloroplast >gi_1223674_emb_CAA77398_ (Z00044) NADH
                   dehydrogenase 49kD subunit [Nicotiana tabacum]
                   >gi 225262 prf__1211235CX ORF 393 [Nicotiana tabacum]
                   169191
Seq. No.
                   LIB3234-080-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3395434
                   420
BLAST score
                   2.0e-41
E value
                   117
Match length
                   77
 % identity
                   (AC004683) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi_742248_prf__2009327B peroxidase [Arabidopsis thaliana]
                   169192
 Seq. No.
                   LIB3234-080-P1-K1-D10
 Seq. ID
                   BLASTN
 Method
                   g2961370
 NCBI GI
                   81
 BLAST score
                   1.0e-37
E value
                   101
Match length
                    95
 % identity
```

22968

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13

Seq. ID



(ESSAII project)

```
169193
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-D11
                  BLASTN
Method
                  g2924257
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                  196
Match length
                  93
% identity
NCBI Description Tobacco chloroplast genome DNA
                  169194
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-D2
                  BLASTX
Method
                  q2769642
NCBI GI
BLAST score
                  532
                  2.0e-54
E value
Match length
                   125
                   78
% identity
                  (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
NCBI Description
                  esculentum]
                   169195
Seq. No.
                  LIB3234-080-P1-K1-D5
Seq. ID
                  BLASTN
Method
                   q4512656
NCBI GI
                   380
BLAST score
E value
                   0.0e + 00
Match length
                   380
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
                   169196
Seq. No.
                   LIB3234-080-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g4589972
NCBI GI
BLAST score
                   503
                   3.0e-51
E value
Match length
                   95
                   100
% identity
                   (AC007195) putative indole-3 acetic acid induced protein
NCBI Description
                   (ARG7) [Arabidopsis thaliana]
                   169197
Seq. No.
                   LIB3234-080-P1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3150407
NCBI GI
BLAST score
                   441
                   7.0e-44
E value
                   83
Match length
                   99
 % identity
                  (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169198
 Seq. No.
```

LIB3234-080-P1-K1-E1

Seq. ID



```
BLASTX
Method
                  g1944518
NCBI GI
                  172
BLAST score
                  3.0e-12
E value
                  35
Match length
                  100
% identity
                  (Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana]
NCBI Description
                  >gi 3047105 (AF058919) protein kinase [Arabidopsis
                  thaliana]
                  169199
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-E12
                  BLASTN
Method
                  g2827513
NCBI GI
                  191
BLAST score
                  1.0e-103
E value
                   294
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
NCBI Description
                   (ESSAII project)
                   169200
Seq. No.
                  LIB3234-080-P1-K1-E2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3047100
                   158
BLAST score
                   9.0e-84
E value
                   245
Match length
                   91
% identity
NCBI Description Arabidopsis thaliana BAC F6N23
                   169201
Seq. No.
                   LIB3234-080-P1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1107501
                   415
BLAST score
                   8.0e-41
E value
                   117
Match length
                   72
% identity
                   (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
NCBI Description
                   Match to gb X91954 orf gene product from A. thaliana. ESTs
                   gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   169202
                   LIB3234-080-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   g2160151
NCBI GI
                   466
BLAST score
                   8.0e-47
E value
                   106
Match length
                   87
% identity
                   (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                   (gb_X77260). [Arabidopsis thaliana]
                   169203
Seq. No.
```

LIB3234-080-P1-K1-F1



```
BLASTX
Method
                  g3924604
NCBI GI
                  475
BLAST score
                  5.0e-48
E value
                  98
Match length
% identity
                   (AF069442) putative leucine-rich repeat protein
NCBI Description
                   [Arabidopsis thaliana]
                  169204
Seq. No.
                  LIB3234-080-P1-K1-F10
Seq. ID
                  BLASTX
Method
                   g266693
NCBI GI
BLAST score
                   210
                   9.0e-17
E value
                   111
Match length
                   50
% identity
                  OLEOSIN >gi 282875 pir_ S22538 oleosin - Arabidopsis
NCBI Description
                   thaliana >gi 16405 emb CAA44225 (X62353) oleosin
                   [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                   169205
Seq. No.
Seq. ID
                   LIB3234-080-P1-K1-F11
                   BLASTX
Method
                   q131336
NCBI GI
                   339
BLAST score
                   6.0e-32
E value
                   73
Match length
                   93
% identity
                   PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_ 72715_pir__F2NT0P
NCBI Description
                   photosystem II phosphoprotein psbH - common tobacco
                   chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
                   >gi_225225_prf__1211235BG photosystem II 10kD
                   phosphoprotein [Nicotiana tabacum]
                   169206
Seq. No.
                   LIB3234-080-P1-K1-F12
Seq. ID
Method
                   BLASTX
                   q4586107
NCBI GI
BLAST score
                   389
                   9.0e-38
E value
Match length
                   123
                   12
 % identity
                   (AL049638) putative disease resistance protein [Arabidopsis
 NCBI Description
                   thaliana]
                   169207
 Seq. No.
                   LIB3234-080-P1-K1-F2
 Seq. ID
                   BLASTN
 Method
                   g4159708
 NCBI GI
                   351
 BLAST score
                   0.0e + 00
 E value
                   367
 Match length
                   93
 % identity
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```



MKP6, complete sequence

```
Seq. No.
                  169208
                  LIB3234-080-P1-K1-F4
Seq. ID
Method
                  BLASTN
                  g4678196
NCBI GI
BLAST score
                  289
                  1.0e-161
E value
                  378
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7H1 genomic
                  sequence, complete sequence
                  169209
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-F6
                  BLASTN
Method
NCBI GI
                  q2924651
BLAST score
                  378
E value
                  0.0e + 00
Match length
                  378
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169210
                  LIB3234-080-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g3540201
NCBI GI
BLAST score
                  538
                  3.0e-55
E value
Match length
                  108
                  100
% identity
NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]
Seq. No.
                  169211
Seq. ID
                  LIB3234-080-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1709129
BLAST score
                  164
                  2.0e-11
E value
Match length
                  55
% identity
                  65
NCBI Description GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3
                  >gi 481018 pir S37642 protein kinase MSK-3 (EC 2.7.1.-) -
                  alfalfa >gi 313148 emb CAA48472 (X68409) protein kinase
                  [Medicago sativa]
                  169212
Seq. No.
                  LIB3234-080-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3892217
BLAST score
                  117
E value
                  4.0e-59
Match length
                  217
                  99
% identity
NCBI Description Arabidopsis thaliana ATP-dependent protease proteolytic
                  subunit (clpP) gene, promoter region and partial cds
```



169213

Seq. No.

```
LIB3234-080-P1-K1-G10
Seq. ID
Method
                  BLASTN
                  g4455339
NCBI GI
                  305
BLAST score
                  1.0e-171
E value
                  373
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
NCBI Description
                  (ESSAII project)
                  169214
Seq. No.
                  LIB3234-080-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  58
                  1.0e-24
E value
Match length
                  74
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169215
                  LIB3234-080-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757399
BLAST score
                  203
E value
                  1.0e-110
Match length
                  203
                  51
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MEE13, complete sequence
                  169216
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4008544
BLAST score
                  167
E value
                  1.0e-11
Match length
                  104
                  37
% identity
                  (AL034492) putative nucleotide-sugar dehydratase
NCBI Description
                   [Streptomyces coelicolor]
                  169217
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  q3096920
                  588
BLAST score
                   4.0e-61
E value
                  114
Match length
% identity
```

Seq. No. 169218

thaliana]

NCBI Description

22973

(AL023094) putative ketoacyl-CoA synthase [Arabidopsis



```
LIB3234-080-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g3063706
NCBI GI
BLAST score
                  621
E value
                  6.0e-65
Match length
                  126
                  87
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                  169219
Seq. No.
                  LIB3234-080-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  q1297184
NCBI GI
BLAST score
                  378
                  0.0e+00
E value
                  378
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome I cosmid g8261 DNA
                  (cytosine-5-) methyltransferase, zinc finger protein 1,
                  nucleoporin 98, poly A+ RNA export protein, plasma membrane
                  ATPase 2, and serine/threonine protein kinase genes, co
                  169220
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-H1
                  BLASTN
Method
NCBI GI
                  q4585952
BLAST score
                  236
E value
                  1.0e-130
Match length
                  369
% identity
                  95
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,
                  complete sequence
                  169221
Seq. No.
                  LIB3234-080-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832625
                  215
BLAST score
                  2.0e-17
E value
Match length
                  60
                  63
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  169222
Seq. ID
                  LIB3234-080-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2982437
BLAST score
                  367
E value
                  3.0e - 35
```

Match length 120 % identity 66

(AL022224) terpene cyclase like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 169223

LIB3234-080-P1-K1-H12 Seq. ID

Method BLASTN



```
NCBI GI
                  g4006885
BLAST score
                  322
                  0.0e + 00
E value
Match length
                   346
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   169224
Seq. No.
Seq. ID
                  LIB3234-080-P1-K1-H2
Method
                  BLASTX
NCBI GI
                   g1864017
BLAST score
                   548
                   2.0e-56
E value
Match length
                   104
                   100
% identity
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   169225
                   LIB3234-080-P1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3242717
BLAST score
                   630
E value
                   5.0e-66
                   125
Match length
                   100
% identity
                   (AC003040) putative APG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169226
                   LIB3234-080-P1-K1-H4
Seq. ID
                   BLASTN
Method
                   q16231
NCBI GI
                   92
BLAST score
                   8.0e-45
E value
                   104
Match length
                   97
% identity
                   Arabidopsis CRA1 gene for 12S seed storage protein
NCBI Description
                   >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage
                   protein CRA1 gene, exons 1-4
                   169227
Seq. No.
                   LIB3234-080-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   g2317731
NCBI GI
                   652
BLAST score
                   1.0e-68
E value
                   120
Match length
                   100
% identity
                   (AF013628) reversibly glycosylated polypeptide-2
NCBI Description
```

[Arabidopsis thaliana]

169228 Seq. No.

LIB3234-080-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI g2317731 BLAST score 637 E value 7.0e-67



```
119
Match length
                   97
% identity
                   (AF013628) reversibly glycosylated polypeptide-2
NCBI Description
                   [Arabidopsis thaliana]
                  169229
Seq. No.
                  LIB3234-080-P1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131276
                   578
BLAST score
                   6.0e-60
E value
                  122
Match length
                   91
% identity
                  PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
NCBI Description
                   PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll
                   a-binding protein psbB - common tobacco chloroplast
                   >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein
                   [Nicotiana tabacum] >gi_225224 prf 1211235BF photosystem
                   II P680 apoprotein [Nicotiana tabacum]
                   169230
Seq. No.
                  LIB3234-081-Q1-K1-A10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3928074
BLAST score
                   211
E value
                   1.0e-115
                   301
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC T7F6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169231
Seq. No.
                   LIB3234-081-Q1-K1-A11
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4757414
                   356
BLAST score
                   0.0e+00
E value
Match length
                   368
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYF24, complete sequence
                   169232
Seq. No.
                   LIB3234-081-Q1-K1-A2
Seq. ID
Method
                   BLASTN
                   g2244788
NCBI GI
                   203
BLAST score
                   1.0e-110
E value
                   368
Match length
% identity
                   96
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
```

Seq. No. 169233

Seq. ID LIB3234-081-Q1-K1-A3

Method BLASTN NCBI GI g4757414



```
356
BLAST score
E value
                  0.0e + 00
                  372
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
                  169234
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-A4
                  BLASTN
Method
                  g2980787
NCBI GI
                   71
BLAST score
E value
                  8.0e-32
                  174
Match length
                   52
% identity
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
NCBI Description
                   (ESSAII project)
Seq. No.
                   169235
                   LIB3234-081-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
                   556
BLAST score
E value
                   2.0e-57
                   120
Match length
                   91
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   169236
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-A8
                   BLASTN
Method
NCBI GI
                   g3449320
BLAST score
                   341
                   0.0e + 00
E value
Match length
                   365
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRB17, complete sequence [Arabidopsis thaliana]
                   169237
Seq. No.
                   LIB3234-081-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1531762
                   179
BLAST score
                   4.0e-13
E value
```

48 Match length 73 % identity

(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis NCBI Description

thaliana]

169238 Seq. No.

LIB3234-081-Q1-K1-B11 Seq. ID

Method BLASTN g4519195 NCBI GI 333 BLAST score

NCBI GI

E value

BLAST score

Match length



```
E value
                  0.0e + 00
Match length
                  370
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
Seq. No.
                  169239
Seq. ID
                  LIB3234-081-Q1-K1-B12
Method
                  BLASTN
NCBI GI
                  g4519195
BLAST score
                  105
                   6.0e-52
E value
Match length
                  225
                   87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
                  169240
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                   q4539004
BLAST score
                   182
                   2.0e-13
E value
Match length
                   92
                   53
% identity
                  (ALO49481) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   169241
Seq. No.
                   LIB3234-081-Q1-K1-B6
Seq. ID
Method
                   BLASTX
                   q3157930
NCBI GI
                   655
BLAST score
                   6.0e-69
E value
Match length
                   123
                   99
% identity
                  (AC002131) Strong similarity to
NCBI Description
                   amino-cyclopropane-carboxylic acid oxidase gb_L27664 from
                   Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from
                   this gene. [Arabidopsis thaliana]
                   169242
Seq. No.
                   LIB3234-081-Q1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4056489
                   480
BLAST score
                   2.0e-48
E value
                   119
Match length
                   75
% identity
                  (AC005896) putative white protein [Arabidopsis thaliana]
NCBI Description
                   169243
Seq. No.
                   LIB3234-081-Q1-K1-C1
Seq. ID
Method
                   BLASTN
```

22978

g3176694

2.0e-10

35

E value

Match length

% identity



```
% identity
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169244
Seq. No.
                  LIB3234-081-Q1-K1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4512656
                  131
BLAST score
                  2.0e-67
E value
                  307
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  169245
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  g3413696
BLAST score
                  369
                  0.0e + 00
E value
                   373
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T19L18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  169246
Seq. No.
                  LIB3234-081-Q1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3510343
                   147
BLAST score
                   5.0e-77
E value
Match length
                   373
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJC20, complete sequence [Arabidopsis thaliana]
                   169247
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   631
                   4.0e-66
E value
                   122
Match length
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   169248
Seq. No.
                   LIB3234-081-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   q3878102
NCBI GI
                   343
BLAST score
```

2.0e-32

123

NCBI GI

E value

BLAST score

Match length

q1345973

406 9.0e-40

93



```
(AL021346) predicted using Genefinder; cDNA EST EMBL:D28058
NCBI Description
                  comes from this gene; cDNA EST EMBL: D67579 comes from this
                  gene; cDNA EST yk275b1.5 comes from this gene; cDNA EST
                  yk208b12.5 comes from this gene; cDNA EST yk395f4.5
                  169249
Seq. No.
                  LIB3234-081-Q1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3176694
BLAST score
                  349
                  0.0e + 00
E value
                  360
Match length
% identity
                   99
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169250
                   LIB3234-081-Q1-K1-C8
Sea. ID
Method
                   BLASTN
                   q3413696
NCBI GI
BLAST score
                   104
                   2.0e-51
E value
Match length
                   299
% identity
                   87
                  Arabidopsis thaliana chromosome II BAC T19L18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169251
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-D10
Method
                   BLASTX
                   q2738248
NCBI GI
BLAST score
                   618
                   1.0e-64
E value
Match length
                   123
                   99
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   169252
                   LIB3234-081-Q1-K1-D11
Seq. ID
Method
                   BLASTX
                   g1169544
NCBI GI
                   583
BLAST score
                   2.0e-60
E value
                   123
Match length
                   97
% identity
                   ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein
NCBI Description
                   - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582)
                   ERD1 protein [Arabidopsis thaliana]
Seq. No.
                   169253
                   LIB3234-081-Q1-K1-D12
Seq. ID
                   BLASTX
Method
```



```
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC
                  1.1\overline{4.99.-} CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >qi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi 1197795_dbj BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  169254
Seq. No.
                  LIB3234-081-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g2194128
NCBI GI
BLAST score
                  88
                  8.0e-60
E value
Match length
                  118
                  98
% identity
                   (AC002062) Strong similarity to Arabidopsis receptor-like
NCBI Description
                  kinase (gb_ATLECGENE) and F20P5.15. [Arabidopsis thaliana]
                  169255
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-D5
Method
                  BLASTX
                  g3451077
NCBI GI
BLAST score
                  152
                   5.0e-10
E value
                   84
Match length
% identity
                   40
                   (AL031326) cysteine proteinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   169256
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-D6
                   BLASTN
Method
                   g4199934
NCBI GI
BLAST score
                   272
                   1.0e-151
E value
Match length
                   353
                   92
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   169257
                   LIB3234-081-Q1-K1-D7
Seq. ID
Method
                   BLASTN
                   g4406752
NCBI GI
                   92
BLAST score
E value
                   3.0e-44
                   145
Match length
```

% identity

Arabidopsis thaliana chromosome II BAC F19B11 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

169258 Seq. No.

LIB3234-081-Q1-K1-D8 Seq. ID

76

Seq. No.

Seq. ID



```
BLASTN
Method
                  g4589427
NCBI GI
                  322
BLAST score
                  0.0e + 00
E value
                  361
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFG13, complete sequence
                  169259
Seq. No.
                  LIB3234-081-Q1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3128168
BLAST score
                  362
                  1.0e-34
E value
                  119
Match length
                  58
% identity
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
                  169260
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-E1
                  BLASTX
Method
                  g3402487
NCBI GI
BLAST score
                   616
                  2.0e-64
E value
                  123
Match length
% identity
                   (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
NCBI Description
                  thaliana]
                   169261
Seq. No.
                   LIB3234-081-Q1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2499327
BLAST score
                   282
                   3.0e-25
E value
Match length
                   102
                   58
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH
                   dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                   >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase
                   [Arabidopsis thaliana]
                   169262
Seq. No.
                   LIB3234-081-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g3036816
NCBI GI
                   255
BLAST score
                   5.0e-22
E value
Match length
                   115
                   49
% identity
                  (AL022373) myosin-like protein [Arabidopsis thaliana]
NCBI Description
                   169263
```

22982

LIB3234-081-Q1-K1-E4



```
BLASTX
Method
NCBI GI
                  q2213615
BLAST score
                  419
                   3.0e-41
E value
Match length
                  121
% identity
                  (AC000103) F21J9.9 [Arabidopsis thaliana]
NCBI Description
                  169264
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-E7
                   BLASTX
Method
                   g399091
NCBI GI
BLAST score
                   457
                   5.0e-46
E value
Match length
                   93
                   97
% identity
                   PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
NCBI Description
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi_282878_pir A38230 inorganic pyrophosphatase
                   (EC 3.6.1.1), \overline{H}+-translocating pyrophosphate-energized -
                   Arabidopsis thaliana >gi_166634 (M81892) vacuolar
                   H+-phosphatase [Arabidopsis thaliana]
                   169265
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-E8
                   BLASTX
Method
NCBI GI
                   q543751
                   179
BLAST score
                   4.0e-13
E value
Match length
                   35
                   94
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                   (ETHYLENE-FORMING ENZYME) (EFE) >gi_541861_pir__JT0755
                   ethylene-forming enzyme - Arabidopsis thaliana
                   >gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme
                   [Arabidopsis thaliana]
                   169266
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-E9
Method
                   BLASTN
NCBI GI
                   q4027862
BLAST score
                   144
                   3.0e-75
E value
                   284
Match length
                   88
% identity
                   Arabidopsis thaliana chromosome 1 BAC T7A14 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169267
Seq. No.
                   LIB3234-081-Q1-K1-F10
Seq. ID
                   BLASTN
Method
                   g3075383
NCBI GI
                   163
BLAST score
                   1.0e-86
E value
                   372
Match length
                   95
 % identity
```

NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic



```
sequence, complete sequence [Arabidopsis thaliana]
```

```
169268
Seq. No.
                  LIB3234-081-Q1-K1-F11
Seq. ID
Method
                  BLASTN
                  q4426938
NCBI GI
BLAST score
                   60
                   4.0e-25
E value
                   108
Match length
                   93
% identity
                   Arabidopsis thaliana senescence-associated protein (SAG29)
NCBI Description
                   mRNA, partial cds
                   169269
Seq. No.
                   LIB3234-081-Q1-K1-F12
Seq. ID
                   BLASTN
Method
                   g3004543
NCBI GI
BLAST score
                   225
                   1.0e-123
E value
                   348
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC F19F24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169270
Seq. No.
                   LIB3234-081-Q1-K1-F2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4757400
BLAST score
                   344
                   0.0e + 00
E value
                   356
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MFJ20, complete sequence
                   169271
Seq. No.
                   LIB3234-081-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g2160189
NCBI GI
                   615
BLAST score
                   3.0e-64
E value
                   123
Match length
                   15
% identity
                   (ACO00132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
                   169272
Seq. No.
                   LIB3234-081-Q1-K1-F4
Seq. ID
Method
                   BLASTN
                   g12218
NCBI GI
                   211
BLAST score
                   1.0e-115
E value
Match length
                   243
                   97
 % identity
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly
```

Seq. ID



```
169273
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-F6
                  BLASTN
Method
NCBI GI
                  q3047074
BLAST score
                  297
                  1.0e-166
E value
                  352
Match length
                  99
% identity
                  Arabidopsis thaliana BAC F21E10
NCBI Description
                  169274
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-F8
Method
                  BLASTX
                  q2160189
NCBI GI
                  332
BLAST score
                   4.0e-31
E value
                  122
Match length
% identity
                   (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb RLK5 ARATH). ESTs gb ATTS0475, gb ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
                  169275
Seq. No.
Seq. ID
                  LIB3234-081-Q1-K1-F9
Method
                  BLASTX
                   g2160189
NCBI GI
                   230
BLAST score
                   4.0e-19
E value
Match length
                   129
% identity
                   24
                   (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   169276
                   LIB3234-081-Q1-K1-G2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4199934
BLAST score
                   323
                   0.0e+00
E value
Match length
                   371
                   97
% identity
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169277
Seq. No.
                   LIB3234-081-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g4581166
NCBI GI
                   293
BLAST score
                   2.0e-26
E value
Match length
                   73
                   81
% identity
                  (AC006220) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169278
Seq. No.
```

LIB3234-081-Q1-K1-G7



```
BLASTN
Method
                  g3299824
NCBI GI
BLAST score
                  157
                   6.0e-83
E value
                   374
Match length
% identity
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                   near 17 cM, complete sequence [Arabidopsis thaliana]
                   169279
Seq. No.
                   LIB3234-081-Q1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3805845
BLAST score
                   389
                   5.0e-38
E value
                   93
Match length
                   85
% identity
                   (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                   169280
Seq. No.
                   LIB3234-081-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   q2335106
NCBI GI
BLAST score
                   151
                   7.0e-10
E value
                   122
Match length
                   6
% identity
                   (AC002339) salt inducible protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   169281
Seq. No.
                   LIB3234-081-Q1-K1-H10
Seq. ID
                   BLASTN
Method
                   g4519193
NCBI GI
BLAST score
                   328
                   0.0e+00
E value
                   371
Match length
                   63
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MDC11, complete sequence
Seq. No.
                   169282
                   LIB3234-081-Q1-K1-H12
Seq. ID
                   BLASTN
Method
                   q2760167
NCBI GI
                   60
BLAST score
                   7.0e-26
E value
                   64
Match length
                   98
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCO15, complete sequence [Arabidopsis thaliana]
                   169283
 Seq. No.
                   LIB3234-081-Q1-K1-H4
 Seq. ID
                   BLASTX
 Method
                   q135406
 NCBI GI
```

671

BLAST score



```
8.0e-71
E value
Match length
                  125
                  98
% identity
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
                  169284
Seq. No.
                  LIB3234-081-Q1-K1-H6
Seq. ID
                  BLASTN
Method
                   g2760167
NCBI GI
BLAST score
                   98
                   8.0e-48
E value
Match length
                   295
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCO15, complete sequence [Arabidopsis thaliana]
                   169285
Seq. No.
Seq. ID
                   LIB3234-081-Q1-K1-H7
                   BLASTN
Method
                   q3046850
NCBI GI
BLAST score
                   89
                   2.0e-42
E value
                   291
Match length
                   81
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24G6, complete sequence [Arabidopsis thaliana]
                   169286
Seq. No.
                   LIB3234-081-Q1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2961390
BLAST score
                   674
                   3.0e-71
E value
Match length
                   123
                   99
% identity
                   (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   169287
Seq. No.
                   LIB3234-082-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115767
                   562
BLAST score
                   4.0e-58
E value
                   108
Match length
                   99
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
```

a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]



Seq. No.

169288

```
LIB3234-082-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g4586249
NCBI GI
                  341
BLAST score
                  4.0e-32
E value
                  95
Match length
                  66
% identity
                  (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                  thaliana]
                  169289
Seq. No.
Seq. ID
                  LIB3234-082-Q1-K1-A11
                  BLASTN
Method
                  g2244991
NCBI GI
                  359
BLAST score
                  0.0e+00
E value
                  359
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                   169290
Seq. No.
Seq. ID
                  LIB3234-082-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                   g1076416
                   390
BLAST score
                   6.0e-38
E value
                   104
Match length
% identity
                   sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor -
NCBI Description
                   Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite
                   reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis
                   thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite
                   reductase [Arabidopsis thaliana]
                   169291
Seq. No.
                   LIB3234-082-Q1-K1-A2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2760167
BLAST score
                   222
                   1.0e-121
E value
                   335
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCO15, complete sequence [Arabidopsis thaliana]
                   169292
Seq. No.
                   LIB3234-082-Q1-K1-A3
Seq. ID
Method
                   BLASTN
                   g4006885
NCBI GI
                   320
BLAST score
                   1.0e-180
E value
                   376
Match length
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
```



169293

```
Seq. No.
                  LIB3234-082-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g2832674
NCBI GI
                  614
BLAST score
                  4.0e-64
E value
                  123
Match length
                  100
% identity
                   (AL021712) fibrillin precursor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   169294
Seq. No.
                  LIB3234-082-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                   g3421102
NCBI GI
                   530
BLAST score
                   3.0e-54
E value
                   113
Match length
% identity
                   (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
NCBI Description
                   thaliana]
                   169295
Seq. No.
                   LIB3234-082-Q1-K1-B1
Seq. ID
                   BLASTN
Method
                   g2749918
NCBI GI
                   138
BLAST score
                   1.0e-71
E value
                   273
Match length
                   88
% identity
                   Arabidopsis thaliana chromosome I BAC F3I6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169296
                   LIB3234-082-Q1-K1-B2
Seq. ID
                   BLASTN
Method
                   q2213606
NCBI GI
                   140
.BLAST score
E value
                   8.0e-73
                   288
Match length
                   98
 % identity
                   Genomic sequence for Arabidopsis thaliana BAC F21J9,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169297
 Seq. No.
Seq. ID
                   LIB3234-082-Q1-K1-B3
                   BLASTN
Method
                   g3738313
 NCBI GI
                   346
 BLAST score
                   0.0e+00
 E value
 Match length
                   361
                   99
 % identity
                   Arabidopsis thaliana chromosome II BAC T29E15 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

169298

Seq. No.



```
LIB3234-082-Q1-K1-B4
Seq. ID
                  BLASTN
Method
                  g495322
NCBI GI
                  83
BLAST score
                  6.0e-39.
E value
                  135
Match length
                  91
% identity
NCBI Description Alnus incana chloroplast 16S rRNA gene, complete sequence
                  169299
Seq. No.
                  LIB3234-082-Q1-K1-B5
Seq. ID
                  BLASTN
Method
                  g4589428
NCBI GI
                  187
BLAST score
                  1.0e-101
E value
                  311
Match length
                   95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MFH8, complete sequence
                   169300
Seq. No.
                  LIB3234-082-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   q3805845
NCBI GI
                   650
BLAST score
                   2.0e-68
E value
                   124
Match length
                   100
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                   169301
Seq. No.
                   LIB3234-082-Q1-K1-B9
Seq. ID
                   BLASTN
Method
                   q4662628
NCBI GI
BLAST score
                   233
                   1.0e-128
E value
                   368
Match length
                   92
 % identity
                   Arabidopsis thaliana chromosome II BAC F27010 genomic
NCBI Description
                   sequence, complete sequence
                   169302
 Seq. No.
                   LIB3234-082-Q1-K1-C1
 Seq. ID
                   BLASTN
 Method
                   q3046853
 NCBI GI
                   327
 BLAST score
                   0.0e+00
 E value
 Match length
                   334
                   99
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MRA19, complete sequence [Arabidopsis thaliana]
```

Seq. No. 169303

Seq. ID LIB3234-082-Q1-K1-C11

Method BLASTX NCBI GI g1170034 BLAST score 348



5.0e-33 E value Match length 72 99 % identity GLUTAMATE--CYSTEINE LIGASE PRECURSOR NCBI Description (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi 2129598 pir_S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >qi 488615 emb CAA82626 (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana] 169304 Seq. No. Seq. ID LIB3234-082-Q1-K1-C12 BLASTN Method NCBI GI q1935913 BLAST score 232 1.0e-127 E value 274 Match length % identity Arabidopsis thaliana lethal leaf-spot 1 homolog (Lls1) NCBI Description mRNA, partial cds 169305 Seq. No. LIB3234-082-Q1-K1-C2 Seq. ID BLASTX Method g2160146 NCBI GI BLAST score 165 2.0e-11 E value 34 Match length 91 % identity (AC000375) Strong similarity to Arabidopsis NCBI Description gb X91953, F21M12.3, F21M12.1. EST gb_H36326 comes from this gene. [Arabidopsis thaliana] 169306 Seq. No. LIB3234-082-Q1-K1-C3 Seq. ID BLASTX Method g2829918 NCBI GI BLAST score 520 3.0e-53 E value Match length 101 99 % identity (AC002291) similar to "tub" protein gp_U82468_2072162 NCBI Description [Arabidopsis thaliana] Seq. No. 169307 LIB3234-082-Q1-K1-C4 Seq. ID BLASTX Method g1172873 NCBI GI 543 BLAST score 9.0e-56 E value 110 Match length

precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]



```
169308
Seq. No.
                  LIB3234-082-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g4558665
NCBI GI
                  233
BLAST score
                  2.0e-19
E value
                  115
Match length
                  43
% identity
NCBI Description (AC007063) putative white protein [Arabidopsis thaliana]
                  169309
Seq. No.
                  LIB3234-082-Q1-K1-C6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4469119
                  116
BLAST score
                  5.0e-59
E value
                  124
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana BBFa gene
                  169310
Seq. No.
                  LIB3234-082-Q1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2505876
BLAST score
                   219
                  8.0e-18
E value
                   47
Match length
                   83
% identity
NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]
                   169311
Seq. No.
Seq. ID
                   LIB3234-082-Q1-K1-D2
                   BLASTN
Method
                   q3766106
NCBI GI
BLAST score
                   307
                   1.0e-172
E value
                   335
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   169312
Seq. ID
                   LIB3234-082-Q1-K1-D3
                   BLASTX
Method
NCBI GI
                   q1586940
                   267
BLAST score
                   2.0e-23
E value
                   92
Match length
                   54
% identity
NCBI Description Ser/Thr kinase [Lycopersicon esculentum]
                   169313
Seq. No.
                   LIB3234-082-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g1345973
NCBI GI
                   698
BLAST score
```

5.0e-74

E value



```
125
Match length
                  100
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi 471091_dbj BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  169314
Seq. No.
                  LIB3234-082-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g2244797
NCBI GI
                  295
BLAST score
                  1.0e-26
E value
                  105
Match length
                  57
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  169315
Seq. No.
                  LIB3234-082-Q1-K1-D7
Seq. ID
                  BLASTN
Method
                  g3659491
NCBI GI
                  193
BLAST score
                  1.0e-104
E value
                   361
Match length
                  100
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   169316
Seq. No.
Seq. ID
                   LIB3234-082-Q1-K1-D8
                   BLASTX
Method
                   g2511725
NCBI GI
                   643
BLAST score
                   1.0e-67
E value
Match length
                   124
                   99
% identity
                  (AF021937) catalase 1 [Arabidopsis thaliana]
NCBI Description
                   169317
Seq. No.
                   LIB3234-082-Q1-K1-E1
Seq. ID
Method
                   BLASTN
                   g4159703
NCBI GI
                   348
BLAST score
                   0.0e+00
E value
Match length
                   372
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
```

K5F14, complete sequence

169318 Seq. No.

LIB3234-082-Q1-K1-E11 Seq. ID

BLASTX Method

NCBI GI

BLAST score



```
g1526424
NCBI GI
                  376
BLAST score
                  3.0e-36
E value
                  75
Match length
                  100
% identity
                  (D64140) LEA protein in group 3 [Arabidopsis thaliana]
NCBI Description
                  169319
Seq. No.
                  LIB3234-082-Q1-K1-E12
Seq. ID
                  {\tt BLASTX}
Method
                  g1946331
NCBI GI
                   613
BLAST score
                   5.0e-64
E value
                   124
Match length
                   98
% identity
                   (U69155) prohibitin [Arabidopsis thaliana] >gi 4097692
NCBI Description
                   (U66593) prohibitin 3 [Arabidopsis thaliana]
                   169320
Seq. No.
                   LIB3234-082-Q1-K1-E2
Seq. ID
Method
                   BLASTX
                   g4490733
NCBI GI
                   334
BLAST score
                   3.0e - 31
E value
                   69
Match length
                   100
% identity
                   (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
                   169321
Seq. No.
                   LIB3234-082-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   q544242
NCBI GI
                   350
BLAST score
                   3.0e - 33
E value
                   111
Match length
                   69
% identity
                   ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                   >gi_485498_pir__S33533 heat shock protein 90 homolog
                   precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                   homologue [Hordeum vulgare]
                   169322
Seq. No.
                   LIB3234-082-Q1-K1-E9
Seq. ID
Method
                   BLASTN
                   q4006885
NCBI GI
BLAST score
                   315
                   1.0e-177
E value
                   355
Match length
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
Seq. No.
                   169323
                   LIB3234-082-Q1-K1-F10
Seq. ID
                   BLASTX
Method
```

22994

g1946331



E value 2.0e-25

Match length 87
% identity 67

NCBI Description (U69155) prohibitin [Arabidopsis thaliana] >gi_4097692

(U66593) prohibitin 3 [Arabidopsis thaliana]

 Seq. No.
 169324

 Seq. ID
 LIB3234-082-Q1-K1-F12

 Method
 BLASTX

NCBI GI g1709970
BLAST score 447
E value 1.0e-44
Match length 114
% identity 79

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 169325

Seq. ID LIB3234-082-Q1-K1-F2

Method BLASTX
NCBI GI g2129642
BLAST score 568
E value 8.0e-59
Match length 107
% identity 96

NCBI Description major latex protein type 3 - Arabidopsis thaliana

>gi_1107495_emb_CAA63027_ (X91961) major latex protein

type3 [Arabidopsis thaliana]

Seq. No. 169326

Seq. ID LIB3234-082-Q1-K1-F6

Method BLASTN
NCBI GI 94757405
BLAST score 137
E value 5.0e-71
Match length 358
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOJ10, complete sequence

Seq. No. 169327

Seq. ID LIB3234-082-Q1-K1-F7

Method BLASTN
NCBI GI 93402745
BLAST score 225
E value 1.0e-123
Match length 371
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

(ESSAII project)

Seq. No. 169328

Seq. ID LIB3234-082-Q1-K1-F9

Method BLASTX
NCBI GI g4191777
BLAST score 642
E value 2.0e-67
Match length 122

NCBI Description



```
% identity
                  (AC005917) putative casein kinase I [Arabidopsis thaliana]
NCBI Description
                  169329
Seq. No.
Seq. ID
                  LIB3234-082-Q1-K1-G10
                  BLASTN
Method
                  g3985958
NCBI GI
BLAST score
                  67
                  3.0e-29
E value
                  243
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZN1, complete sequence [Arabidopsis thaliana]
                  169330
Seq. No.
                  LIB3234-082-Q1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455338
BLAST score
                  320
                  1.0e-29
E value
                  113
Match length
                  53
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
                  169331
Seq. No.
Seq. ID
                  LIB3234-082-Q1-K1-G12
Method
                  BLASTX
                  q2832620
NCBI GI
BLAST score
                   467
E value
                   6.0e-47
                   121
Match length
                   70
% identity
                  (ALO21711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169332
                   LIB3234-082-Q1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2499872
BLAST score
                   176
E value
                   9.0e-13
Match length
                   83
                   45
% identity
                   TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL
NCBI Description
                   AMINOPEPTIDASE) >gi_2137836_pir__I48855
                   tripeptidyl-peptidase II (EC 3.4.14.10) - mouse
                   >gi 575955 emb CAA57103 (X81323) tripeptidyl-peptidase ii
                   [Mus musculus]
                   169333
Seq. No.
                   LIB3234-082-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g118926
NCBI GI
                   263
BLAST score
                   6.0e - 23
E value
                   102
Match length
                   53
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
```



>gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No. 169334

Seq. ID LIB3234-082-Q1-K1-G6

Method BLASTX
NCBI GI g3128180
BLAST score 488
E value 2.0e-49
Match length 118
% identity 85

NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No. 169335

Seq. ID LIB3234-082-Q1-K1-G7

Method BLASTN
NCBI GI g2656025
BLAST score 71
E value 1.0e-31
Match length 98
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCD7

Seq. No. 169336

Seq. ID LIB3234-082-Q1-K1-G9

Method BLASTX
NCBI GI g2842490
BLAST score 290
E value 4.0e-26
Match length 74
% identity 74

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 169337

Seq. ID LIB3234-082-Q1-K1-H1

Method BLASTX
NCBI GI g1170939
BLAST score 514
E value 2.0e-52
Match length 104
% identity 94

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi_1084408_pir__S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 169338

Seq. ID LIB3234-082-Q1-K1-H8

Method BLASTX NCBI GI g1169601 BLAST score 394



E value 2.0e-38
Match length 93
% identity 85

NCBI Description OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR

>gi_493068 (U09503) chloroplast omega-6 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 169339

Seq. ID LIB3234-083-Q1-K1-A1

Method BLASTX
NCBI GI g2262113
BLAST score 373
E value 6.0e-36
Match length 80
% identity 85

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 169340

Seq. ID LIB3234-083-Q1-K1-A10

Method BLASTX
NCBI GI g1335862
BLAST score 587
E value 5.0e-61
Match length 123
% identity 94

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 169341

Seq. ID LIB3234-083-Q1-K1-A11

Method BLASTX
NCBI GI g4406780
BLAST score 522
E value 2.0e-53
Match length 123
% identity 84

NCBI Description (AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No. 169342

Seq. ID LIB3234-083-Q1-K1-A12

Method BLASTN
NCBI GI g2853071
BLAST score 324
E value 0.0e+00
Match length 328
% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7

(ESSA project)

Seq. No. 169343

Seq. ID LIB3234-083-Q1-K1-A3

Method BLASTN
NCBI GI g4662628
BLAST score 158
E value 1.0e-83
Match length 382
% identity 88

NCBI Description



```
NCBI Description Arabidopsis thaliana chromosome II BAC F27010 genomic
                  sequence, complete sequence
                  169344
Seq. No.
Seq. ID
                  LIB3234-083-Q1-K1-A5
                  BLASTN
Method
NCBI GI
                  q4314374
BLAST score
                   32
                  2.0e-08
E value
                   497
Match length
                   15
% identity
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169345
Seq. ID
                   LIB3234-083-Q1-K1-A6
                   BLASTX
Method
                   g3193293
NCBI GI
BLAST score
                   583
E value
                   2.0e-60
                   122
Match length
                   98
% identity
                   (AF069298) contains a short region of similarity to another
NCBI Description
                   Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                   [Arabidopsis thaliana]
                   169346
Seq. No.
Seq. ID
                   LIB3234-083-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   q404688
                   213
BLAST score
                   4.0e-17
E value
                   57
Match length
                   61
% identity
                   (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
Seq. No.
                   169347
                   LIB3234-083-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   g3355477
NCBI GI
BLAST score
                   395
                   7.0e-39
E value
                   77
Match length
                   59
% identity
                   (AC004218) putative P-glycoprotein, pgpl [Arabidopsis
NCBI Description
                   thaliana]
                   169348
Seq. No.
                   LIB3234-083-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   g4204298
NCBI GI
                   599
BLAST score
                   2.0e-62
E value
                   119
Match length
                   97
% identity
```

22999

[Arabidopsis thaliana]

(AC003027) lcl_prt_seq No definition line found



```
169349
Seq. No.
                  LIB3234-083-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g2088651
NCBI GI
                  233
BLAST score
                  2.0e-19
E value
                  100
Match length
                  52
% identity
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                  169350
Seq. No.
                  LIB3234-083-Q1-K1-B5
Seq. ID
                  BLASTN
Method
                  g2454181
NCBI GI
BLAST score
                   343
                   0.0e + 00
E value
                   377
Match length
% identity
                  Arabidopsis thaliana pyruvate dehydrogenase El alpha
NCBI Description
                   subunit mRNA, nuclear gene encoding plastid protein,
                   complete cds
                   169351
Seq. No.
                   LIB3234-083-Q1-K1-B7
Seq. ID
                   BLASTN
Method
                   g4220636
NCBI GI
                   122
BLAST score
E value
                   3.0e-62
                   174
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFB16, complete sequence [Arabidopsis thaliana]
                   169352
Seq. No.
                   LIB3234-083-Q1-K1-B9
Seq. ID
                   BLASTN
Method
                   g3449327
NCBI GI
BLAST score
                   216
                   1.0e-118
E value
Match length
                   236
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
                   169353
Seq. No.
                   LIB3234-083-Q1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129773
BLAST score
                   512
                   4.0e-52
E value
Match length
                   96
                   100
% identity
                   xyloglucan endotransglycosylase-related protein XTR3 -
NCBI Description
                   Arabidopsis thaliana (fragment) >gi_1244752 (U43485)
```

23000

xyloglucan endotransglycosylase-related protein



[Arabidopsis thaliana]

```
169354
Seq. No.
                  LIB3234-083-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  q4191794
NCBI GI
                  393
BLAST score
                  3.0e - 38
E value
                  71
Match length
                  99
% identity
                  (AC005917) putative zinc finger-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  169355
Seq. No.
Seq. ID
                  LIB3234-083-Q1-K1-C11
                  BLASTX
Method
NCBI GI
                  q2505876
                  201
BLAST score
E value
                  9.0e-16
                  44
Match length
                  82
% identity
                  (Y12776) MYB-related protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169356
                  LIB3234-083-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                   q2583125
NCBI GI
                   424
BLAST score
E value
                   7.0e-42
Match length
                   98
                   81
% identity
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana]
                   169357
Seq. No.
                   LIB3234-083-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g3660471
NCBI GI
BLAST score
                   572
                   3.0e-59
E value
                   125
Match length
                   86
% identity
                  (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   169358
Seq. No.
                   LIB3234-083-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g114193
NCBI GI
                   620
BLAST score
                   7.0e-65
E value
Match length
                   125
                   95
% identity
                  PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR
NCBI Description
                   (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP
                   SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
```

23001

SYNTHASE 1) >gi_170225 (M64261)



3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Nicotiana tabacum] >gi_228697_prf__1808327A deoxyheptulosonate phosphate synthase [Nicotiana tabacum]

Seq. No. 169359 Seq. ID LIB3234-083-Q1-K1-C6 BLASTN Method NCBI GI q4678266 BLAST score 150 3.0e-79E value 150 Match length 74 % identity Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 NCBI Description (ESSA project) 169360 Seq. No. Seq. ID LIB3234-083-Q1-K1-C7 BLASTX Method NCBI GI g2570342 BLAST score 209 1.0e-16 E value Match length 38 100 % identity (U90929) glyoxalase II cytoplasmic isozyme [Arabidopsis NCBI Description thaliana] 169361 Seq. No. Seq. ID LIB3234-083-Q1-K1-C8 Method BLASTX NCBI GI q112681 516 BLAST score 1.0e-52 E value 123 Match length % identity 82 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana] 169362 Seq. No. LIB3234-083-Q1-K1-C9 Seq. ID Method BLASTN g3133272 NCBI GI 153 BLAST score 1.0e-80 E value

Seq. No. 169363

Match length

Seq. ID LIB3234-083-Q1-K1-D1

219

Method BLASTX
NCBI GI g3176690
BLAST score 627
E value 1.0e-65



Match length 126 % identity 99

NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 169364

Seq. ID LIB3234-083-Q1-K1-D11

Method BLASTN
NCBI GI 94757411
BLAST score 270
E value 1.0e-150
Match length 365

% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXC7, complete sequence

Seq. No. 169365

Seq. ID LIB3234-083-Q1-K1-D12

Method BLASTN
NCBI GI g3366536
BLAST score 352
E value 0.0e+00
Match length 360
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T25N20,

complete sequence [Arabidopsis thaliana]

Seq. No. 169366

Seq. ID LIB3234-083-Q1-K1-D7

Method BLASTX
NCBI GI g1352347
BLAST score 453
E value 3.0e-45
Match length 89
% identity 100

NCBI Description ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)

>gi_480620_pir__S37103 translation elongation factor eEF-1

beta-A1 chain - Arabidopsis thaliana (cv. Colombia)

>gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta

Al [Arabidopsis thaliana]

Seq. No. 169367

Seq. ID LIB3234-083-Q1-K1-D8

Method BLASTN
NCBI GI g599626
BLAST score 126
E value 2.0e-64
Match length 259
% identity 34

NCBI Description A.thaliana minisatellite sequence 1, chromosome

Seq. No. 169368

Seq. ID LIB3234-083-Q1-K1-E10

Method BLASTX NCBI GI g1170040 BLAST score 399

Seq. No.

Seq. ID

Method

NCBI GI

169373

BLASTX

g123620

LIB3234-083-Q1-K1-F11



```
E value
                  6.0e-39
Match length
                  98
                  81
% identity
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
NCBI Description
                  >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase
                  precursor [Arabidopsis thaliana] >gi_1944448 dbj_BAA19653
                  (D89620) glutathione reductase precursor [Arabidopsis
                  thaliana] >gi_740576_prf__2005376A glutathione reductase
                   [Arabidopsis thaliana]
                  169369
Seq. No.
                  LIB3234-083-Q1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4662609
BLAST score
                  368
                  0.0e + 00
E value
Match length
                  372
                  100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
NCBI Description
                  complete sequence
                  169370
Seq. No.
                  LIB3234-083-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                   g3869253
NCBI GI
BLAST score
                   636
                   1.0e-66
E value
                   126
Match length
% identity
                   99
                   (U39288) ferredoxin-dependent glutamate synthase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   169371
Seq. No.
                   LIB3234-083-Q1-K1-E7
Seq. ID
                   BLASTN
Method
                   g2435510
NCBI GI
                   350
BLAST score
                   0.0e+00
E value
Match length
                   370
% identity
                   99
                  Arabidopsis thaliana BAC TM017A05
NCBI Description
                   169372
Seq. No.
                   LIB3234-083-Q1-K1-F10
Seq. ID
Method
                   BLASTN
                   g2264306
NCBI GI
                   56
BLAST score
                   1.0e-22
E value
Match length
                   60
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBK5, complete sequence [Arabidopsis thaliana]
```



```
BLAST score
                  632
                  3.0e-66
E value
Match length
                  126
% identity
                  99
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir_ S14950
NCBI Description
                  heat shock cognate protein 70 - tomato
                  >qi 19258 emb CAA37971 (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
                  169374
Seq. No.
                  LIB3234-083-Q1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g421969
                  144
BLAST score
                  2.0e-09
E value
Match length
                   31
% identity
                   90
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
NCBI Description
                   - coffee chloroplast (fragment) >gi_1322147_emb_CAA49827_
                   (X70364) rbcL [Coffea arabica]
                   169375
Seq. No.
                  LIB3234-083-Q1-K1-F3
Seq. ID
Method
                  BLASTN
                   g3702731
NCBI GI
BLAST score
                   343
                   0.0e + 00
E value
                   367
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
                   169376
Seq. No.
Seq. ID
                   LIB3234-083-Q1-K1-F4
                   BLASTX
Method
                   g4581166
NCBI GI
                   302
BLAST score
                   1.0e-27
E value
Match length
                   76
% identity
                   80
                   (AC006220) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169377
Seq. No.
                   LIB3234-083-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2104535
                   378
BLAST score
                   2.0e-36
E value
                   118
Match length
                   64
% identity
                  (AF001308) T10M13.13 [Arabidopsis thaliana]
```

NCBI Description

Seq. No.

LIB3234-083-Q1-K1-F6 Seq. ID

169378

BLASTX Method NCBI GI g3184281 454 BLAST score

NCBI Description



```
2.0e-45
E value
Match length
                  100
                   89
% identity
                  (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  169379
Seq. No.
                  LIB3234-083-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                   q4538912
NCBI GI
                   482
BLAST score
                   9.0e-49
E value
                   110
Match length
% identity
                   87
                  (ALO49482) putative protein [Arabidopsis thaliana]
NCBI Description
                   169380
Seq. No.
                   LIB3234-083-Q1-K1-G11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3461810
BLAST score
                   182
                   6.0e-98
E value
                   294
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T17M13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169381
Seq. No.
                   LIB3234-083-Q1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   111
                   2.0e-55
E value
                   230
Match length
                   95
% identity
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                   sequence, complete sequence
                   169382
Seq. No.
                   LIB3234-083-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   q4586116
NCBI GI
                   456
BLAST score
                   1.0e-45
E value
Match length
                   121
                   72
% identity
                   (AL049638) putative C-4 sterol methyl oxidase [Arabidopsis
NCBI Description
                   thaliana]
                   169383
Seq. No.
                   LIB3234-083-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   q4580389
NCBI GI
BLAST score
                   375
                   3.0e-36
E value
                   89
Match length
                   82
% identity
```

(AC007171) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  169384
                  LIB3234-083-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135858
                  483
BLAST score
                  8.0e-49
E value
Match length
                  115
% identity
                  82
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >gi 99760 pir S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi 16182_emb_CAA45114_ (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                  thaliana] >gi 166623 (M84343) tonoplast intrinsic protein
                  [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast
                  intrinsic protein alpha [Arabidopsis thaliana]
                  169385
Seq. No.
Seq. ID
                  LIB3234-083-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q114330
                  335
BLAST score
                  8.0e-32
E value
                  79
Match length
                  78
% identity
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                  >gi 67972 pir PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                  type 1, plasma membrane - Arabidopsis thaliana >gi 166746
                   (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                  thaliana]
                  169386
Seq. No.
Seq. ID
                  LIB3234-083-Q1-K1-H12
                  BLASTX
Method
NCBI GI
                  g1361982
BLAST score
                  465
                  7.0e-47
E value
                  97
Match length
                   96
% identity
NCBI Description
                   4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
                  thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase
                   [Arabidopsis thaliana]
                  169387
Seq. No.
                  LIB3234-083-Q1-K1-H5
Seq. ID
Method
                  BLASTN
                   g2264312
NCBI GI
                   275
BLAST score
                   1.0e-153
E value
                   370
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOK16, complete sequence [Arabidopsis thaliana]
```

Seq. No. 169388

Seq. ID LIB3234-083-Q1-K1-H6

Method BLASTN



```
g2702261
NCBI GI
BLAST score
                  3.0e-26
E value
Match length
                  256
                  81
% identity
                  Arabidopsis thaliana chromosome II BAC T21L14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169389
Seq. No.
                  LIB3234-083-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  g4585997
NCBI GI
BLAST score
                   208
                   1.0e-24
E value
                   117
Match length
                   47
% identity
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169390
Seq. No.
                  LIB3234-083-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4006934
BLAST score
                   442
                   5.0e-44
E value
                   103
Match length
                   79
% identity
NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]
                   169391
Seq. No.
                   LIB3234-083-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   q4678299
NCBI GI
BLAST score
                   581
                   3.0e-60
E value
Match length
                   114
                   99
% identity
                   (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   169392
                   LIB3234-084-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   q3859116
NCBI GI
                   331
BLAST score
                   6.0e-31
E value
                   82
Match length
                   73
% identity
                  (AF031609) unknown [Oryza sativa]
NCBI Description
                   169393
Seq. No.
                   LIB3234-084-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g1550740
NCBI GI
                   481
BLAST score
                   1.0e-48
E value
                   92
Match length
```

100

% identity

BLAST score

E value

163 1.0e-86



```
NCBI Description
                  (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
                  169394
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g114330
BLAST score
                  363
E value
                  1.0e-34
                  93
Match length
                  74
% identity
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                  >gi 67972 pir PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                  type 1, plasma membrane - Arabidopsis thaliana >gi 166746
                  (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                  thaliana]
                  169395
Seq. No.
                  LIB3234-084-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  q134853
NCBI GI
                  176
BLAST score
                  8.0e-13
E value
Match length
                  96
                  15
% identity
                  TRANSCRIPTION INITIATION PROTEIN SPT5
NCBI Description
                  >gi 101643 pir A40253 acidic nuclear protein SPT5 - yeast
                  (Saccharomyces cerevisiae) >gi 172680 (M62882) SPT5 protein
                   [Saccharomyces cerevisiae] >gi 854480 emb CAA89942
                   (Z49810) Spt5p [Saccharomyces cerevisiae]
Seq. No.
                  169396
Seq. ID
                  LIB3234-084-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3925363
BLAST score
                  220
E value
                  6.0e-18
Match length
                  103
% identity
                  45
NCBI Description
                  (AF067961) homeodomain protein [Malus domestica]
                  169397
Seq. No.
                  LIB3234-084-Q1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264316
BLAST score
                  378
                  0.0e+00
E value
                  378
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169398
                  LIB3234-084-Q1-K1-B1
Seq. ID
                  BLASTN
Method
                  q3659491
NCBI GI
```



Match length 210 % identity 95 NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana] 169399 Seq. No. LIB3234-084-Q1-K1-B10 Seq. ID Method BLASTX NCBI GI q3641836 BLAST score 534 9.0e-55 E value 124 Match length % identity 80 (AL023094) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] Seq. No. 169400 LIB3234-084-Q1-K1-B12 Seq. ID Method BLASTX NCBI GI q1922242 BLAST score 339 4.0e-32 E value Match length 68 % identity 100 (Y10084) hypothetical protein [Arabidopsis thaliana] NCBI Description 169401 Seq. No. LIB3234-084-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI q4584548 BLAST score 576 E value 1.0e-59 Match length 124 % identity 90 (AL049608) putative protein [Arabidopsis thaliana] NCBI Description 169402 Seq. No. LIB3234-084-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI g3080427 BLAST score 481 1.0e-48 E value Match length 118 75 % identity (AL022604) putative protein [Arabidopsis thaliana] NCBI Description 169403 Seq. No.

LIB3234-084-Q1-K1-B9 Seq. ID

Method BLASTX NCBI GI g633890 BLAST score 408 E value 5.0e-40125 Match length 66 % identity

(S72926) glucose and ribitol dehydrogenase homolog [Hordeum NCBI Description

vulgare]



```
169404
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-C1
                  BLASTX
Method
                  g1628583
NCBI GI
                   365
BLAST score
                   5.0e-35
E value
                   111
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   169405
Seq. No.
Seq. ID
                   LIB3234-084-Q1-K1-C10
                   BLASTN
Method
                   g2245073
NCBI GI
                   370
BLAST score
                   0.0e + 00
E value
                   378
Match length
                   100
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   169406
Seq., No.
Seq. ID
                   LIB3234-084-Q1-K1-C12
                   BLASTX
Method
                   g4581166
NCBI GI
BLAST score
                   308
                   3.0e-28
E value
Match length
                   76
                   82
% identity
                   (AC006220) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169407
Seq. No.
                   LIB3234-084-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g542125
BLAST score
                   83
                   9.0e-40
E value
Match length
                   94
                   91
% identity
                   translation elongation factor eEF-1 alpha chain - barley
NCBI Description
                   >gi 396134 emb CAA80666 (Z23130) protein synthesis
                   elongation factor-1 alpha [Hordeum vulgare]
Seq. No.
                   169408
                   LIB3234-084-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g4586249
NCBI GI
BLAST score
                   368
                   3.0e - 35
E value
Match length
                   118
% identity
                   58
                   (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No.



```
LIB3234-084-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  302
                  1.0e-27
E value
                  64
Match length
                  98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  169410
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-C6
                  BLASTX
Method
NCBI GI
                  g1628583
                  305
BLAST score
                  5.0e-28
E value
                  64
Match length
                  100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   169411
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-C8
                  {\tt BLASTN}
Method
                   g3985933
NCBI GI
                   302
BLAST score
                   1.0e-169
E value
Match length
                   366
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9E15, complete sequence [Arabidopsis thaliana]
                   169412
Seq. No.
                   LIB3234-084-Q1-K1-C9
Seq. ID
Method
                   BLASTN
                   g3241925
NCBI GI
                   50
BLAST score
E value
                   5.0e-19
                   246
Match length
% identity
                   87
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MOK9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169413
                   LIB3234-084-Q1-K1-D1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3600029
BLAST score
                   375
```

E value 0.0e + 00379 Match length % identity 100

Arabidopsis thaliana BAC T12H20 NCBI Description

Seq. No. 169414

LIB3234-084-Q1-K1-D10 Seq. ID

NCBI GI



```
BLASTX
Method
                  g2494121
NCBI GI
                  477
BLAST score
                  4.0e-48
E value
                  93
Match length
                  100
% identity
                  (AC002376) Strong similarity to Triticum ABA induced
NCBI Description
                  membrane protein (gb U80037). EST gb_Z27032 comes from this
                  gene. [Arabidopsis thaliana]
                  169415
Seq. No.
                  LIB3234-084-Q1-K1-D11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2104546
                  208
BLAST score
                  1.0e-113
E value
                   280
Match length
                   95
% identity
                  Arabidopsis thaliana chromosome IV cosmid AGAA, complete
NCBI Description
                  sequence
                   169416
Seq. No.
                  LIB3234-084-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                   g3850914
NCBI GI
                   597
BLAST score
E value
                   4.0e-62
                   122
Match length
                   98
% identity
NCBI Description (AF060397) ATP synthase beta subunit [Stirlingia latifolia]
                   169417
Seq. No.
                   LIB3234-084-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2494610
                   248
BLAST score
                   2.0e-37
E value
                   92
Match length
                   95
% identity
                  CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR
NCBI Description
                   >gi 1079732 (U39877) cpFtsZ [Arabidopsis thaliana]
Seq. No.
                   169418
                   LIB3234-084-Q1-K1-D6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2815519
BLAST score
                   378
                   0.0e + 00
E value
Match length
                   378
                   100
% identity
                   Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169419
Seq. No.
                   LIB3234-084-Q1-K1-D7
Seq. ID
Method
                   BLASTN
```

g3413696

NCBI GI

BLAST score



```
BLAST score
                  279
E value
                  1.0e-156
                  370
Match length
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T19L18 genomic
NCBI Description
                · sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169420
                  LIB3234-084-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g3334244
NCBI GI
                   507
BLAST score
E value
                   1.0e-51
                   114
Match length
                   84
% identity
                  LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
NCBI Description
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                   MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                   >gi 2113825 emb CAA73691 (Y13239) Glyoxalase I [Brassica
                   juncea]
                   169421
Seq. No.
                  LIB3234-084-Q1-K1-E1
Seq. ID
Method
                   BLASTX
                   g3122626
NCBI GI
BLAST score
                   183
                   1.0e-13
E value
                                                        " national.
Match length
                   86
% identity
                   49
                  26S PROTEASE REGULATORY SUBUNIT 8 > qi 2245467 (U97538) DUG
NCBI Description
                   [Drosophila melanogaster]
                   169422
Seq. No.
                   LIB3234-084-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g4454013
NCBI GI
                   570
BLAST score
                   5.0e-59
E value
Match length
                   111
                   100
% identity
                  (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
                   169423
Seq. No.
                   LIB3234-084-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   g2618686
NCBI GI
BLAST score
                   175
                   1.0e-12
E value
Match length
                   76
                   41
% identity
                  (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169424
Seq. No.
                   LIB3234-084-Q1-K1-E2
Seq. ID
Method
                   BLASTX
```

23014

g4314396



```
1.0e-33
E value
Match length
                  103
                  72
% identity
                   (AC006232) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  169425
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-E3
Method
                  BLASTX
                  q1769905
NCBI GI
                   370
BLAST score
                   2.0e-35
E value
Match length
                   112
                   65
% identity
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
                   169426
Seq. No.
Seq. ID
                   LIB3234-084-Q1-K1-E5
Method
                   BLASTX
                   g1592675
NCBI GI
                   268
BLAST score
                   1.0e-23
E value
                   99
Match length
                   58
% identity
                  (X91919) LEA76 homologue typel [Arabidopsis thaliana]
NCBI Description
                   169427
Seq. No.
Seq. ID
                   LIB3234-084-Q1-K1-E6
Method
                   BLASTX
                   g4584110
NCBI GI
BLAST score
                   269
                   8.0e-24
E value
Match length
                   99
% identity
                   54
                  (AJ133639) SAH7 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169428
Seq. ID
                   LIB3234-084-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q4454013
BLAST score
                   564
                   3.0e-58
E value
                   110
Match length
% identity
                   100
                  (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
                   169429
Seq. No.
                   LIB3234-084-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g3377835
NCBI GI
BLAST score
                   398
                   8.0e-39
E value
                   112
Match length
                   71
% identity
                   (AF075598) contains similarity to Arabidopsis thaliana
NCBI Description
```

downy mildew resistance protein RPP5 (GB:U97106)



[Arabidopsis thaliana]

```
169430
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-E9
Method
                  BLASTN
                  g4079614
NCBI GI
                  72
BLAST score
E value
                  3.0e - 32
                  204
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169431
Seq. No.
                  LIB3234-084-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076414
                   147
BLAST score
E value
                   2.0e-09
                   77
Match length
                   38
% identity
                  subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi 757534 emb CAA59963 (X85974)
                   subtilisin-like protease [Arabidopsis thaliana]
                   169432
Seq. No.
                   LIB3234-084-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1352463
BLAST score
                   465
                   1.0e-46
E value
Match length
                   105
% identity
                   87
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi 1161312
NCBI Description
                   (U04876) myo-inositol-1-phosphate synthase [Arabidopsis
                   thaliana]
                   169433
Seq. No.
Seq. ID
                   LIB3234-084-Q1-K1-F6
Method
                   BLASTN
                   g4199934
NCBI GI
                   258
BLAST score
                   1.0e-143
E value
Match length
                   356
                   92
% identity
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169434
Seq. No.
                   LIB3234-084-Q1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3747111
BLAST score
                   455
                   2.0e-45
E value
                   97
Match length
% identity
                   51
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
```



```
Seq. No.
                   169435
                  LIB3234-084-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1363526
BLAST score
                   58
                   4.0e - 34
E value
Match length
                   74
                   100
% identity
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
NCBI Description
                   cytochrome b6 - maize chloroplast >qi 902251 emb CAA60315
                   (X86563) cytochrome B6 [Zea mays]
                   169436
Seq. No.
Seq. ID -
                   LIB3234-084-Q1-K1-F9
                   BLASTN
Method
NCBI GI
                   q4835223
BLAST score
                   187
E value
                   1.0e-101
                   309
Match length
                   88
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3
NCBI Description
                   (ESSA project)
Seq. No.
                   169437
Seq. ID
                   LIB3234-084-Q1-K1-G1
Method
                   BLASTN
NCBI GI
                   g4589425
BLAST score
                   195
E value
                   1.0e-106
Match length
                   228
                   96
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBA10, complete sequence
                   169438
Seq. No.
                   LIB3234-084-Q1-K1-G10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3985958
BLAST score
                   67
                   3.0e-29
E value
Match length
                   233
                   88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169439
Seq. ID
                   LIB3234-084-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1109699
BLAST score
                   505
E value
                   3.0e-51
Match length
                   96
% identity
                   100
                   (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

BLAST score

E value

608 2.0e-63



LIB3234-084-Q1-K1-G4 Seq. ID BLASTX Method NCBI GI g549977 235 BLAST score 1.0e-19 E value 123 Match length 50 % identity NCBI Description (U12859) cDNA-5-encoded protein [Arabidopsis thaliana] 169441 Seq. No. LIB3234-084-Q1-K1-G5 Seq. ID BLASTX Method g4510383 NCBI GI BLAST score 390 E value 7.0e-38 110 Match length 75 % identity NCBI Description (AC007017) unknown protein [Arabidopsis thaliana] Seq. No. 169442 Seq. ID LIB3234-084-Q1-K1-G7 BLASTN Method NCBI GI q3985932 BLAST score 251 E value 1.0e-139 251 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K22J17, complete sequence [Arabidopsis thaliana] 169443 Seq. No. LIB3234-084-Q1-K1-G8 Seq. ID BLASTX Method NCBI GI q3413705 BLAST score 526 7.0e-54E value Match length 118 88 % identity (AC004747) putative glycine dehydrogenase [Arabidopsis NCBI Description thaliana] 169444 Seq. No. LIB3234-084-Q1-K1-H11 Seq. ID Method BLASTX NCBI GI q3758833 BLAST score 246 5.0e-21 E value 96 Match length 51 % identity NCBI Description (Y18225) MtN6 [Medicago truncatula] 169445 Seq. No. LIB3234-084-Q1-K1-H12 Seq. ID Method BLASTX g2494113 NCBI GI



```
Match length
% identity
                   (AC002376) Strong similarity to Musa pectate lyase
NCBI Description
                   (gb X92943). ESTs gb_AA042458, gb_ATTS4502, gb N38552 come
                  from this gene. [Arabidopsis thaliana]
                  169446
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g166708
                  490
BLAST score
                  1.0e-49
E value
                   97
Match length
                  100
% identity
                   (M64118) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                  169447
Seq. No.
Seq. ID
                  LIB3234-084-Q1-K1-H5
Method
                  BLASTX
                   q2392769
NCBI GI
                   180
BLAST score
                   2.0e-13
E value
                   73
Match length
                   47
% identity
                   (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
                   thaliana]
                   169448
Seq. No.
Seq. ID
                   LIB3234-084-Q1-K1-H7
Method
                   BLASTN
                   q4220641
NCBI GI
                   327
BLAST score
                   0.0e+00
E value
Match length
                   375
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169449
Seq. ID
                   LIB3234-085-Q1-K1-A1
Method
                   BLASTN
                   g4220644
NCBI GI
BLAST score
                   67
E value
                   3.0e-29
                   137
Match length
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MXL8, complete sequence [Arabidopsis thaliana]
                   169450
Seq. No.
                   LIB3234-085-Q1-K1-A10
Seq. ID
                   BLASTN
```

Method BLASTN
NCBI GI g343239
BLAST score 353
E value 0.0e+00
Match length 369



```
% identity
NCBI Description Mustard (S.alba) chloroplast 16S rRNA, 5' end, and Val-tRNA
                  169451
Seq. No.
                  LIB3234-085-Q1-K1-A11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4432829
BLAST score
                   361
                  0.0e + 00
E value
                   369
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169452
Seq. No.
                  LIB3234-085-Q1-K1-A12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2264311
BLAST score
                   33
                   5.0e-09
E value
                   37
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MLN1, complete sequence [Arabidopsis thaliana]
                   169453
Seq. No.
                   LIB3234-085-Q1-K1-A2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3449313
BLAST score
                   58
                   6.0e-24
E value
Match length
                   82
                   93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21P3, complete sequence [Arabidopsis thaliana]
                   169454
Seq. No.
                   LIB3234-085-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g2160146
NCBI GI
                   475
BLAST score
                   8.0e-48
E value
                   111
Match length
                   87
% identity
                   (AC000375) Strong similarity to Arabidopsis
NCBI Description
                   gb_X91953,F21M12.3,F21M12.1. EST gb_H36326 comes from this
                   gene. [Arabidopsis thaliana]
                   169455
Seq. No.
                   LIB3234-085-Q1-K1-A4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2281648
BLAST score
                   134
                   3.0e-69
E value
                   138
Match length
% identity
                   Arabidopsis thaliana AP2 domain containing protein RAP2.12
NCBI Description
```

Method



mRNA, partial cds

```
Seq. No.
                  169456
Seq. ID
                  LIB3234-085-Q1-K1-A5
                  BLASTX
Method
NCBI GI
                  g1001311
                  155
BLAST score
                  2.0e-10
E value
                  81
Match length
                  48
% identity
                  (D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
                  169457
Seq. No.
Seq. ID
                  LIB3234-085-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  g3047100
                  306
BLAST score
                   1.0e-172
E value
                   354
Match length
                   95
% identity
NCBI Description Arabidopsis thaliana BAC F6N23
                   169458
Seq. No.
                  LIB3234-085-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                   g2160187
NCBI GI
                   303
BLAST score
E value
                   8.0e-28
                   105
Match length
                   54
% identity
                  (AC000132) Similar to Nicotiana tumor-related protein
NCBI Description
                   (gb_26453). [Arabidopsis thaliana]
                   169459
Seq. No.
Seq. ID
                   LIB3234-085-Q1-K1-A8
Method
                   BLASTX
                   q4580471
NCBI GI
BLAST score
                   178
                   5.0e-13
E value
Match length
                   93
                   38
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169460
                   LIB3234-085-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   g4160573
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
Match length
                   112
                   33
% identity
                  (AL035226) guanine nucleotide binding protein beta
NCBI Description
                   subunit-like [Schizosaccharomyces pombe]
                   169461
Seq. No.
                   LIB3234-085-Q1-K1-B1
Seq. ID
```

23021

BLASTX



NCBI GI g2447107 BLAST score 216 2.0e-17 E value Match length 117 % identity 36 (U42580) A638R [Paramecium bursaria Chlorella virus 1] NCBI Description 169462 Seq. No. LIB3234-085-Q1-K1-B10 Seq. ID BLASTX Method q1176529 NCBI GI 252 BLAST score E value 1.0e-21 117 Match length 43 % identity HYPOTHETICAL 100.9 KD PROTEIN C34E10.3 IN CHROMOSOME III NCBI Description >gi_500726 (U10402) C34E10.3 gene product [Caenorhabditis elegans] 169463 Seq. No. LIB3234-085-Q1-K1-B11 Seq. ID

Method BLASTN
NCBI GI g2264321
BLAST score 206
E value 1.0e-112
Match length 437
% identity 55

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

 Seq. No.
 169464

 Seq. ID
 LIB3234-085-Q1-K1-B2

 Method
 BLASTX

 NCBI GI
 g322596

 BLAST score
 649

 E value
 3.0e-68

E value 3.0e-6
Match length 126
% identity 100

NCBI Description serine/threonine protein kinase (EC 2.7.-.-) AK21 -

Arabidopsis thaliana >gi_166600 (M93023) SNF1-related

protein kinase [Arabidopsis thaliana]

>gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase

[Arabidopsis thaliana]

Seq. No. 169465

Seq. ID LIB3234-085-Q1-K1-B3

Method BLASTN
NCBI GI g2864607
BLAST score 224
E value 1.0e-123
Match length 318
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 169466

Seq. ID LIB3234-085-Q1-K1-B4

Seq. ID

Method



```
BLASTX
Method
                  g2832620
NCBI GI
BLAST score
                  400
                  5.0e-39
E value
                  110
Match length
                  69
% identity
                 (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  169467
Seq. No.
                  LIB3234-085-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g133960
NCBI GI
BLAST score
                  408
                  4.0e-40
E value
                  94
Match length
                  86
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi 70876 pir R3NT4
NCBI Description
                  ribosomal protein S4 - common tobacco chloroplast
                  >gi 11834 emb CAA77354 (Z00044) ribosomal protein S4
                   [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal
                  protein S4 [Nicotiana tabacum]
                  169468
Seq. No.
                  LIB3234-085-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4325354
                  619
BLAST score
                  1.0e-64
E value
                  123
Match length
                   88
% identity
                  (AF128395) contains similarity to retrovirus-related
NCBI Description
                  polyproteins and to CCHC zinc finger protein (Pfam:
                   PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
Seq. No.
                   169469
                   LIB3234-085-Q1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1592677
BLAST score
                   271
                   6.0e-24
E value
Match length
                   126
% identity
                   48
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169470
                   LIB3234-085-Q1-K1-C1
Seq. ID
Method
                   BLASTN
                   g2058295
NCBI GI
BLAST score
                   186
                   1.0e-100
E value
Match length
                   202
                   98
% identity
NCBI Description A.thaliana chloroplast ndhG gene
                   169471
Seq. No.
```

23023

LIB3234-085-Q1-K1-C10

BLASTX



NCBI GI g2809253 BLAST score 469 E value 4.0e-47 Match length 89 % identity 100

NCBI Description (AC002560) F21B7.22 [Arabidopsis thaliana]

Seq. No. 169472

Seq. ID LIB3234-085-Q1-K1-C11

Method BLASTX
NCBI GI g2444176
BLAST score 443
E value 4.0e-44
Match length 123
% identity 71

NCBI Description (U94782) unconventional myosin [Helianthus annuus]

Seq. No. 169473

Seq. ID LIB3234-085-Q1-K1-C12

Method BLASTN
NCBI GI g4678371
BLAST score 334
E value 0.0e+00
Match length 372
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15

(ESSA project)

Seq. No. 169474

Seq. ID LIB3234-085-Q1-K1-C2

Method BLASTX
NCBI GI g2494112
BLAST score 634
E value 2.0e-66
Match length 125
% identity 94

NCBI Description (AC002376) Match to Arabidopsis ATHKCP (gb_L40948). ESTs

gb_ATTS0764, gb_R90646, gb_AA389809, gb_ATTS2615 come from this gene. [Arabidopsis thaliana] >gi_3126868 (AF061570)

potassium channel beta subunit homolog [Arabidopsis

thaliana]

Seq. No. 169475

Seq. ID LIB3234-085-Q1-K1-C3

Method BLASTX
NCBI GI g1169598
BLAST score 338
E value 9.0e-32
Match length 75
% identity 84

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No. 169476

Seq. ID LIB3234-085-Q1-K1-C4

Method BLASTX



```
NCBI GI
                  g1592679
                  287
BLAST score
                  8.0e-26
E value
                  107
Match length
                  59
% identity
                  (X91915) LEA D113 homologue type1 [Arabidopsis thaliana]
NCBI Description
                  169477
Seq. No.
                  LIB3234-085-Q1-K1-C5
Seq. ID
Method
                  BLASTN
                  g4512656
NCBI GI
BLAST score
                  108
                  1.0e-53
E value
Match length
                  287
                  81
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
                  169478
Seq. No.
                  LIB3234-085-Q1-K1-C6
Seq. ID
                  BLASTN
Method
                  g2564048
NCBI GI
                  91
BLAST score
                  1.0e-43
E value
                  234
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKD15, complete sequence [Arabidopsis thaliana]
                  169479
Seq. No.
                  LIB3234-085-Q1-K1-D11
Seq. ID
Method
                  BLASTN
                  g2398520
NCBI GI
BLAST score
                  346
                  0.0e+00
E value
                  374
Match length
                  98
% identity
                  Arabidopsis thaliana mRNA for Hap2a transcription factor
NCBI Description
                  169480
Seq. No.
                  LIB3234-085-Q1-K1-D2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3859840
BLAST score
                  364
E value
                  0.0e+00
Match length
                  376
                   99
% identity
                  Plastid transformation vector pGS31A 16S ribosomal RNA
NCBI Description
                   gene, partial sequence; aminoglycoside 3'-adenyltransferase
                   (aadA) gene, complete cds
```

Seq. No. 169481

Seq. ID LIB3234-085-Q1-K1-D3

Method BLASTX NCBI GI g1246019 BLAST score 600 E value 2.0e-62



Match length 115 % identity 100

NCBI Description (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg

erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]

Seq. No. 169482

Seq. ID LIB3234-085-Q1-K1-D4

Method BLASTX
NCBI GI g4206208
BLAST score 282
E value 3.0e-25
Match length 92
% identity 68

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

>gi_4263041_gb_AAD15310_ (AC005142) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 169483

Seq. ID LIB3234-085-Q1-K1-D5

Method BLASTX
NCBI GI g3915961
BLAST score 608
E value 2.0e-63
Match length 126
% identity 91

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)

>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi 2924285 emb_CAA77438_ (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 169484

Seq. ID LIB3234-085-Q1-K1-D6

Method BLASTN
NCBI GI 94220641
BLAST score 362
E value 0.0e+00
Match length 383
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUL3, complete sequence [Arabidopsis thaliana]

Seq. No. 169485

Seq. ID LIB3234-085-Q1-K1-D7

Method BLASTX
NCBI GI g112740
BLAST score 225
E value 1.0e-18
Match length 106
% identity 51

NCBI Description NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)

>gi_81691_pir__A25997 napin precursor (napA) - rape

>gi $^-$ 16715 $^-$ 3 (J $^-$ 02586) prepronapin [Brassica napus] >gi $^-$ 167155

(J02798) napin [Brassica napus]

Seq. No. 169486

Seq. ID LIB3234-085-Q1-K1-D8

Method BLASTX



```
NCBI GI
                  g1171577
BLAST score
                  191
                  1.0e-14
E value
Match length
                  115
% identity
                  33
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
Seq. No.
                  169487
                  LIB3234-085-Q1-K1-D9
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4115352
                  178
BLAST score
                  2.0e-95
E value
                  318
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T15J14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169488
                  LIB3234-085-Q1-K1-E1
Seq. ID
Method
                  BLASTN
                  q2924653
NCBI GI
                  166
BLAST score
E value
                  2.0e-88
                  335
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169489
                  LIB3234-085-Q1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4335761
BLAST score
                  620
E value
                  7.0e-65
Match length
                  119
% identity
                  97
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169490
Seq. ID
                  LIB3234-085-Q1-K1-E2
Method
                  BLASTN
                  q4218109
NCBI GI
BLAST score
                  249
E value
                  1.0e-138
Match length
                  356
                  97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16
                   (ESSAII project)
                  169491
Seq. No.
                  LIB3234-085-Q1-K1-E7
Seq. ID
```

Method BLASTX
NCBI GI g2827546
BLAST score 397
E value 1.0e-38
Match length 105



```
% identity
NCBI Description
                   (AL021635) cytochrome P450 like protein [Arabidopsis
                  thaliana]
                  169492
Seq. No.
                  LIB3234-085-Q1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3962377
BLAST score
                  440
                  8.0e-44
E value
                  87
Match length
                  98
% identity
                  (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
NCBI Description
                  169493
Seq. No.
Seq. ID
                  LIB3234-085-Q1-K1-F10
Method
                  BLASTX
                  g3962377
NCBI GI
BLAST score
                  512
E value
                  3.0e-52
                  96
Match length
                  100
% identity
                  (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169494
Seq. ID
                  LIB3234-085-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g544122
BLAST score
                   648
E value
                   4.0e-68
Match length
                  126
                   98
% identity
NCBI Description APOCYTOCHROME F PRECURSOR >gi 629599 pir S45661
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  cytochrome f precursor - turnip chloroplast
                   >gi 441282_emb_CAA54307_ (X77011) cytochrome f [Brassica
                   rapa]
Seq. No.
                   169495
Seq. ID
                   LIB3234-085-Q1-K1-F12
Method
                   BLASTN
NCBI GI
                   q4455168
BLAST score
                   372
                   0.0e+00
E value
Match length
                   372
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                   (ESSAII project)
Seq. No.
                   169496
                   LIB3234-085-Q1-K1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1931636
BLAST score
                   149
E value
                   1.0e-78
Match length
                   153
```

99

% identity



```
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
                  169497
Seq. No.
                  LIB3234-085-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3785976
BLAST score
                  49
E value
                  2.0e-20
                  92
Match length
                  68
% identity
                  (AC005560) Sec12p-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169498
                  LIB3234-085-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1771160
BLAST score
                  445
E value
                  3.0e-44
Match length
                  127
                  68
% identity
NCBI Description
                  (X98929) SBT1 [Lycopersicon esculentum]
                  >gi 3687305 emb CAA06999 (AJ006378) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                  169499
Seq. ID
                  LIB3234-085-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1064887
BLAST score
                  166
E value
                  1.0e-11
Match length
                  65
% identity
                  48
                  (X92955) pollen coat protein [Brassica oleracea]
NCBI Description
                  169500
Seq. No.
                  LIB3234-085-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g2661179
NCBI GI
BLAST score
                  569
                  7.0e-59
E value
                  118
Match length
                  97
% identity
                  (U80984) AtZW10 [Arabidopsis thaliana]
NCBI Description
                  169501
Seq. No.
                  LIB3234-085-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130052
                  578
BLAST score
E value
                   6.0e-60
                  125
Match length
                   82
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                   >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase
                   [Hordeum vulgare]
```

Seq. No. 169502



```
LIB3234-085-Q1-K1-G2
 Seq. ID
 Method
                   BLASTN
                   g3241925
 NCBI GI
 BLAST score
                    226
 E value
                   1.0e-124
                    308
 Match length
                    59
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MOK9, complete sequence [Arabidopsis thaliana]
                   169503
 Seq. No.
                   LIB3234-085-Q1-K1-G4
 Seq. ID
 Method
                   BLASTN
                   g1402874
 NCBI GI
                    190
 BLAST score
                    1.0e-102
 E value
 Match length
                    254
                    100
 % identity
 NCBI Description A.thaliana 81kb genomic sequence
                    169504
 Seq. No.
                   LIB3234-085-Q1-K1-G5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1531762
BLAST score
                    187
 E value
                    5.0e-14
                    51
 Match length
 % identity
                    (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
 NCBI Description
                    thaliana]
                    169505
 Seq. No.
 Seq. ID
                    LIB3234-085-Q1-K1-G7
 Method
                    BLASTX
 NCBI GI
                    g2914707
 BLAST score
                    163
                    1.0e-11
 E value
 Match length
                    71
 % identity
                    7
                    (AC003974) putative disease resistance protein (Cf-2.2)
 NCBI Description
                    [Arabidopsis thaliana] >gi_3298554 (AC004681) putative
                    disease resistance protein [Arabidopsis thaliana]
                    169506
 Seq. No.
                    LIB3234-085-Q1-K1-G8
 Seq. ID
                    BLASTX
 Method
                    g2244909
 NCBI GI
                    250
 BLAST score
 E value
                    8.0e-22
                    55
 Match length
                    89
 % identity
                   (Z97339) pyruvate, orthophosphate dikinase [Arabidopsis
 NCBI Description
                    thaliana]
```

169507

BLASTX

LIB3234-085-Q1-K1-G9

Seq. No.

Seq. ID Method



```
NCBI GI
                  g1703108
BLAST score
                  610
                  1.0e-63
E value
Match length
                  120
% identity
                  98
                  ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
NCBI Description
                  thaliana >qi 2129528 pir S68107 actin 7 - Arabidopsis
                  thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >qi 1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
                  169508
Seq. No.
Seq. ID
                  LIB3234-085-Q1-K1-H1
                  BLASTX
Method
                  q3834316
NCBI GI
BLAST score
                  587
E value
                  5.0e-61
                  119
Match length
% identity
                  100
                  (AC005679) Similar to qb X16648 pathogenesis related
NCBI Description
                  protein from Hordeum vulgare. EST gb Z18206 comes from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  169509
                  LIB3234-085-Q1-K1-H10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2143322
BLAST score
                  35
E value
                  2.0e-10
Match length
                  110
                  84
% identity
NCBI Description P.deltoides chloroplast DNA for psbB operon
Seq. No.
                  169510
                  LIB3234-085-Q1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220638
BLAST score
                  316
E value
                  1.0e-178
Match length
                  383
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  169511
Seq. No.
                  LIB3234-085-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210330
BLAST score
                  648
                  4.0e-68
E value
                  122
Match length
                  98
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit
NCBI Description
                   [Arabidopsis thaliana]
```

169512

LIB3234-085-Q1-K1-H6

Seq. No.

Seq. ID

Seq. No.

Seq. ID

169517

LIB3234-086-Q1-K1-A5



```
BLASTX
Method
NCBI GI
                  q226120
                  214
BLAST score
E value
                  3.0e-17
Match length
                  102
% identity
                  41
                  vicilin gene B [Saguinus oedipus]
NCBI Description
                  169513
Seq. No.
                  LIB3234-086-Q1-K1-A1
Seq. ID
Method
                  BLASTN
                  g4589437
NCBI GI
BLAST score
                  353
                  0.0e + 00
E value
Match length
                  361
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPN9, complete sequence
                  169514
Seq. No.
                  LIB3234-086-01-K1-A10
Seq. ID
Method
                  BLASTX
                  q2829894
NCBI GI
BLAST score
                  146
                  2.0e-09
E value
                  30
Match length
% identity
                  93
                  (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169515
Seq. ID
                  LIB3234-086-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q120667
BLAST score
                  394
                  2.0e-38
E value
Match length
                   91
% identity
                   82
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                   thaliana >gi 166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate
                   dehydrogenase [Arabidopsis thaliana]
                  169516
Seq. No.
                  LIB3234-086-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                   g4006827
NCBI GI
BLAST score
                   439
E value
                   1.0e-43
                   98
Match length
                   86
% identity
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
```



BLASTN Method NCBI GI q3337347 324 BLAST score 0.0e + 00E value Match length 355 53 % identity Arabidopsis thaliana chromosome II BAC F13P17 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 169518 Seq. No. LIB3234-086-Q1-K1-A8 Seq. ID BLASTX Method NCBI GI q4753651 BLAST score 563 3.0e-58 E value 115 Match length 92 % identity (ALO49751) ribosomal protein L13a like protein [Arabidopsis NCBI Description thaliana] 169519 Seq. No. LIB3234-086-Q1-K1-A9 Seq. ID BLASTX Method NCBI GI g4038040 BLAST score 296 6.0e-27 E value 57 Match length 100 % identity (AC005936) proteinase inhibitor II [Arabidopsis thaliana] NCBI Description 169520 Seq. No. LIB3234-086-Q1-K1-B1 Seq. ID BLASTN Method NCBI GI q2264316 BLAST score 354 0.0e + 00E value Match length 361 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana] 169521 Seq. No. LIB3234-086-Q1-K1-B10 Seq. ID BLASTX Method NCBI GI g3135611 612 BLAST score 6.0e-64E value 117 Match length

100 % identity

NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]

169522 Seq. No.

LIB3234-086-Q1-K1-B11 Seq. ID

BLASTX Method q3548802 NCBI GI 81 BLAST score 4.0e-24 E value



Match length 114 % identity 51

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi 4335769 gb AAD17446_ (AC006284) putative axil protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 169523

Seq. ID LIB3234-086-Q1-K1-B12

Method BLASTX
NCBI GI g3421384
BLAST score 255
E value 4.0e-22
Match length 63
% identity 81

NCBI Description (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase

[Arabidopsis thaliana]

Seq. No. 169524

Seq. ID LIB3234-086-Q1-K1-B2

Method BLASTX
NCBI GI g2160151
BLAST score 472
E value 2.0e-47
Match length 119
% identity 77

NCBI Description (ACO00375) Strong similarity to Brassica aspartic protease

(gb X77260). [Arabidopsis thaliana]

Seq. No. 169525

Seq. ID LIB3234-086-Q1-K1-B3

Method BLASTX
NCBI GI g2499610
BLAST score 423
E value 8.0e-42
Match length 97
% identity 86

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6)

(ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein

kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana

>gi_457404_dbj_BAA04869 (D21842) MAP kinase [Arabidopsis
thaliana] >gi 2281091 (AC002333) MAP Kinase 6 [Arabidopsis

thaliana]

Seq. No. 169526

Seq. ID LIB3234-086-Q1-K1-B4

Method BLASTN
NCBI GI 94063735
BLAST score 206
E value 1.0e-112
Match length 286
% identity 100

NCBI Description Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 169527

Seq. ID LIB3234-086-Q1-K1-B6

Method BLASTN



NCBI GI g3983533 BLAST score 70 4.0e-31 E value Match length 129 % identity 89 Arabidopsis thaliana BAC T24G3 from chromosome V near 70 NCBI Description cM, complete sequence [Arabidopsis thaliana] Seq. No. 169528 LIB3234-086-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI g3337356

Method BLASTX
NCBI GI g3337356
BLAST score 455
E value 1.0e-45
Match length 88
% identity 100
NCBI Description (AC004481) putati

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 169529

Seq. ID LIB3234-086-Q1-K1-C1

Method BLASTN
NCBI GI g3241922
BLAST score 276
E value 1.0e-154
Match length 284
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLM24, complete sequence [Arabidopsis thaliana]

Seq. No. 169530

Seq. ID LIB3234-086-Q1-K1-C10

Method BLASTN
NCBI GI g4455339
BLAST score 244
E value 1.0e-135
Match length 89

% identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5

(ESSAII project)

Seq. No. 169531

Seq. ID LIB3234-086-Q1-K1-C12

Method BLASTN
NCBI GI 94589414
BLAST score 150
E value 8.0e-79
Match length 336
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14B15, complete sequence

Seq. No. 169532

Seq. ID LIB3234-086-Q1-K1-C2

Method BLASTX NCBI GI g82223 BLAST score 55



```
3.0e-11
E value
                  60
Match length
                  72
% identity
                  hypothetical protein 70B - common tobacco chloroplast
NCBI Description
                  >gi 11878 emb CAA77391 (Z00044) hypothetical protein
                  [Nicotiana tabacum] >gi_1223681_emb_CAA77402_ (Z00044)
                  hypothetical protein [Nicotiana tabacum]
                  >gi 225250 prf 1211235CJ ORF 70B [Nicotiana tabacum]
Seq. No.
                  169533
Seq. ID
                  LIB3234-086-Q1-K1-C3
                  BLASTN
Method
NCBI GI
                  g4510323
BLAST score
                  32
E value
                  1.0e-08
                  118
Match length
                  99
% identity
                  Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
NCBI Description
                  cM, complete sequence
                  169534
Seq. No.
Seq. ID
                  LIB3234-086-Q1-K1-C4
                  BLASTN
Method
NCBI GI
                  g2656031
BLAST score
                  283
                  1.0e-158
E value
                  308
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
                  169535
Seq. No.
                  LIB3234-086-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2224933
BLAST score
                  512
E value
                  3.0e-52
Match length
                  116
                  86
% identity
                  (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
NCBI Description
                  >gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
                  thaliana]
```

Seq. No. 169536

Seq. ID LIB3234-086-Q1-K1-C7

Method BLASTX
NCBI GI g3647355
BLAST score 230
E value 4.0e-19
Match length 104
% identity 47

NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w),

Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No. 169537

Seq. ID Method



```
LIB3234-086-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4584387
BLAST score
                  77
                  8.0e-36
E value .
                  93
Match length
                   96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
NCBI Description
                   (ESSA project)
                  169538
Seq. No.
                  LIB3234-086-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                   g66179
NCBI GI
                   556
BLAST score
                   2.0e-57
E value
Match length
                   114
                   90
% identity
                  NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -
NCBI Description
                   common tobacco chloroplast >gi_225255_prf__1211235CP NADH
                   dehydrogenase 4-like ORF 509B [Nicotiana tabacum]
                   169539
Seq. No.
                   LIB3234-086-Q1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4101589
BLAST score
                   307
                   3.0e-28
E value
Match length
                   103
% identity
                   53
                   (AF005050) aspartyl aminopeptidase [Homo sapiens]
NCBI Description
                   169540
Seq. No.
                   LIB3234-086-Q1-K1-D12
Seq. ID
                   BLASTN
Method
                   g4199934
NCBI GI
                   337
BLAST score
                   0.0e+00
E value
Match length
                   341
                   100
% identity
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169541
Seq. No.
                   LIB3234-086-Q1-K1-D2
Seq. ID
                   BLASTN
Method
                   g2864607
NCBI GI
                   361
BLAST score
                   0.0e+00
E value
                   361
Match length
                   100
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                   (ESSAII project)
                   169542
Seq. No.
```

LIB3234-086-Q1-K1-D3

BLASTX



% identity

NCBI Description

```
NCBI GI
                  g1246019
BLAST score
                  551
                   9.0e-57
E value
Match length
                  105
% identity
                  100
                  (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
NCBI Description
                  erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
                  169543
Seq. No.
                  LIB3234-086-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                   g3929364
NCBI GI
BLAST score
                   290
                   3.0e-26
E value
                   99
Match length
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-23KD) (CI-23KD) >gi 1076356 pir S52380 NADH
                   dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                   >qi 666977 emb CAA59061 (X84318) NADH dehydrogenase
                   [Arabidopsis thaliana] >gi 3152573 (AC002986) Match to
                   NADH: ubiquinone oxidoreductase gb X84318 from A.thaliana.
                   ESTs gb Z27005, gb T04711, gb T45\overline{0}78 and gb Z28689 come
                   from this gene. [Arabidopsis thaliana]
                   169544
Seq. No.
                   LIB3234-086-Q1-K1-D7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2864607
BLAST score
                   124
E value
                   2.0e-63
Match length
                   200
                   91
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                   (ESSAII project)
                   169545
Seq. No.
                   LIB3234-086-Q1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4079614
                   96
BLAST score
                   4.0e-47
E value
Match length
                   112
                   93
% identity
                   Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169546
Seq. No.
                   LIB3234-086-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172816
                   187
BLAST score
                   4.0e-14
E value
Match length
                   98
```

60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395_

(X81799) ribosomal protein L16 [Arabidopsis thaliana]



LIB3234-086-Q1-K1-E12

Seq. No.

Seq. ID

```
Method
                  BLASTN
NCBI GI
                  q3402695
BLAST score
                  338
                  0.0e + 00
E value
Match length
                  350
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T3K9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169548
                  LIB3234-086-Q1-K1-E2
Seq. ID
Method
                  BLASTN
                  g4510392
NCBI GI
BLAST score
                  125
                  7.0e-64
E value
Match length
                  203
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T17D12 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  169549
                  LIB3234-086-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  q1864017
NCBI GI
BLAST score
                   534
E value
                  8.0e-55
Match length
                  101
                   100
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. No.
                  169550
                  LIB3234-086-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132901
BLAST score
                   320
E value
                   1.0e-29
Match length
                   66
% identity
                   86
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L33 >gi 71356 pir R5NT33
NCBI Description
                   ribosomal protein L33 - common tobacco chloroplast
                   >gi_11850_emb_CAA77370_ (Z00044) ribosomal protein L33
                   [Nicotiana tabacum] >gi 225219 prf 1211235BA ribosomal
                   protein L33 [Nicotiana tabacum]
                   169551
Seq. No.
                   LIB3234-086-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   g4263694
NCBI GI
                   165
BLAST score
                   9.0e-88
E value
Match length
                   319
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

169557



```
Seq. No.
                  169552
                  LIB3234-086-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2541886
BLAST score
                  316
                  3.0e-29
E value
                  115
Match length
                  51
% identity
NCBI Description
                  (D63675) acetolactate synthase [Cyanidioschyzon merolae]
Seq. No.
                  169553
                  LIB3234-086-Q1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3763915
BLAST score
                  97
E value
                  3.0e-47
                  348
Match length
                  41
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14B2 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169554
                  LIB3234-086-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695380
BLAST score
                  118
E value
                  5.0e-06
Match length
                  118
% identity
                  14
                  (AF096370) partial CDS; contains similarity to Nicotiana
NCBI Description
                  tabacum membrane-associated salt-inducible protein
                  (GB:U08285) [Arabidopsis thaliana]
Seq. No.
                  169555
Seq. ID
                  LIB3234-086-Q1-K1-F1
Method
                  BLASTX
NCBÍ GI
                  q3335169
BLAST score
                  595
E value
                  6.0e-62
Match length
                  112
                  100
% identity
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  169556
Seq. ID
                  LIB3234-086-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2961379
BLAST score
                  460
E value
                  4.0e-46
Match length
                  109
% identity
                  87
NCBI Description
                  (AL022141) hypothatical protein [Arabidopsis thaliana]
```

Method NCBI GI



```
LIB3234-086-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  270
E value
                  7.0e-24
                  116
Match length
                  56
% identity
NCBI Description
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                  - spinach >gi 1066153 dbj BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
                  169558
Seq. No.
Seq. ID
                  LIB3234-086-Q1-K1-F2
Method
                  BLASTN
                  q2656030
NCBI GI
BLAST score
                  337
E value
                  0.0e + 00
                  357
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUL8
                  169559
Seq. No.
Seq. ID
                  LIB3234-086-Q1-K1-F3
Method
                  BLASTX
                  q3250695
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
Match length
                  114
% identity
                   52
NCBI Description
                  (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                  169560
Seq. ID
                  LIB3234-086-Q1-K1-F4
Method
                  BLASTN
NCBI GI
                   g3341671
BLAST score
                   57
                   8.0e-24
E value
Match length
                   94
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F16B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169561
                  LIB3234-086-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                   g1619602
NCBI GI
BLAST score
                   342
                   3.0e-32
E value
                  78
Match length
                   83
% identity
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                   169562
Seq. No.
                  LIB3234-086-Q1-K1-F6
Seq. ID
```

23041

BLASTX

g2739010



```
BLAST score
                  208
                  1.0e-16
E value
Match length
                  58
                   66
% identity
                  (AF022464) CYP77A3p [Glycine max]
NCBI Description
Seq. No.
                  169563
                  LIB3234-086-Q1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  203
E value
                  1.0e-110
                   345
Match length
                   99
% identity
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                  chromosome IV, complete sequence [Arabidopsis thaliana]
                  169564
Seq. No.
Seq. ID
                  LIB3234-086-Q1-K1-F8
                  BLASTX
Method
                   g3264778
NCBI GI
                   345
BLAST score
                   1.0e-32
E value
                   118
Match length
                   65
% identity
                  (AF072536) H-protein promoter binding factor-1 [Arabidopsis
NCBI Description
                   thaliana]
                   169565
Seq. No.
Seq. ID
                   LIB3234-086-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g16245
                   145
BLAST score
                   3.0e-09
E value
Match length
                   51
% identity
                   (X51514) precursor acetolactate synthase (670 AA)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   169566
Seq. ID
                   LIB3234-086-Q1-K1-G10
Method
                   BLASTN
NCBI GI
                   g3831437
BLAST score
                   138
E value
                   1.0e-71
Match length
                   324
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC T3A4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169567
                   LIB3234-086-Q1-K1-G11
Seq. ID
Method
                   BLASTX
                   g3860260
NCBI GI
BLAST score
                   312
                   8.0e-29
E value
```

23042

99

Match length



% identity

NCBI Description

```
thaliana]
                  169568
Seq. No.
                  LIB3234-086-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1943751
                  56
BLAST score
E value
                  8.0e-12
                  107
Match length
                  40
% identity
                  (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                  protein, complete sequence >gi_2078292 (U96455) ER-type
                  Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
Seq. No.
                  169569
                  LIB3234-086-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678299
BLAST score
                  554
                  4.0e-57
E value
                  109
Match length
                  99
% identity
                   (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  169570
Seq. No.
Seq. ID
                  LIB3234-086-Q1-K1-G4
Method
                  BLASTX
                  q82200
NCBI GI
BLAST score
                  251
                   4.0e-22
E value
Match length
                  69
                  72
% identity
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
Seq. No.
                  169571
Seq. ID
                  LIB3234-086-Q1-K1-G5
Method
                  BLASTN
NCBI GI
                  g3004543
                  301
BLAST score
                  1.0e-169
E value
                   330
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F19F24 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169572
                  LIB3234-086-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g4185141
NCBI GI
BLAST score
                   580
E value
                   3.0e-60
                  114
Match length
                   96
% identity
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
NCBI Description
```

(AC005824) putative acidic ribosomal protein [Arabidopsis

169578



thaliana]

```
169573
Seq. No.
                  LIB3234-086-Q1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2887500
                  159
BLAST score
                  7.0e-11
E value
                  29
Match length
                  90
% identity
                   (AC002339) putative AP2 domain-containing protein
NCBI Description
                   [Arabidopsis thaliana]
                  169574
Seq. No.
Seq. ID
                  LIB3234-086-Q1-K1-G9
Method
                  BLASTN
                  q3335356
NCBI GI
BLAST score
                  147
                  5.0e-77
E value
                  325
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169575
Seq. No.
                  LIB3234-086-Q1-K1-H1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3335331
BLAST score
                  63
                  7.0e-27
E value
                  95
Match length
                  92
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  169576
Seq. No.
                  LIB3234-086-Q1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4580732
BLAST score
                   36
E value
                   9.0e-11
Match length
                  72
                   88
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F5J5,
NCBI Description
                   complete sequence
Seq. No.
                   169577
Seq. ID
                   LIB3234-086-Q1-K1-H11
Method
                   BLASTX
NCBI GI
                   g3747111
                   412
BLAST score
                   2.0e-40
E value
Match length
                   94
% identity
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
```



```
LIB3234-086-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  q3335171
NCBI GI
BLAST score
                  420
E value
                  2.0e-41
                  116
Match length
                  68
% identity
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
                  169579
Seq. No.
                  LIB3234-086-Q1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4558566
                  620
BLAST score
                  7.0e-65
E value
                  118
Match length
                  100
% identity
NCBI Description
                  (AC007138) putative raffinose synthase or seed imbibition
                  protein [Arabidopsis thaliana]
                  169580
Seq. No.
                  LIB3234-086-Q1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1935913
                  216
BLAST score
                  1.0e-118
E value
                   308
Match length
                   96
% identity
NCBI Description
                  Arabidopsis thaliana lethal leaf-spot 1 homolog (Lls1)
                  mRNA, partial cds
Seq. No.
                   169581
                  LIB3234-086-Q1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832681
BLAST score
                   176
                   8.0e-13
E value
Match length
                   36
% identity
                   83
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                   169582
Seq. No.
                   LIB3234-086-Q1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3550519
                   399
BLAST score
                   5.0e-39
E value
Match length
                   114
                   66
% identity
NCBI Description (AJ007630) oxygenase [Nicotiana tabacum]
                   169583
Seq. No.
                   LIB3234-087-Q1-K1-A1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q12219
```

23045

117

4.0e-59

BLAST score

E value



263 Match length % identity 97 Mustard chloroplast trnk gene for tRNA-Lys(UUU) NCBI Description Seq. No. 169584 LIB3234-087-Q1-K1-A10 Seq. ID BLASTX Method NCBI GI q4589954 BLAST score 151 3.0e-10 E value Match length 83 % identity 42 (AC007169) hypothetical protein [Arabidopsis thaliana] NCBI Description 169585 Seq. No. LIB3234-087-Q1-K1-A11 Seq. ID Method BLASTN q4519196 NCBI GI BLAST score 38 4.0e-12 E value 66 Match length 89 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSK10, complete sequence 169586 Seq. No. LIB3234-087-Q1-K1-A12 Seq. ID BLASTN Method NCBI GI g2358139 BLAST score 358 0.0e + 00E value 358 Match length 100 % identity NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana] 169587 Seq. No. LIB3234-087-Q1-K1-A2 Seq. ID Method BLASTX g3056584 NCBI GI 595 BLAST score 6.0e-62E value 115 Match length 98 % identity (AC004255) T1F9.5 [Arabidopsis thaliana] NCBI Description 169588 Seq. No. LIB3234-087-Q1-K1-A4 Seq. ID BLASTN Method

Method BLASTN
NCBI GI g166870
BLAST score 314
E value 1.0e-176
Match length 370
% identity 96

NCBI Description Arabidopsis thaliana 5S ribosomal RNA gene, complete cds

Seq. No. 169589

23046

4.-



```
Seq. ID
                  LIB3234-087-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  q3059018
BLAST score
                  360
                  0.0e + 00
E value
Match length
                  367
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
NCBI Description
                  (ESSAII project)
                  169590
Seq. No.
Seq. ID
                  LIB3234-087-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                  g12219
BLAST score
                  117
E value
                  4.0e-59
Match length
                  271
                  97
% identity
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.
                  169591
                  LIB3234-087-Q1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2656029
BLAST score
                  187
                  1.0e-101
E value
Match length
                  274
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQB2
                  169592
Seq. No.
                  LIB3234-087-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g3043415
NCBI GI
BLAST score
                  523
                  2.0e-53
E value
Match length
                  100
% identity
                  100
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]
                  169593
Seq. No.
                  LIB3234-087-Q1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2642427
BLAST score
                  335
                  0.0e+00
E value
Match length
                  364
                  92
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20D16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB3234-087-Q1-K1-B5

Method BLASTX NCBI GI g99688 BLAST score 633



E value 2.0e-66 122 Match length % identity 100

translation elongation factor eEF-1 alpha chain (gene A4) -NCBI Description

Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)

elongation factor 1-alpha [Arabidopsis thaliana]

169595 Seq. No.

LIB3234-087-Q1-K1-B6 Seq. ID

Method BLASTN NCBI GI g2828186 BLAST score 93 E value 9.0e-45372 Match length 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

169596 Seq. No.

LIB3234-087-Q1-K1-B8 Seq. ID

Method BLASTN NCBI GI g1053092 BLAST score 147 3.0e-77E value Match length 155 % identity 99

Arabidopsis thaliana pre zeta-carotene desaturase precursor NCBI Description

(zds) mRNA, complete cds

169597 Seq. No.

LIB3234-087-Q1-K1-B9 Seq. ID

BLASTN Method NCBI GI g2924651 BLAST score 203 1.0e-110 E value 350 Match length 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 169598

LIB3234-087-Q1-K1-C10 Seq. ID

Method BLASTX NCBI GI g1352347 BLAST score 479 2.0e-48 E value Match length 99 % identity 96

ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) NCBI Description

>gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia)

>gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta

Al [Arabidopsis thaliana]

169599 Seq. No.

LIB3234-087-Q1-K1-C11 Seq. ID

Method BLASTN

NCBI GI

BLAST score

g548847



```
NCBI GI
                   g2656026
BLAST score
                   343
                   0.0e + 00
E value
Match length
                   365
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   169600
Seq. No.
Seq. ID
                   LIB3234-087-Q1-K1-C12
                   BLASTX
Method
NCBI GI
                   g3421070
BLAST score
                   418
                   2.0e-41
E value
Match length
                   86
% identity
                   95
                   (AF043518) 20S proteasome subunit PAA1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   169601
Seq. ID
                   LIB3234-087-Q1-K1-C2
                   BLASTN
Method
NCBI GI
                   g4580454
BLAST score
                   339
                   0.0e + 00
E value
Match length
                   347
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   169602
                   LIB3234-087-Q1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3449320
                   199
BLAST score
                   1.0e-108
E value
                   366
Match length
                   87
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRB17, complete sequence [Arabidopsis thaliana]
                   169603
Seq. No.
                   LIB3234-087-Q1-K1-C6
Seq. ID
                   BLASTN
Method
                   g4199934
NCBI GI
BLAST score
                   246
                   1.0e-136
E value
                   274
Match length
                   97
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169604
Seq. No.
                   LIB3234-087-Q1-K1-C7
Seq. ID
Method
                   BLASTX
```



```
E value
                  9.0e-42
                  83
Match length
                  98
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi_1086182_pir__S39501 ribosomal protein S12 -
                  curled-leaved tobacco >gi 225248 prf 1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
                  169605
Seq. No.
                  LIB3234-087-Q1-K1-C8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g166870
                  271
BLAST score
                  1.0e-151
E value
Match length
                  340
% identity
                  95
                  Arabidopsis thaliana 5S ribosomal RNA gene, complete cds
NCBI Description
                  169606
Seq. No.
                  LIB3234-087-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166870
BLAST score
                  92
                  3.0e-44
E value
Match length
                  204
                  87
% identity
                  Arabidopsis thaliana 5S ribosomal RNA gene, complete cds
NCBI Description
Seq. No.
                  169607
                  LIB3234-087-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                  g2459445
NCBI GI
BLAST score
                  204
                  3.0e-16
E value
                  43
Match length
                  93
% identity
                  (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                  thaliana]
                  169608
Seq. No.
                  LIB3234-087-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  g4587986
NCBI GI
                  367
BLAST score
                  0.0e+00
E value
                  367
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete
                   sequence
```

Seq. ID LIB3234-087-Q1-K1-D11

Method BLASTN
NCBI GI g4580454
BLAST score 360
E value 0.0e+00
Match length 367



% identity 100 Arabidopsis thaliana chromosome II BAC T2G17 genomic NCBI Description sequence, complete sequence 169610 Seq. No. LIB3234-087-Q1-K1-D12 Seq. ID Method BLASTX NCBI GI q4567275 BLAST score 504 3.0e-51 E value Match length 95 39 % identity (AC006841) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 169611 Seq. ID LIB3234-087-Q1-K1-D2 Method BLASTX NCBI GI g3176874 BLAST score 494 4.0e-50 E value Match length 94 100 % identity NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis thaliana] Seq. No. 169612 LIB3234-087-Q1-K1-D3 Seq. ID Method BLASTX NCBI GI g2244750 BLAST score 499 9.0e-51 E value Match length 98 100 % identity (Z97335) adenosylhomocysteinase [Arabidopsis thaliana] NCBI Description >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana] 169613 Seq. No. Seq. ID LIB3234-087-Q1-K1-D4 BLASTN Method NCBI GI g2924257 59 BLAST score 9.0e-25 E value Match length 113 92 % identity NCBI Description Tobacco chloroplast genome DNA 169614 Seq. No. LIB3234-087-Q1-K1-D5 Seq. ID BLASTN Method g2832639 NCBI GI 161 BLAST score 9.0e-86 E value Match length 161 100 % identity

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NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. ID

169620

LIB3234-087-Q1-K1-E11



```
Seq. No.
                  169615
Seq. ID
                  LIB3234-087-Q1-K1-D6
Method
                  BLASTN
NCBI GI
                  q4468976
BLAST score
                  195
E value
                  1.0e-106
Match length
                  195
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18
NCBI Description
                  (ESSA project)
Seq. No.
                  169616
                  LIB3234-087-Q1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4206762
BLAST score
                  247
E value
                  1.0e-136
Match length
                  282
% identity
                  96
NCBI Description
                  Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  169617
Seq. ID
                  LIB3234-087-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  494
E value
                  3.0e-50
Match length
                  101
                  97
% identity
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  169618
Seq. No.
                  LIB3234-087-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3445209
                  382
BLAST score
                  6.0e-37
E value
                  95
Match length
                  71
% identity
NCBI Description
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
                  169619
Seq. No.
                  LIB3234-087-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063472
                  536
BLAST score
E value
                  5.0e - 55
Match length
                  100
                  99
% identity
NCBI Description
                  (AC003981) F22013.34 [Arabidopsis thaliana]
```



```
Method
                  BLASTN
NCBI GI
                  q3869068
BLAST score
                  69
                  1.0e-30
E value
Match length
                  163
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC16, complete sequence [Arabidopsis thaliana]
                  169621
Seq. No.
                  LIB3234-087-Q1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220636
BLAST score
                  212
                  1.0e-116
E value
Match length
                  357
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169622
Seq. ID
                  LIB3234-087-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3355311
BLAST score
                   375
                   4.0e-36
E value
Match length
                   83
% identity
NCBI Description
                   (AJ009737) eukaryotic translation initiation factor 6 [Beta
                   vulgaris]
                  169623
Seq. No.
                  LIB3234-087-Q1-K1-E3
Seq. ID
Method
                  BLASTN
                   g4757413
NCBI GI
                   157
BLAST score
                   6.0e-83
E value
Match length
                   319
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXO21, complete sequence
                   169624
Seq. No.
                   LIB3234-087-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129780
BLAST score
                   362
                   1.0e-34
E value
                   66
Match length
                   100
% identity
                   photosystem I protein A1 - Arabidopsis thaliana chloroplast
NCBI Description
                   (fragment) >gi_538202 (L36246) anoxia-induced protein
                   [Arabidopsis thaliana]
```

Seq. No. 169625
Seq. ID LIB3234-087-Q1-K1-E5

Seq. ID LIB3234-087-Method BLASTX

letilod blasia

E value

Match length



```
NCBI GI
                     g3212870
  BLAST score
                     204
  E value
                     6.0e-24
  Match length
                     117
  % identity
                     48
                     (AC004005) putative N-myristoyltransferase [Arabidopsis
  NCBI Description
                     thaliana]
                     169626
Seq. No.
                     LIB3234-087-Q1-K1-E6
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g4220635
  BLAST score
                     344
                     0.0e+00
  E value
  Match length
                     352
                     99
  % identity
                     Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
  NCBI Description
                     MDB19, complete sequence [Arabidopsis thaliana]
                     169627
  Seq. No.
                     LIB3234-087-Q1-K1-E7
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3170525
  BLAST score
                     328
                     1.0e-30
  E value
  Match length
                     83
                     77
  % identity
  NCBI Description
                    (AF054615) cellulase [Fragaria x ananassa]
                     169628
  Seq. No.
                     LIB3234-087-Q1-K1-E8
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g3004543
                     281
  BLAST score
                     1.0e-157
  E value
                     342
  Match length
                     95
  % identity
  NCBI Description Arabidopsis thaliana chromosome II BAC F19F24 genomic
                     sequence, complete sequence [Arabidopsis thaliana]
                     169629
  Seq. No.
                     LIB3234-087-Q1-K1-E9
  Seq. ID
  Method
                     BLASTX
                     g2244749
  NCBI GI
  BLAST score
                     503
                     4.0e-51
  E value
                     96
  Match length
                     100
  % identity
                    (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
  NCBI Description
                     169630
  Seq. No.
                     LIB3234-087-Q1-K1-F1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     q1360645
                     35
  BLAST score
```

23054

4.0e-10

Match length

120



% identity 100 Arabidopsis thaliana cyclin (cyclbAt) mRNA, complete cds NCBI Description 169631 Seq. No. LIB3234-087-Q1-K1-F10 Seq. ID BLASTX Method NCBI GI q3915847 333 BLAST score 3.0e-31 E value 75 Match length 88 % identity 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative NCBI Description 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 169632 Seq. ID LIB3234-087-Q1-K1-F11 Method BLASTX NCBI GI q860891 456 BLAST score 1.0e-45 E value 92 Match length 95 % identity (X87636) PSII cytochome b559 alpha chain [Beta vulgaris] NCBI Description >gi 860897 emb CAA60972 (X87637) PSII cytochrome b599 alpha chain [Beta vulgaris] 169633 Seq. No. Seq. ID LIB3234-087-Q1-K1-F12 Method BLASTX NCBI GI g860891 456 BLAST score 1.0e-45 E value 92 Match length 95 % identity (X87636) PSII cytochome b559 alpha chain [Beta vulgaris] NCBI Description >gi_860897_emb_CAA60972_ (X87637) PSII cytochrome b599 alpha chain [Beta vulgaris] Seq. No. 169634 LIB3234-087-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI q2244970 575 BLAST score E value 1.0e-59 113 Match length % identity 100 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana] 169635 Seq. No. LIB3234-087-Q1-K1-F3 Seq. ID Method BLASTX NCBI GI g4204299 BLAST score 619 E value 9.0e-65



% identity 100 (AC003027) 1cl prt seq No definition line found NCBI Description [Arabidopsis thaliana] Seq. No. 169636 LIB3234-087-Q1-K1-F6 Seq. ID Method BLASTX NCBI GI g1402884 BLAST score 536 4.0e-55 E value Match length 103 98 % identity NCBI Description (X98130) unknown [Arabidopsis thaliana] >gi 1495265 emb CAA66120 (X97488) beta-transducin like protein [Arabidopsis thaliana] Seq. No. 169637 Seq. ID LIB3234-087-Q1-K1-F8 Method BLASTX NCBI GI g2245138 BLAST score 571 4.0e-59 E value Match length 112 % identity 100 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana] 169638 Seq. No. Seq. ID LIB3234-087-Q1-K1-G1 Method BLASTX NCBI GI q3462351 BLAST score 229 5.0e-19 E value Match length 114 % identity 40 (U85647) small optic lobes homolog [Homo sapiens] NCBI Description 169639 Seq. No. LIB3234-087-Q1-K1-G10 Seq. ID Method BLASTX NCBI GI g3402716 BLAST score 184 9.0e-14 E value Match length 85 49 % identity (AC004261) unknown protein [Arabidopsis thaliana] NCBI Description 169640 Seq. No. Seq. ID LIB3234-087-Q1-K1-G11 Method BLASTN g4732167 NCBI GI 284

Method BLASTN
NCBI GI g4732167
BLAST score 284
E value 1.0e-159
Match length 370
% identity 97

NCBI Description Arabidopsis thaliana BAC F28D6

Seq. No. 169641



Seq. ID LIB3234-087-Q1-K1-G12

Method BLASTX
NCBI GI g4204308
BLAST score 530
E value 2.0e-54
Match length 103
% identity 89

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 169642

Seq. ID LIB3234-087-Q1-K1-G3

Method BLASTN
NCBI GI g3337347
BLAST score 187
E value 1.0e-101
Match length 318
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F13P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169643

Seq. ID LIB3234-087-Q1-K1-G4

Method BLASTN
NCBI GI g2494110
BLAST score 269
E value 1.0e-150
Match length 305
% identity 99

NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 169644

Seq. ID LIB3234-087-Q1-K1-G5

Method BLASTN
NCBI GI g3860243
BLAST score 355
E value 0.0e+00
Match length 355
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169645

Seq. ID LIB3234-087-Q1-K1-G6

Method BLASTN
NCBI GI g3860243
BLAST score 317
E value 1.0e-178
Match length 349
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169646

Seq. ID LIB3234-087-Q1-K1-G8

Method BLASTX

Method

NCBI GI

BLASTX

g225279



```
NCBI GI
                  g1703115
                  446
BLAST score
                  2.0e-44
E value
Match length
                  83
                  100
% identity
                  ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                  thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]
                  >qi 3236244 (AC004684) actin 3 protein [Arabidopsis
                  thaliana]
                  169647
Seq. No.
                  LIB3234-087-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g3983125
NCBI GI
                  590
BLAST score
E value
                  2.0e-61
                  117
Match length
                  99
% identity
                  (AF097648) phosphate/triose-phosphate translocator
NCBI Description
                  precursor [Arabidopsis thaliana]
                  169648
Seq. No.
                  LIB3234-087-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g2129767
NCBI GI
                  469
BLAST score
                  4.0e-47
E value
Match length
                  101
                  88
% identity
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
NCBI Description
                  precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                   (D61394) beta-VPE [Arabidopsis thaliana]
                  169649
Seq. No.
                  LIB3234-087-Q1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3747111
BLAST score
                  327
                  1.0e-30
E value
Match length
                  69
                   91
% identity
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                  169650
Seq. No.
                  LIB3234-087-Q1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1742951
BLAST score
                   287
E value
                   3.0e-26
Match length
                   69
                   77
% identity
                  (Y09817) Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169651
                  LIB3234-087-Q1-K1-H2
Seq. ID
```



BLAST score 50 E value 5.0e-28 Match length 93 % identity 76

NCBI Description rpoC-like ORF 236 [Nicotiana tabacum]

Seq. No. 169652

Seq. ID LIB3234-087-Q1-K1-H3

Method BLASTX
NCBI GI g225279
BLAST score 50
E value 3.0e-27
Match length 92
% identity 76

NCBI Description rpoC-like ORF 236 [Nicotiana tabacum]

Seq. No. 169653

Seq. ID LIB3234-087-Q1-K1-H5

Method BLASTX
NCBI GI g119351
BLAST score 216
E value 2.0e-17
Match length 60
% identity 73

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 84950 pir S07586

phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly

(Drosophila melanogaster) >gi 7946 emb CAA34895 (X17034)

enolase (AA 1-433) [Drosophila melanogaster]

Seq. No. 169654

Seq. ID LIB3234-087-Q1-K1-H7

Method BLASTN
NCBI GI g2564048
BLAST score 351
E value 0.0e+00
Match length 363
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKD15, complete sequence [Arabidopsis thaliana]

Seq. No. 169655

Seq. ID LIB3234-087-Q1-K1-H8

Method BLASTN
NCBI GI g2564048
BLAST score 288
E value 1.0e-161
Match length 331
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKD15, complete sequence [Arabidopsis thaliana]

Seq. No. 169656

Seq. ID LIB3234-088-Q1-K1-A10

Method BLASTX NCBI GI g2505870 BLAST score 593



E value 1.0e-61 Match length 120 % identity 98

NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 169657

Seq. ID LIB3234-088-Q1-K1-A11

Method BLASTN
NCBI GI g4510392
BLAST score 98
E value 9.0e-48
Match length 162
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic

sequence, complete sequence

Seq. No. 169658

Seq. ID LIB3234-088-Q1-K1-A2

Method BLASTN
NCBI GI g719276
BLAST score 73
E value 7.0e-33
Match length 144
% identity 88

NCBI Description Arabidopsis thaliana SABRE gene, exon

Seq. No. 169659

Seq. ID LIB3234-088-Q1-K1-A3

Method BLASTN
NCBI GI g4733953
BLAST score 89
E value 2.0e-42
Match length 128
% identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F13011 genomic

sequence, complete sequence

Seq. No. 169660

Seq. ID LIB3234-088-Q1-K1-A4

Method BLASTX
NCBI GI g1724100
BLAST score 290
E value 3.0e-26
Match length 100
% identity 57

NCBI Description (U79765) porin [Mesembryanthemum crystallinum]

Seq. No. 169661

Seq. ID LIB3234-088-Q1-K1-A5

Method BLASTN
NCBI GI g1279616
BLAST score 170
E value 1.0e-90
Match length 344
% identity 88

NCBI Description O.argillicola chloroplast 16S rRNA, trnI, trnA and 23S rRNA

genes

Match length

% identity

111 87



```
169662
Seq. No.
                   LIB3234-088-Q1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1345973
                   400
BLAST score
                   4.0e-39
E value
                   92
Match length
                   80
 % identity
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi 471091_dbj BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi 1197795_dbj BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
                   169663
 Seq. No.
                   LIB3234-088-Q1-K1-A7
 Seq. ID
                   BLASTN
 Method
                   q719276
 NCBI GI
BLAST score
                   333
 E value
                   0.0e+00
                   356
 Match length
                   98
 % identity
 NCBI Description Arabidopsis thaliana SABRE gene, exon
 Seq. No.
                   169664
                   LIB3234-088-Q1-K1-A8
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3935152
 BLAST score
                   501
 E value
                   6.0e-51
 Match length
                   112
                   77
 % identity
 NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]
 Seq. No.
                   169665
 Seq. ID
                   LIB3234-088-Q1-K1-A9
 Method
                   BLASTN
                   g1279569
 NCBI GI
                   41
 BLAST score
                   6.0e-14
 E value
                   49
 Match length
                   96
 % identity
 NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
                   169666
 Seq. No.
                   LIB3234-088-Q1-K1-B11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3152581
 BLAST score
                   498
                   1.0e-50
 E value
```



NCBI Description (AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come

from this gene. [Arabidopsis thaliana]

Seq. No. 169667

Seq. ID LIB3234-088-Q1-K1-B12

Method BLASTX
NCBI GI g1169598
BLAST score 328
E value 1.0e-30
Match length 73
% identity 84

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No. 169668

Seq. ID LIB3234-088-Q1-K1-B2

Method BLASTX
NCBI GI g3953471
BLAST score 653
E value 9.0e-69
Match length 121
% identity 100

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 169669

Seq. ID LIB3234-088-Q1-K1-B4

Method BLASTX
NCBI GI g2191151
BLAST score 624
E value 2.0e-65
Match length 121
% identity 100

NCBI Description (AF007269) contains similarity to membrane associated

salt-inducible protein [Arabidopsis thaliana]

Seq. No. 169670

Seq. ID LIB3234-088-Q1-K1-B5

Method BLASTN
NCBI GI g2191126
BLAST score 94
E value 2.0e-45
Match length 223
% identity 95

NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 169671

Seq. ID LIB3234-088-Q1-K1-B6

Method BLASTX
NCBI GI g2459445
BLAST score 300
E value 2.0e-27
Match length 114
% identity 26

NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

thaliana]



```
      Seq. No.
      169672

      Seq. ID
      LIB3234-088-Q1-K1-B7

      Method
      BLASTX

      NCBI GI
      g1565227

      BLAST score
      504

      E value
      3.0e-51
```

94

% identity 100
NCBI Description (X95573) salt-tolerance zinc finger protein [Arabidopsis

thaliana]

Seq. No. 169673

Match length

Seq. ID LIB3234-088-Q1-K1-C1

Method BLASTX
NCBI GI g3169059
BLAST score 208
E value 2.0e-16
Match length 81
% identity 49

NCBI Description (AL023704) weak similarity to B.subtilis spore outgrowth f

actor B [Schizosaccharomyces pombe]

Seq. No. 169674

Seq. ID LIB3234-088-Q1-K1-C10

Method BLASTX
NCBI GI g1345973
BLAST score 392
E value 4.0e-38
Match length 92
% identity 79

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 169675

Seq. ID LIB3234-088-Q1-K1-C11

Method BLASTX
NCBI GI 94538923
BLAST score 175
E value 1.0e-12
Match length 48
% identity 71

NCBI Description (AL049483) predicted protein destination factor

[Arabidopsis thaliana]

Seq. No. 169676

Seq. ID LIB3234-088-Q1-K1-C12

Method BLASTN
NCBI GI g4678371
BLAST score 321



```
E value
                  0.0e + 00
Match length
                  359
% identity
                  97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
NCBI Description
                  (ESSA project)
Seq. No.
                  169677
Seq. ID
                  LIB3234-088-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4567286
BLAST score
                  492
E value
                  7.0e-50
Match length
                  117
% identity
                  85.
NCBI Description
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
                  thaliana]
Seq. No.
                  169678
Seq. ID
                  LIB3234-088-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  q2494110
BLAST score
                  297
E value
                  1.0e-166
Match length
                  332
% identity
                  99
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169679
                  LIB3234-088-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510397
BLAST score
                  509
E value
                  7.0e-52
                  100
Match length
                  98
% identity
NCBI Description
                  (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
                  169680
Seq. No.
                  LIB3234-088-Q1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4678371
BLAST score
                  121
E value
                  1.0e-61
Match length
                  257
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
                   (ESSA project)
                  169681
Seq. No.
Seq. ID
                  LIB3234-088-Q1-K1-C7
```

Method BLASTN NCBI GI g2924257

BLAST score 70 E value 4.0e-31 Match length 184 % identity 90



```
NCBI Description Tobacco chloroplast genome DNA
                  169682
Seq. No.
Seq. ID
                  LIB3234-088-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q1402914
BLAST score
                   547
E value
                   2.0e-56
Match length
                  108
                   100
% identity
                  (X98318) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169683
                  LIB3234-088-Q1-K1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3395421
BLAST score
                   356
                   0.0e + 00
E value
Match length
                   360
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T19C21 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169684
                   LIB3234-088-Q1-K1-D2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4455168
BLAST score
                   307
E value
                   1.0e-172
Match length
                   355
                   99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                   (ESSAII project)
                   169685
Seq. No.
                   LIB3234-088-Q1-K1-D4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2459406
BLAST score
                   199
E value
                   1.0e-108
                   207
Match length
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   169686
Seq. No.
                   LIB3234-088-Q1-K1-D5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2459406
                   102
BLAST score
                   1.0e-50
E value
Match length
                   122
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic
```

23065

sequence, complete sequence [Arabidopsis thaliana]



Seq. ID LIB3234-088-Q1-K1-D6

Method BLASTX
NCBI GI g4587520
BLAST score 361
E value 2.0e-34
Match length 70
% identity 100

NCBI Description (AC007060) Strong similarity to gb_X71057 protein kinase

from Nicotiana tabacum and contains PF_00069 eukaryotic

protein kinase domain. [Arabidopsis thaliana]

Seq. No. 169688

Seq. ID LIB3234-088-Q1-K1-D8

Method BLASTX
NCBI GI g2347098
BLAST score 331
E value 5.0e-31
Match length 61
% identity 100

NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]

>qi 4490742 emb CAB38904.1 (AL035708) ubiquitin-specific

protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 169689

Seq. ID LIB3234-088-Q1-K1-D9

Method BLASTN
NCBI GI g4519193
BLAST score 362
E value 0.0e+00
Match length 362
% identity 50

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 169690

Seq. ID LIB3234-088-Q1-K1-E1

Method BLASTN
NCBI GI 94467131
BLAST score 285
E value 1.0e-159
Match length 305
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13

(ESSA project)

Seq. No. 169691

Seq. ID LIB3234-088-Q1-K1-E11

Method BLASTX
NCBI GI g529353
BLAST score 204
E value 1.0e-16
Match length 58
% identity 59

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 169692

Seq. ID LIB3234-088-Q1-K1-E12



```
BLASTX
Method
NCBI GI
                  q529353
                  283
BLAST score
                  3.0e-31
E value
Match length
                  96
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                  169693
Seq. No.
                  LIB3234-088-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  q4263753
NCBI GI
BLAST score
                  307
                  1.0e-172
E value
                  383
Match length
% identity
                  95
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  169694
Seq. No.
Seq. ID
                  LIB3234-088-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  g529353
BLAST score
                  330
                  4.0e-31
E value
                  84
Match length
                   64
% identity
NCBI Description
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
Seq. No.
                  169695
                  LIB3234-088-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267073
BLAST score
                  494
                   4.0e-50
E value
                  91
Match length
                  99
% identity
NCBI Description
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  169696
Seq. No.
                  LIB3234-088-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1730512
                  550
BLAST score
                  1.0e-56
E value
Match length
                  119
                   91
% identity
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST
NCBI Description
                   >gi_2129669_pir__S71368 phosphoglycerate kinase -
                  Arabidopsis thaliana (fragment) >gi_1022805 (U37701)
                  phosphoglycerate kinase [Arabidopsis thaliana]
```

23067

169697

LIB3234-088-Q1-K1-F10

Seq. No.

Seq. ID



```
Method
                  BLASTN
                  q2760169
NCBI GI
BLAST score
                  216
                  1.0e-118
E value
Match length
                  232
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFB13, complete sequence [Arabidopsis thaliana]
                  169698
Seq. No.
                  LIB3234-088-Q1-K1-F11
Seq. ID
Method
                  BLASTN
                  q4199934
NCBI GI
                  58
BLAST score
E value
                  7.0e-24
Match length
                  122
% identity
                  87
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  169699
Seq. No.
                  LIB3234-088-Q1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449326
BLAST score
                  301
                  1.0e-169
E value
Match length
                  366
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19M22, complete sequence [Arabidopsis thaliana]
                  169700
Seq. No.
                  LIB3234-088-Q1-K1-F2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2880038
                  180
BLAST score
                  1.0e-96
E value
Match length
                   359
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T11J7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169701
                  LIB3234-088-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1169598
BLAST score
                   305
E value
                   6.0e-28
Match length
                   75
                   76
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
```

Seq. ID LIB3234-088-Q1-K1-F6

Method BLASTX

desaturase [Arabidopsis thaliana]



NCBI GI g544415 BLAST score 341 E value 4.0e-32 Match length 123 % identity 58

NCBI Description GLYCEROL-3-PHOSPHATE DEHYDROGENASE MITOCHONDRIAL PRECURSOR

(GPD-M) (GPDH-M) >gi 627996 pir A54051

glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) precursor - rat >gi_493022 (U08027) glycerolphosphate dehydrogenase [Rattus norvegicus] >gi_603583_emb_CAA55329_(X78593) glycerol-3-phosphate dehydrogenase [Rattus norvegicus]

Seq. No. 169703

Seq. ID LIB3234-088-Q1-K1-F7

Method BLASTN
NCBI GI g4159708
BLAST score 343
E value 0.0e+00
Match length 355
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence

Seq. No. 169704

Seq. ID LIB3234-088-Q1-K1-F8

Method BLASTX
NCBI GI g543841
BLAST score 471
E value 2.0e-47
Match length 91
% identity 100

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875

ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747 gb AAD26597.1 AC007236 2 (AC007236)

ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 169705

Seq. ID LIB3234-088-Q1-K1-F9

Method BLASTN
NCBI GI g2264302
BLAST score 70
E value 5.0e-31
Match length 139
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 169706

Seq. ID LIB3234-088-Q1-K1-G11

Method BLASTX
NCBI GI g4490292
BLAST score 490
E value 1.0e-49
Match length 96
% identity 100

169712



```
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
                   169707
 Seq. No.
                   LIB3234-088-Q1-K1-G12
 Seq. ID
 Method
                   BLASTX
                   g3935152
 NCBI GI
 BLAST score
                   445
                   2.0e-44
 E value
                   107
 Match length
                   72
 % identity
                   (AC005106) T25N20.16 [Arabidopsis thaliana]
 NCBI Description
                   169708
 Seq. No.
                   LIB3234-088-Q1-K1-G2
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g2842474
                   76
 BLAST score
                   3.0e-35
 E value
                   92
 Match length
                    96
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
 NCBI Description
                    (ESSAII project)
                   169709
∞Seq. No.
                   LIB3234-088-Q1-K1-G3
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g3869067
                   56
 BLAST score
                   8.0e-23
 E value
                   210
 Match length
                    91
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCK7, complete sequence [Arabidopsis thaliana]
                   169710
 Seq. No.
 Seq. ID
                   LIB3234-088-Q1-K1-G4
 Method
                   BLASTN
                    g3449327
 NCBI GI
 BLAST score
                    114
                    2.0e-57
 E value
 Match length
                    249
                    93
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
                    169711
 Seq. No.
 Seq. ID
                   LIB3234-088-Q1-K1-G5
 Method
                   BLASTN
 NCBI GI
                    q3449327
 BLAST score
                    92
 E value
                    2.0e-44
 Match length
                    165
 % identity
                    93
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

23070

MCA23, complete sequence [Arabidopsis thaliana]



```
Seq. ID
                  LIB3234-088-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                  g2564050
BLAST score
                  363
                  0.0e+00
E value
Match length
                  371
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUA22, complete sequence [Arabidopsis thaliana]
                  169713
Seq. No.
Seq. ID
                  LIB3234-088-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q913631
BLAST score
                  158
                  1.0e-10
E value
                  88
Match length
% identity
                  39
                  class-3 aldehyde dehydrogenase, class-3 ALDH
NCBI Description
                  [Synechococcus, PCC7942, Peptide, 459 aa]
                  >qi 2351120 dbj BAA22052 (D32049) Aldehyde dehydrogenase
                   [Synechococcus PCC7942] >gi 1092933 prf 2102241A aldehyde
                  dehydrogenase [Synechococcus sp.]
Seq. No.
                  169714
                  LIB3234-088-Q1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4376087
                  66
BLAST score
E value
                  5.0e-29
Match length
                  109
                  91
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  169715
Seq. ID
                  LIB3234-088-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2924512
BLAST score
                  638
                  5.0e-67
E value
Match length
                  121
                  98
% identity
                  (AL022023) beta-galactosidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  169716
Seq. ID
                  LIB3234-088-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q4586594
BLAST score
                  494
                  4.0e-50
E value
Match length
                  102
```

% identity

NCBI Description

75

(AB025001) polyubiquitin [Cicer arietinum]

Seq. ID

Method



Seq. ID LIB3234-088-Q1-K1-H12 Method BLASTN NCBI GI g870791 BLAST score 69 - E value 1.0e-30 Match length 216 58 % identity Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete NCBI Description Seq. No. 169718 Seq. ID LIB3234-088-Q1-K1-H2 Method BLASTX NCBI GI q21913 BLAST score 176 5.0e-13 E value Match length 87 % identity NCBI Description (X62626) vicilin [Theobroma cacao] Seq. No. 169719 LIB3234-088-Q1-K1-H3 Seq. ID Method BLASTN NCBI GI g2182287 BLAST score 107 3.0e-53E value Match length 298 85 % identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana] Seq. No. 169720 LIB3234-088-Q1-K1-H4 Seq. ID Method BLASTX NCBI GI g4469408 BLAST score 296 7.0e-27 E value Match length 115 % identity 55 NCBI Description (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] >gi 4469410 gb AAD21249 (AF116528) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] Seq. No. 169721 Seq. ID LIB3234-088-Q1-K1-H5 Method BLASTN NCBI GI g870791 BLAST score 61 E value 8.0e-26 Match length 69 52 % identity Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete NCBI Description 169722 Seq. No.

23072

LIB3234-088-Q1-K1-H6

BLASTN

Match length

% identity

371 99



```
NCBI GI
                  g2764733
BLAST score
                  251
                  1.0e-139
E value
Match length
                  251
% identity
                  100
NCBI Description Arabidopsis thaliana plastid ndhB gene, exon
Seq. No.
                  169723
                  LIB3234-088-Q1-K1-H7
Seq. ID
                  BLASTN
Method
                  g4757407
NCBI GI
BLAST score
                  61
E value
                  9.0e-26
                  93
Match length
                  91
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQD19, complete sequence
Seq. No.
                  169724
                  LIB3234-088-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191185
BLAST score
                  501
E value
                  6.0e-51
                  103
Match length
% identity
                  99
                  (AF007271) A TM021B04.6 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  169725
Seq. ID
                  LIB3234-089-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q2924257
BLAST score
                  49
E value
                  7.0e-19
Match length
                  65
% identity
                  94
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  169726
                  LIB3234-089-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3402747
BLAST score
                  335
E value
                  0.0e + 00
Match length
                  362
                  98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22
                   (ESSAII project)
Seq. No.
                  169727
Seq. ID
                  LIB3234-089-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g4757415
BLAST score
                  359
E value
                  0.0e + 00
```



```
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYN21, complete sequence
                  169728
Seq. No.
                  LIB3234-089-P1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1778141
                  302
BLAST score
                  1.0e-27
E value
                  83
Match length
                  76
% identity
                  (U66321) phosphate/phosphoenolpyruvate translocator
NCBI Description
                  precursor; PPT [Arabidopsis thaliana]
                  169729
Seq. No.
                  LIB3234-089-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g4586249
NCBI GI
BLAST score
                  341
                  4.0e-32
E value
Match length
                  114
% identity
                  57
                  (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                  thaliana]
                  169730
Seq. No.
                  LIB3234-089-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262250
BLAST score
                  618
                  1.0e-64
E value
Match length
                  121
                   98
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                  169731
Seq. No.
                  LIB3234-089-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                   597
                   3.0e-62
E value
Match length
                  118
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                  169732
Seq. No.
```

LIB3234-089-P1-K1-A6 Seq. ID

Method BLASTX NCBI GI g3128199 BLAST score 180 3.0e-13 E value 73 Match length % identity 53

(AC004521) putative proteinase [Arabidopsis thaliana] NCBI Description

169733 Seq. No.

LIB3234-089-P1-K1-A7 Seq. ID



Method BLASTX
NCBI GI g112682
BLAST score 341
E value 4.0e-32
Match length 97
% identity 71

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 169734

Seq. ID LIB3234-089-P1-K1-A8

Method BLASTX
NCBI GI g99992
BLAST score 326
E value 2.0e-30
Match length 88
% identity 42

NCBI Description protein disulfide-isomerase (EC 5.3.4.1) precursor -

alfalfa (clone B2) >gi_166418 (M82973) putative endomembrane protein; putative [Medicago sativa]

Seq. No. 169735

Seq. ID LIB3234-089-P1-K1-A9

Method BLASTN
NCBI GI g3449314
BLAST score 20
E value 3.0e-01
Match length 177
% identity 49

% identity 49
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22F20, complete sequence [Arabidopsis thaliana]

Seq. No. 169736

Seq. ID LIB3234-089-P1-K1-B1

Method BLASTN
NCBI GI g2673901
BLAST score 312
E value 1.0e-175
Match length 364
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169737

Seq. ID LIB3234-089-P1-K1-B10

Method BLASTX
NCBI GI g1402904
BLAST score 579
E value 5.0e-60
Match length 115
% identity 97

NCBI Description (X98313) peroxidase [Arabidopsis thaliana]

Seq. No. 169738



Seq. ID LIB3234-089-P1-K1-B11

Method BLASTX
NCBI GI g128838
BLAST score 126
E value 4.0e-47
Match length 120
% identity 77

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE 49 KD SUBUNIT, CHLOROPLAST (ORF 393) >gi 82215 pir A05216 NADH

dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 393 - common tobacco chloroplast >gi 1223674 emb CAA77398 (Z00044) NADH

dehydrogenase 49kD subunit [Nicotiana tabacum]

>gi 225262 prf 1211235CX ORF 393 [Nicotiana tabacum]

Seq. No. 169739

Seq. ID LIB3234-089-P1-K1-B12

Method BLASTX
NCBI GI g3980380
BLAST score 461
E value 2.0e-46
Match length 94
% identity 100

NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]

Seq. No. 169740

Seq. ID LIB3234-089-P1-K1-B2

Method BLASTX
NCBI GI g76189
BLAST score 163
E value 3.0e-11
Match length 98
% identity 41

NCBI Description hypothetical 17K protein (bioA 3' region) - Escherichia

coli >gi_455168 (J04423) ORF 1 [Escherichia coli]

Seq. No. 169741

Seq. ID LIB3234-089-P1-K1-B4

Method BLASTN
NCBI GI g1313927
BLAST score 57
E value 3.0e-23
Match length 251
% identity 81

NCBI Description B.oleracea mRNA for IFA binding protein (sp10)

Seq. No. 169742

Seq. ID LIB3234-089-P1-K1-B5

Method BLASTN
NCBI GI g1313927
BLAST score 57
E value 3.0e-23
Match length 251
% identity 81

NCBI Description B.oleracea mRNA for IFA binding protein (sp10)

Seq. No. 169743

Seq. ID LIB3234-089-P1-K1-B6



Method BLASTX
NCBI GI g2760606
BLAST score 168
E value 1.0e-38
Match length 123
% identity 62

NCBI Description (AB001568) phospholipid hydroperoxide glutathione

peroxidase-like protein [Arabidopsis thaliana] >gi 3004869

(AF030132) glutathione peroxidase; ATGP1 [Arabidopsis

thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase

[Arabidopsis thaliana]

Seq. No. 169744

Seq. ID LIB3234-089-P1-K1-B8

Method BLASTN
NCBI GI g1402935
BLAST score 64
E value 2.0e-27

E value 2.0e
Match length 121
% identity 85

NCBI Description A.thaliana genomic DNA fragment (ecotype MARBURG-0)

Seq. No. 169745

Seq. ID LIB3234-089-P1-K1-C1

Method BLASTX
NCBI GI g266693
BLAST score 282
E value 2.0e-25
Match length 89
% identity 73

NCBI Description OLEOSIN >gi 282875 pir S22538 oleosin - Arabidopsis

thaliana >gi 16405_emb CAA44225 (X62353) oleosin [Arabidopsis thaliana] >gi 4455257_emb CAB36756.1 (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 169746

Seq. ID LIB3234-089-P1-K1-C10

Method BLASTX
NCBI GI g131150
BLAST score 516
E value 1.0e-52
Match length 106
% identity 92

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2

>gi_81515_pir__S00445 photosystem I protein A2 - spinach
chloroplast >gi_12271_emb_CAA27745_ (X04131) psaB gene
product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia
oleracea] >gi_225422_prf__1303218B gene psaB [Spinacia

oleracea]

Seq. No. 169747

Seq. ID LIB3234-089-P1-K1-C11

Method BLASTN
NCBI GI g4581138
BLAST score 33
E value 3.0e-09



73 Match length % identity Arabidopsis thaliana chromosome II BAC F1011 genomic NCBI Description sequence, complete sequence 169748 Seq. No. Seq. ID LIB3234-089-P1-K1-C12 Method BLASTN q4585952 NCBI GI 156 BLAST score 1.0e-82 E value 160 Match length % identity 99 Genomic sequence for Arabidopsis thaliana BAC F26F24, NCBI Description complete sequence 169749 Seq. No. LIB3234-089-P1-K1-C2 Seq. ID Method BLASTX q4512615 NCBI GI 422 BLAST score E value 8.0e-42 98 Match length 86 % identity (AC004793) Strong similarity to gb X59970 3-isopropylmalate NCBI Description dehydrogenase (IMDH) from Brassica napus. EST gb F14478 comes from this gene. [Arabidopsis thaliana] Seq. No. 169750 Seq. ID LIB3234-089-P1-K1-C4 BLASTX Method NCBI GI q16245 BLAST score 163 1.0e-11 E value Match length 76 49 % identity (X51514) precursor acetolactate synthase (670 AA) NCBI Description [Arabidopsis thaliana]

169751 Seq. No.

LIB3234-089-P1-K1-C6 Seq. ID

Method BLASTX q399091 NCBI GI 410 BLAST score 2.0e-40 E value 91 Match length 91 % identity

PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP NCBI Description (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi 282878_pir__A38230 inorganic pyrophosphatase

(EC 3.6.1.1), H+-translocating pyrophosphate-energized -

Arabidopsis thaliana >gi_166634 (M81892) vacuolar

H+-phosphatase [Arabidopsis thaliana]

169752 Seq. No.

LIB3234-089-P1-K1-D1 Seq. ID

Method BLASTN

NCBI Description

thaliana]



```
NCBI GI
                   q4159699
BLAST score
                   337
                   0.0e + 00
E value
Match length
                   362
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K16E1, complete sequence
                   169753
Seq. No.
                   LIB3234-089-P1-K1-D10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3810584
BLAST score
                   40
                   4.0e-13
E value
                   40
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC T6B13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169754
Seq. No.
                   LIB3234-089-P1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1345973
BLAST score
                   431
                   1.0e-42
E value
                   97
Match length
                   81
% identity
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                    [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
                   169755
Seq. No.
                   LIB3234-089-P1-K1-D2
Seq. ID
                   BLASTX
Method
                   g3869088
NCBI GI
                   542
BLAST score
                   1.0e-55
E value
                   105
Match length
                    99
% identity
                   (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                   169756
Seq. No.
                   LIB3234-089-P1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2462746
                    287
BLAST score
                    8.0e-26
E value
Match length
                    65
                    88
% identity
```

(AC002292) Similar to ATP-citrate-lyase [Arabidopsis

NCBI Description

Seq. No.

169762



```
169757
Seq. No.
                  LIB3234-089-P1-K1-D5
Seq. ID
                  BLASTX
Method
                  q129868
NCBI GI
                  303
BLAST score
E value
                   5.0e-28
Match length
                  72
% identity
                  85
                  CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)
NCBI Description
                  >gi_100816_pir__S14962 plastoquinol--plastocyanin reductase
                   (EC 1.10.99.1) 17K protein - wheat chloroplast
                  >gi 12364 emb CAA38552 (X54751) subunit IV of cytochrome
                  bf complex [Triticum aestivum]
Seq. No.
                  169758
                  LIB3234-089-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2828180
BLAST score
                   337
                   0.0e + 00
E value
Match length
                   368
                   98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169759
Seq. ID
                   LIB3234-089-P1-K1-D8
Method
                   BLASTX
                   g1800281
NCBI GI
BLAST score
                   492
                   7.0e-50
E value
Match length
                   104
% identity
                   19
                  (U82086) polyubiquitin [Fragaria x ananassa]
NCBI Description
                   169760
Seq. No.
Seq. ID
                   LIB3234-089-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1724100
                   359
BLAST score
                   3.0e - 34
E value
Match length
                   96
                   72
% identity
                  (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
                   169761
Seq. No.
                   LIB3234-089-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1698582
BLAST score
                   245
                   7.0e-21
E value
Match length
                   112
% identity
```

23080

(U60767) integral membrane protein OsNramp3 [Oryza sativa]



```
LIB3234-089-P1-K1-E12
Seq. ID
Method
                BLASTN
NCBI GI
                  q3860243
BLAST score
                  301
E value
                  1.0e-169
                  379
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169763
Seq. No.
                  LIB3234-089-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  q3668087
NCBI GI
                  283
BLAST score
                  2.0e-25
E value
Match length
                  74
% identity
                  21
NCBI Description
                  (AC004667) hypothetical protein [Arabidopsis thaliana]
                  169764
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-E3
Method
                  BLASTN
                  q3176695
NCBI GI
                 . 140
BLAST score
                  5.0e-73
E value
                  260
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F14J9 genomic
NCBI Description
                  sequence contains phyA marker, complete sequence
                  [Arabidopsis thaliana]
Seq. No.
                  169765
Seq. ID
                  LIB3234-089-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g3059018
BLAST score
                  272
                  1.0e-151
E value
Match length
                  335
% identity
                  95
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
NCBI Description
                   (ESSAII project)
                  169766
Seq. No.
                  LIB3234-089-P1-K1-E5
Seq. ID
Method
                  BLASTN
                  g3059018
NCBI GI
                  277
BLAST score
E value
                  1.0e-154
                   336
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
                  (ESSAII project)
```

Seq. No. 169767

Seq. ID LIB3234-089-P1-K1-E6

Method BLASTX

NCBI GI BLAST score



```
NCBI GI
                  g1350965
BLAST score
                  518
                  7.0e-53
E value
                  100
Match length
                  98
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12)
                  169768
Seq. No.
                  LIB3234-089-P1-K1-E8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3695386
                  251
BLAST score
                  1.0e-139
E value
                  326
Match length
                  94
% identity
NCBI Description Arabidopsis thaliana BAC T2L5
                  169769
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  q4432829
BLAST score
                  68
E value
                  4.0e-30
                  159
Match length
                  86
% identity
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169770
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-F10
                  BLASTX
Method
                  q1109699
NCBI GI
BLAST score
                   604
                   6.0e-63
E value
Match length
                  125
% identity
                  (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169771
                  LIB3234-089-P1-K1-F11
Seq. ID
Method
                   BLASTX
                   q3157937
NCBI GI
                   540
BLAST score
                   2.0e-55
E value
Match length
                   122
% identity
                   84
                  (AC002131) Identical to aspartic proteinase cDNA gb_U51036
NCBI Description
                   from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                   gb T21482, gb T43650, gb R64749, gb R65157, gb T88269,
                   gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591,
                   gb AA728734, gb
                   169772
Seq. No.
                   LIB3234-089-P1-K1-F12
Seq. ID
                   BLASTN
Method
```

23082

g3510345



```
3.0e-59
E value
                  188
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ8, complete sequence [Arabidopsis thaliana]
                  169773
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-F2
                  BLASTN
Method
NCBI GI
                  q4756963
BLAST score
                  223
                  1.0e-122
E value
                  344
Match length
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                  (ESSA project)
                  169774
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-F3
Method
                  BLASTX
                  g4263722
NCBI GI
BLAST score
                  456
                  1.0e-45
E value
                  99
Match length
                  92
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                  169775
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-F4
Method
                  BLASTX
                  g2262167
NCBI GI
BLAST score
                  222
                  2.0e-18
E value
Match length
                  71
% identity
                  68
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  169776
Seq. ID
                  LIB3234-089-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2443329
BLAST score
                  266
                  2.0e-23
E value
                  94
Match length
% identity
                   64
                  (D86122) Mei2-like protein [Arabidopsis thaliana]
NCBI Description
                  169777
Seq. No.
                  LIB3234-089-P1-K1-F7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3402695
BLAST score
                  262
E value
                  1.0e-145
                  321
Match length
                   92
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic
```

Seq. No.



```
sequence, complete sequence [Arabidopsis thaliana]
```

```
169778
Seq. No.
                  LIB3234-089-P1-K1-F8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4756963
                  56
BLAST score
                  8.0e-23
E value
Match length
                  79
                  94
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                  (ESSA project)
                  169779
Seq. No.
Seq. ID
                  LIB3234-089-P1-K1-G1
                  BLASTX
Method
                  g1168258
NCBI GI
BLAST score
                  501
                  6.0e-51
E value
Match length
                  118
                  84
% identity
                  ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (TRANSAMINASE A) >gi 693692 (U15034) aspartate
                  aminotransferase [Arabidopsis thaliana]
                  169780
Seq. No.
                  LIB3234-089-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4063552
BLAST score
                   609
                   1.0e-63
E value
                  125
Match length
                   98
% identity
                  (AF035908) ATP synthase beta subunit [Muntingia calabura]
NCBI Description
                   169781
Seq. No.
                  LIB3234-089-P1-K1-G12
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3510339
BLAST score
                   154
                   4.0e-81
E value
Match length
                   331
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   169782
Seq. No.
                   LIB3234-089-P1-K1-G2
Seq. ID
                   BLASTN
Method
                   g2098816
NCBI GI
                   273
BLAST score
                   1.0e-152
E value
                   348
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
                   169783
```

Seq. ID

Method



```
LIB3234-089-P1-K1-G4
Seq. ID
                  BLASTN
Method
                  g3063438
NCBI GI
BLAST score
                  324
                  0.0e+00
E value
                  363
Match length
                  76
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                   169784
Seq. No.
                  LIB3234-089-P1-K1-G5
Seq. ID
                  BLASTN
Method
                   g3063438
NCBI GI
                   339
BLAST score
                   0.0e+00
E value
                   363
Match length
                   77
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                   169785
Seq. No.
Seq. ID
                   LIB3234-089-P1-K1-G6
                   BLASTN
Method
                   g3510339
NCBI GI
                   33
BLAST score
                   3.0e-09
E value
                   49
Match length
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   169786
Seq. No.
                   LIB3234-089-P1-K1-G7
Seq. ID
Method
                   BLASTX
                   g4204298
NCBI GI
                   517
BLAST score
                   8.0e-53
E value
                   99
Match length
% identity
                   99
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   169787
Seq. ID
                   LIB3234-089-P1-K1-G8
Method
                   BLASTN
NCBI GI
                   g4585891
BLAST score
                   341
                   0.0e+00
E value
Match length
                   353
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC T103 genomic
NCBI Description
                   sequence, complete sequence
                   169788
Seq. No.
```

23085

LIB3234-089-P1-K1-G9

BLASTX

E value

Match length % identity



```
g1345973
NCBI GI
BLAST score
                  656
                   4.0e-69
E value
Match length
                  122
% identity
                   98
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >qi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
                   169789
Seq. No.
Seq. ID
                   LIB3234-089-P1-K1-H1
                   BLASTX
Method
NCBI GI
                   q4249382
                   96
BLAST score
                   5.0e-42
E value
                   120
Match length
                   76
% identity
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   169790
Seq. No.
Seq. ID
                   LIB3234-089-P1-K1-H10
Method
                   BLASTN
                   q3319359
NCBI GI
BLAST score
                   288
                   1.0e-161
E value
Match length
                   381
                   92
% identity
NCBI Description Arabidopsis thaliana BAC T7M24
                   169791
Seq. No.
Seq. ID
                   LIB3234-089-P1-K1-H12
Method
                   BLASTX
                   q4249382
NCBI GI
                   412
BLAST score
                   2.0e-40
E value
Match length
                   91
                   84
% identity
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb_AC004481. [Arabidopsis thaliana]
                   169792
Seq. No.
                   LIB3234-089-P1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3334124
BLAST score
                   448
```

23086

1.0e-44

105



NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

 Seq. No.
 169793

 Seq. ID
 LIB3234-089-P1-K1-H3

 Method
 BLASTX

Method BLASTX
NCBI GI g2894574
BLAST score 521
E value 3.0e-53
Match length 105
% identity 97

NCBI Description (AL021890) peroxidase prxrl [Arabidopsis thaliana]

>gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No. 169794

Seq. ID LIB3234-089-P1-K1-H4

Method BLASTN
NCBI GI g3319359
BLAST score 111
E value 1.0e-55
Match length 202
% identity 91

NCBI Description Arabidopsis thaliana BAC T7M24

Seq. No. 169795

Seq. ID LIB3234-089-P1-K1-H6

Method BLASTX
NCBI GI g66179
BLAST score 575
E value 1.0e-59
Match length 125
% identity 87

NCBI Description NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -

common tobacco chloroplast >gi 225255_prf__1211235CP NADH

dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. No. 169796

Seq. ID LIB3234-089-P1-K1-H7

Method BLASTX
NCBI GI g2498731
BLAST score 208
E value 1.0e-16
Match length 77
% identity 56

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog -

Arabidopsis thaliana >gi 886428 emb CAA89838 (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 169797

Seq. ID LIB3234-089-P1-K1-H8

Method BLASTN
NCBI GI g3128143
BLAST score 350



```
0.0e + 00
E value
Match length
                  370
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTI20, complete sequence [Arabidopsis thaliana]
                  169798
Seq. No.
                  LIB3234-089-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g1170939
NCBI GI
                  442
BLAST score
                  5.0e-44
E value
                  90
Match length
                  92
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi 1084408 pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi 429108 emb CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  169799
Seq. No.
                  LIB3234-090-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  g1170619
NCBI GI
                   197
BLAST score
                   2.0e-26
E value
                  77
Match length
% identity
                   90
                  KINESIN-LIKE PROTEIN A >gi 479594 pir S34830
NCBI Description
                   kinesin-related protein katA - Arabidopsis thaliana
                   >gi_303502 dbj_BAA01972 (D11371) kinesin-like motor
                   protein heavy chain [Arabidopsis thaliana]
                   >gi 2911084 emb CAA17546.1_ (AL021960) kinesin-related
                   protein katA [Arabidopsis thaliana]
                   169800
Seq. No.
                   LIB3234-090-P1-K1-A11
Seq. ID
Method
                   BLASTN
                   g4388714
NCBI GI
                   249
BLAST score
                   1.0e-138
E value
                   374
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F5K7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169801
Seq. No.
                   LIB3234-090-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   g2851508
NCBI GI
BLAST score
                   624
                   2.0e-65
E value
Match length
                   118
                   100
% identity
                   60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
NCBI Description
```

ribosomal protein L21 (gb_L38826). ESTs



gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

```
169802
Seq. No.
                  LIB3234-090-P1-K1-A3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2244747
                  51
BLAST score
                  6.0e-20
E value
                  103
Match length
                  87
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  169803
Seq. No.
                  LIB3234-090-P1-K1-A5
Seq. ID
                  BLASTN
Method
NCBI GI
                   q2342717
                   82
BLAST score
                   6.0e-39
E value
                   82
Match length
                   62
% identity
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169804
Seq. No.
                   LIB3234-090-P1-K1-A6
Seq. ID
Method
                   BLASTX
                   g3421102
NCBI GI
BLAST score
                   464
                   1.0e-46
E value
                   87
Match length
                   100
% identity
                   (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
NCBI Description
                   thaliana]
                   169805
Seq. No.
                   LIB3234-090-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   g1531762
NCBI GI
                   .
195
BLAST score
                   5.0e-15
E value
                   51
Match length
                   75
 % identity
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   169806
 Seq. No.
                   LIB3234-090-P1-K1-A9
 Seq. ID
                   BLASTX
 Method
                   q461903
 NCBI GI
                   501
 BLAST score
                   6.0e-51
 E value
                   106
 Match length
                   89
 % identity
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
```



(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_405129 (L14844) cyclophilin [Arabidopsis thaliana] >gi_4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl isomerase ROC1 [Arabidopsis thaliana]

Seq. No. 169807

Seq. ID LIB3234-090-P1-K1-B1

Method BLASTN
NCBI GI g4199934
BLAST score 281
E value 1.0e-157
Match length 346
% identity 92

% identity 92 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 169808

Seq. ID LIB3234-090-P1-K1-B10

Method BLASTN
NCBI GI g4753195
BLAST score 71

E value 1.0e-31 Match length 184 % identity 84

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 169809

Seq. ID LIB3234-090-P1-K1-B11

Method BLASTX
NCBI GI g99749
BLAST score 547
E value 3.0e-56
Match length 119
% identity 90

NCBI Description probable serine/threonine-specific protein kinase ATPK64

(EC 2.7.1.-) - Arabidopsis thaliana

>gi_217843_dbj_BAA01731_ (D10937) protein kinase

[Arabidopsis thaliana]

Seq. No. 169810

Seq. ID LIB3234-090-P1-K1-B12

Method BLASTN
NCBI GI g4159707
BLAST score 151
E value 2.0e-79
Match length 324
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJK13, complete sequence

Seq. No. 169811

Seq. ID LIB3234-090-P1-K1-B4

Method BLASTX
NCBI GI g4415920
BLAST score 507
E value 2.0e-51



```
115
Match length
% identity
                  90
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  169812
Seq. No.
                  LIB3234-090-P1-K1-B6
Seq. ID
                  BLASTN
Method
                  q3355463
NCBI GI
                  378
BLAST score
                  0.0e + 00
E value
                  378
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169813
                   LIB3234-090-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2982452
                   337
BLAST score
E value
                   1.0e-31
                   122
Match length
% identity
                   (AL022223) receptor protein kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   169814
Seq. No.
                   LIB3234-090-P1-K1-B8
Seq. ID
                   BLASTX
Method
                   g3170525
NCBI GI
BLAST score
                   541
                   1.0e-55
E value
                   120
Match length
                   84
% identity
NCBI Description (AF054615) cellulase [Fragaria x ananassa]
                   169815
Seq. No.
                   LIB3234-090-P1-K1-B9
Seq. ID
                   BLASTX
Method
                   g140285
NCBI GI
                   199
BLAST score
                   2.0e-15
E value
Match length
                   62
                   69
% identity
                   HYPOTHETICAL 19 KD PROTEIN (ORF 168)
NCBI Description
                   >gi 2924263 emb CAA77415 (Z00044) Ycf3 protein [Nicotiana
                   tabacum]
                   169816
 Seq. No.
                   LIB3234-090-P1-K1-C10
Seq. ID
                   BLASTX
Method
                   q4455223
NCBI GI
 BLAST score
                   223
                   3.0e-18
 E value
 Match length
                   79
```

57

% identity



```
(AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  169817
Seq. No.
Seq. ID
                  LIB3234-090-P1-K1-C12
                  BLASTX
Method
                  g1002803
NCBI GI
BLAST score
                  398
                  8.0e-39
E value
                  95
Match length
% identity
                  (U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]
NCBI Description
                  169818
Seq. No.
Seq. ID
                  LIB3234-090-P1-K1-C5
                   BLASTN
Method
NCBI GI
                   q4557061
BLAST score
                   141
                   2.0e-73
E value
                   177
Match length
                   38
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F23M2 genomic
                   sequence, complete sequence
                   169819
Seq. No.
Seq. ID
                   LIB3234-090-P1-K1-C8
                   BLASTX
Method
                   q1109699
NCBI GI
BLAST score
                   526
                   8.0e-54
E value
                   100
Match length
                   100
% identity
                   (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169820
                   LIB3234-090-P1-K1-D1
Seq. ID
                   BLASTN
Method
                   g4220641
NCBI GI
BLAST score
                   38
E value
                   1.0e-12
Match length
                   67
 % identity
                   83
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUL3, complete sequence [Arabidopsis thaliana]
                   169821
 Seq. No.
                   LIB3234-090-P1-K1-D10
 Seq. ID
                   BLASTX
 Method
                   g4454480
 NCBI GI
                   299
 BLAST score
                   3.0e-27
 E value
                   85
 Match length
                   59
 % identity
                   (AC006234) putative (1-4)-beta-mannan endohydrolase
 NCBI Description
                   [Arabidopsis thaliana]
```

169822

Seq. No.



```
LIB3234-090-P1-K1-D11
Seq. ID
                  BLASTN
Method
                  g4662640
NCBI GI
                  355
BLAST score
                  0.0e+00
E value
                  370
Match length
                  51
% identity
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
NCBI Description
                  sequence, complete sequence
                  169823
Seq. No.
                  LIB3234-090-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  q544424
NCBI GI
                  434
BLAST score
                  4.0e-43
E value
                  85
Match length
                   99
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi 16301_emb_CAA78711_ (Z14987) glycine rich protein
                   [Arabidopsis Thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   169824
                   LIB3234-090-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g3273743
NCBI GI
                   611
BLAST score
                   8.0e-64
E value
                   116
Match length
                   100
% identity
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                   thaliana] >gi_3786019 (AC005499) unknown protein
                   [Arabidopsis Thaliana]
                   169825
Seq. No.
Seq. ID
                   LIB3234-090-P1-K1-D4
                   BLASTX
Method
                   g1490554
NCBI GI
                   547
BLAST score
                   3.0e-56
E value
                   124
Match length
 % identity
                   (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   169826
 Seq. No.
                   LIB3234-090-P1-K1-D5
 Seq. ID
                   BLASTN
 Method
                   q3869074
 NCBI GI
 BLAST score
                   154
                   3.0e-81
 E value
 Match length
                   258
```

99

% identity



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMI9, complete sequence [Arabidopsis thaliana]
                  169827
Seq. No.
                  LIB3234-090-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  q1142594
NCBI GI
BLAST score
                  217
                  1.0e-17
E value
                  43
Match length
                  98
% identity
                 (U13703) ATP synthase CF-0 subunit I [Brassica oleracea]
NCBI Description
                  169828
Seq. No.
                  LIB3234-090-P1-K1-D7
Seq. ID
                  BLASTN
Method
                  q4699904
NCBI GI
BLAST score
                   132
                   2.0e-68
E value
Match length
                   136
                   64
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F1E22,
NCBI Description
                   complete sequence
                   169829
Seq. No.
Seq. ID
                   LIB3234-090-P1-K1-E10
                   BLASTX
Method
                   g140299
NCBI GI
BLAST score
                   270
                   8.0e-24
E value
                   124
Match length
                   50
% identity
                   CYTOCHROME C BIOGENESIS PROTEIN CCSA >gi_82213_pir__A05213
NCBI Description
                   hypothetical protein 313 - common tobacco chloroplast
                   >qi 1223666 emb CAA77395_ (Z00044) c-type cytochrome
                   synthesis protein [Nicotiana tabacum]
                   >gi 225254_prf__1211235CN ORF 313 [Nicotiana tabacum]
Seq. No.
                   169830
                   LIB3234-090-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   q4006827
NCBI GI
                   428
BLAST score
                   2.0e-42
E value
Match length
                   125
 % identity
                   67
                   (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   169831
 Seq. No.
                   LIB3234-090-P1-K1-E12
 Seq. ID
                   BLASTX
 Method
                   g1345944
 NCBI GI
                   279
 BLAST score
                   7.0e-25
 E value
                   69
 Match length
                   78
 % identity
 NCBI Description 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR
```



(BETA-KETOACYL-ACP SYNTHASE III) (KAS III) >gi_598075 (L31891) 3-ketoacyl-acyl carrier protein synthase III (KAS III) [Arabidopsis thaliana]

 Seq. No.
 169832

 Seq. ID
 LIB3234-090-P1-K1-E2

 Method
 BLASTX

Method BLASTX
NCBI GI g135858
BLAST score 292
E value 2.0e-26
Match length 57
% identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 169833

Seq. ID LIB3234-090-P1-K1-E5

Method BLASTX
NCBI GI g2789434
BLAST score 146
E value 3.0e-09
Match length 98
% identity 30

NCBI Description (AB001389) CLB1 [Lycopersicon esculentum]

Seq. No. 169834

Seq. ID LIB3234-090-P1-K1-E6

Method BLASTX
NCBI GI g2129642
BLAST score 640
E value 3.0e-67
Match length 117
% identity 99

NCBI Description major latex protein type 3 - Arabidopsis thaliana

>gi_1107495_emb_CAA63027_ (X91961) major latex protein

type3 [Arabidopsis thaliana]

Seq. No. 169835

Seq. ID LIB3234-090-P1-K1-E7

Method BLASTX
NCBI GI g3643602
BLAST score 477
E value 4.0e-48
Match length 88
% identity 100

NCBI Description (AC005395) putative tonoplast intrinsic protein

[Arabidopsis thaliana]

Seq. No. 169836

Seq. ID LIB3234-090-P1-K1-F1

Method BLASTX NCBI GI g114661

Seq. ID



```
599
BLAST score
                  2.0e-62
E value
                  123
Match length
                  93
% identity
                  ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV)
NCBI Description
                  >gi 67924_pir _LWNT6 H+-transporting ATP synthase (EC
                  3.6.1.34) chain a - common tobacco chloroplast
                  >gi_11813_emb_CAA77344_ (Z00044) ATPase sunthase IV subunit
                   [Nicotiana tabacum] >gi 225273 prf 1211235H ATPase a
                   [Nicotiana tabacum]
                   169837
Seq. No.
                  LIB3234-090-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  g4741196
NCBI GI
                   390
BLAST score
                   7.0e-38
E value
                   125
Match length
                   70
% identity
                   (AL049746) ABC-type transport-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   169838
Seq. No.
                   LIB3234-090-P1-K1-F2
Seq. ID
                   BLASTN
Method
                   g3894179
NCBI GI
                   203
BLAST score
                   1.0e-110
E value
                   323
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F13H10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169839
Seq. No.
                   LIB3234-090-P1-K1-F3
Seq. ID
                   BLASTN
Method
                   g4757403
NCBI GI
BLAST score
                   262
                   1.0e-145
 E value
 Match length
                   379
                   100
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MJL12, complete sequence
                   169840
 Seq. No.
                   LIB3234-090-P1-K1-F5
 Seq. ID
                   BLASTN
 Method
                   g2564051
 NCBI GI
                   155
 BLAST score
                   6.0e-82
 E value
 Match length
                   232
                   90
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MWD9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   169841
```

LIB3234-090-P1-K1-F6

Method



```
BLASTN
Method
                  g4741184
NCBI GI
                  44
BLAST score
                  2.0e-15
E value
                  89
Match length
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7
NCBI Description
                   (ESSA project)
                  169842
Seq. No.
                  LIB3234-090-P1-K1-F7
Seq. ID
                  BLASTN
Method
                   g2618599
NCBI GI
                   366
BLAST score
                   0.0e+00
E value
                   378
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBD2, complete sequence [Arabidopsis thaliana]
                   169843
Seq. No.
                   LIB3234-090-P1-K1-F9
Seq. ID
                   BLASTX
Method
                   g728868
NCBI GI
                   155
BLAST score
                   2.0e-10
E value
                   75
Match length
                   43
% identity
                   ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                   >gi_99824_pir__S16748 proline-rich protein - rape
                   (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                   protein [Brassica napus]
                   169844
Seq. No.
                   LIB3234-090-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   q4581146
NCBI GI
                   415
BLAST score
                   6.0e-41
E value
                   85
Match length
                   99
 % identity
                   (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                   cytoplasmic [Arabidopsis thaliana]
                   169845
 Seq. No.
Seq. ID
                   LIB3234-090-P1-K1-G11
Method
                   BLASTX
                   g1864017
 NCBI GI
                   578
 BLAST score
                   6.0e-60
 E value
 Match length
                   110
                   100
 % identity
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
 NCBI Description
                   169846
 Seq. No.
                   LIB3234-090-P1-K1-G12
 Seq. ID
```

23097

BLASTN



```
q4519194
NCBI GI
                  301
BLAST score
                  1.0e-169
E value
                  378
Match length
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                  169847
Seq. No.
                  LIB3234-090-P1-K1-G3
Seq. ID
                  BLASTN
Method
                  g1495254
NCBI GI
                  175
BLAST score
                  1.0e-93
E value
                   212
Match length
                   100
% identity
NCBI Description A.thaliana mRNA for unknown protein, ORF02
                   169848
Seq. No.
                   LIB3234-090-P1-K1-G4
Seq. ID
                   BLASTN
Method
                   g3746057
NCBI GI
                   356
BLAST score
                   0.0e+00
E value
                   381
Match length
                   98
% identity
                   Arabidopsis thaliana chromosome II BAC T16B12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169849
Seq. No.
                   LIB3234-090-P1-K1-G5
Seq. ID
                   BLASTN
Method
                   a4191760
NCBI GI
                   383
BLAST score
                   0.0e + 00
E value
                   383
Match length
                   100
 % identity
                   Genomic sequence for Arabidopsis thaliana BAC F17F8,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169850
 Seq. No.
                   LIB3234-090-P1-K1-G6
 Seq. ID
                   BLASTN
Method
                   g3449333
 NCBI GI
 BLAST score
                   371
                   0.0e+00
 E value
                   387
 Match length
                    35
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MXF12, complete sequence [Arabidopsis thaliana]
                    169851
 Seq. No.
                   LIB3234-090-P1-K1-H10
 Seq. ID
                    BLASTX
 Method
                    q4559384
 NCBI GI
```

215

2.0e-17

BLAST score

E value



```
Match length
% identity
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                  169852
Seq. No.
                  LIB3234-090-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g3212877
NCBI GI
                  527
BLAST score
                  6.0e-54
E value
                  120
Match length
% identity
                  (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
                   169853
Seq. No.
                  LIB3234-090-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   g267073
NCBI GI
BLAST score
                   674
                   3.0e-71
E value
                   124
Match length
% identity
                   TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                   beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                   beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                   beta-3 tubulin [Arabidopsis thaliana]
                   169854
Seq. No.
                   LIB3234-090-P1-K1-H4
Seq. ID
                   BLASTX
Method
                   q3021282
NCBI GI
                   668
BLAST score
                   2.0e-70
E value
                   124
Match length
                   100
% identity
                   (AL022347) serine/threonine - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   169855
Seq. No.
                   LIB3234-090-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3021282
                   233
BLAST score
                   1.0e-19
E value
Match length
                   79
                   62
 % identity
                   (AL022347) serine/threonine - like protein [Arabidopsis -
 NCBI Description
                   thaliana]
                   169856
 Seq. No.
                   LIB3234-090-P1-K1-H6
 Seq. ID
                   BLASTX
 Method
                   q2961373
 NCBI GI
                   288
 BLAST score
                   6.0e-26
 E value
                   102
 Match length
```

57

% identity



```
NCBI Description (AL022141) putative disease resistance protein [Arabidopsis
                  thaliana]
                  169857
Seq. No.
                  LIB3234-090-P1-K1-H7
Seq. ID
                  BLASTN
Method
                  g4580520
NCBI GI
                  194
BLAST score
                  1.0e-105
E value
                  198
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana scarecrow-like 7 (SCL7) mRNA, partial
                   169858
Seq. No.
                  LIB3234-090-P1-K1-H9
Seq. ID
                  BLASTX
Method
                   g2078350
NCBI GI
                   239
BLAST score
                   3.0e-20
E value
                   85
Match length
                   61
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                   169859
Seq. No.
                   LIB3234-091-P1-K1-A1
Seq. ID
                   BLASTX
Method
                   g1592677
NCBI GI
                   188
BLAST score
                   3.0e-14
E value
                   38
Match length
                   97
% identity
                   (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
                   169860
Seq. No.
                   LIB3234-091-P1-K1-A10
Seq. ID
                   BLASTN
Method
                   g3449320
NCBI GI
                   327
 BLAST score
                   0.0e+00
 E value
                   368
 Match length
                   97
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MRB17, complete sequence [Arabidopsis thaliana]
                   169861
 Seq. No.
 Seq. ID
                   LIB3234-091-P1-K1-A11
                   BLASTX
 Method
                   g729486
 NCBI GI
                   144
 BLAST score
                   5.0e-09
 E value
                   79
 Match length
                    42
 % identity
 NCBI Description PRE-RRNA PROCESSING PROTEIN FHL1 >gi 626950 pir S43738
                   transcription activator FHL1 - yeast (Saccharomyces
                    cerevisiae) >gi_454255_emb_CAA82202_ (Z28348) Fhllp
```

[Saccharomyces cerevisiae] >gi_914975 (U32445) Pre-rRNA



processing protein Fhll (Swiss Prot. accession number P39521) [Saccharomyces cerevisiae]

Seq. ID LIB3234-091-P1-K1-A12
Method BLASTX
NCBI GI g2827528
BLAST score 304
E value 8.0e-28
Match length 95
% identity 59

Seq. No.

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 169863

Seq. ID LIB3234-091-P1-K1-A2

Method BLASTX
NCBI GI g3335169
BLAST score 483
E value 9.0e-49
Match length 113
% identity 76

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi 4455197 emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 169864

Seq. ID LIB3234-091-P1-K1-A3

Method BLASTX
NCBI GI g2605714
BLAST score 338
E value 6.0e-32
Match length 65
% identity 100

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 169865

Seq. ID LIB3234-091-P1-K1-A4

Method BLASTX
NCBI GI g114654
BLAST score 289
E value 5.0e-26
Match length 81
% identity 79

NCBI Description ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)

>gi_67898_pir__LWNTA H+-transporting ATP synthase (EC

3.6.1.34) lipid-binding protein - common tobacco

chloroplast >gi_11812_emb_CAA77343_ (Z00044) ATPase III subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A

ATPase III, H translocating [Nicotiana sp.]

>gi 225272_prf__1211235G ATPase III [Nicotiana tabacum]

Seq. No. 169866

Seq. ID LIB3234-091-P1-K1-A5

Method BLASTX NCBI GI g2980798

Match length

78



```
118
BLAST score
                  5.0e-20
E value
Match length
                  68
% identity
                  84
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                  169867
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3935151
BLAST score
                  495
                  3.0e-50
E value
                  91
Match length
                  100
% identity
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
                  169868
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2894574
BLAST score
                  472
                  1.0e-47
E value
                  90
Match length
                  99
% identity
NCBI Description
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
                  >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
                  169869
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-B1
Method
                  BLASTN
                  q2182289
NCBI GI
BLAST score
                   323
E value
                   0.0e+00
Match length
                   373
                   96
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F11P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169870
Seq. ID
                  LIB3234-091-P1-K1-B10
Method
                  BLASTN
                  g2924653
NCBI GI
BLAST score
                   226
E value
                   1.0e-124
                   370
Match length
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169871
                  LIB3234-091-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  q132939
NCBI GI
BLAST score
                   406
E value
                   5.0e-40
```



```
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal
NCBI Description
                  protein L3 (ARP1) - Arabidopsis thaliana >gi_166858
                  (M32654) ribosomal protein [Arabidopsis thaliana]
                  169872
Seq. No.
                  LIB3234-091-P1-K1-B12
Seq. ID
                  BLASTX
Method
                  q1710530
NCBI GI
                  550
BLAST score
                  1.0e-56
E value
                  103
Match length
                  96
% identity
                  60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487_emb CAA63025 (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
                  169873
Seq. No.
                  LIB3234-091-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2645971
                   580
BLAST score
                   3.0e-60
E value
                   110
Match length
% identity
                   (AF034255) reversibly glycosylated polypeptide-3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   169874
                   LIB3234-091-P1-K1-B3
Seq. ID
                   BLASTN
Method
                   q2656030
NCBI GI
BLAST score
                   337
                   0.0e+00
E value
Match length
                   375
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUL8
Seq. No.
                   169875
                   LIB3234-091-P1-K1-B4
Seq. ID
                   BLASTX
Method
                   g207905
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
                   123
Match length
                   41
% identity
                   (M18027) alpha globulin B [Artificial gene]
NCBI Description
                   169876
Seq. No.
                   LIB3234-091-P1-K1-B8
Seq. ID
                   BLASTN
Method
                   g4757390
NCBI GI
                   334
BLAST score
```

0.0e + 00

362

E value

Match length



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F24B18, complete sequence
                  169877
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-B9
                  BLASTN
Method
                  g4519195
NCBI GI
                  172
BLAST score
                   6.0e-92
E value
                   321
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
                   169878
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-C1
                   BLASTN
Method
                   g3600029
NCBI GI
BLAST score
                   368
                   0.0e + 00
E value
                   368
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana BAC T12H20
                   169879
Seq. No.
Seq. ID
                   LIB3234-091-P1-K1-C10
                   BLASTN
Method
NCBI GI
                   q4589408
BLAST score
                   358
                   0.0e + 00
E value
                   370
Match length
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F14A1, complete sequence
                   169880
Seq. No.
                   LIB3234-091-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169273
BLAST score
                   218
                   1.0e-17
E value
                   96
Match length
                   49
% identity
                   DEOXYCYTIDINE KINASE (DCK) >gi_1083283_pir__A55122
NCBI Description
                   deoxycytidine kinase (EC 2.7.1.74) - mouse
                   >gi_456677_emb_CAA54787_ (X77731) deoxycytidine kinase [Mus
                   musculus]
                   169881
Seq. No.
                   LIB3234-091-P1-K1-C5
Seq. ID
                   BLASTN
Method
                   g343239
NCBI GI
                   210
BLAST score
                   1.0e-115
E value
```

98

Match length

% identity

Seq. ID

```
1
```

```
NCBI Description Mustard (S.alba) chloroplast 16S rRNA, 5' end, and Val-tRNA
                  169882
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-C6
                  BLASTX
Method
NCBI GI
                  g2462750
BLAST score
                  312
                  8.0e-29
E value
Match length
                  75
                  79
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
                  169883
Seq. No.
                  LIB3234-091-P1-K1-D1
Seq. ID
                  BLASTN
Method
                  g4589969
NCBI GI
BLAST score
                  37
E value
                  2.0e-11
Match length
                  61
                  90
% identity
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
NCBI Description
                  sequence, complete sequence
                  169884
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-D10
                  BLASTX
Method
                  g4102582
NCBI GI
BLAST score
                  269
E value
                  3.0e-24
                  67
Match length
% identity
NCBI Description (AF013115) CAO [Arabidopsis thaliana]
Seq. No.
                  169885
                  LIB3234-091-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  335
                  0.0e + 00
E value
Match length
                  371
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSL1, complete sequence [Arabidopsis thaliana]
                  169886
Seq. No.
                  LIB3234-091-P1-K1-D12
Seq. ID
                  BLASTX
Method
                  g1709970
NCBI GI
                  437
BLAST score
                  2.0e-43
E value
                  110
Match length
                  79
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                  169887
Seq. No.
```

23105

LIB3234-091-P1-K1-D3

NCBI GI

g225115



```
BLASTN
Method
NCBI GI
                  g2244829
                  125
BLAST score
                   9.0e-64
E value
Match length
                   166
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   169888
Seq. No.
                   LIB3234-091-P1-K1-D4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4127298
                   45
BLAST score
                   4.0e-16
E value
                   104
Match length
% identity
                   91
                  Allium altaicum chloroplast psaA-trnS intergenic spacer,
NCBI Description
                   partial sequence (cultivar TAX2760)
                   169889
Seq. No.
                   LIB3234-091-P1-K1-D7
Seq. ID
                   BLASTN
Method
                   g2264321
NCBI GI
                   338
BLAST score
                   0.0e+00
E value
                   370
Match length
                   45
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXM12, complete sequence [Arabidopsis thaliana]
                   169890
Seq. No.
                   LIB3234-091-P1-K1-D8
Seq. ID
Method
                   BLASTN
                   g4159712
NCBI GI
                   346
BLAST score
                   0.0e+00
E value
Match length
                   370
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MWI23, complete sequence
                   169891
Seq. No.
                   LIB3234-091-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g4038491
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
                   113
Match length
                   40
% identity
                   (AJ131705) poly(ADP-ribose) polymerase [Arabidopsis
NCBI Description
                   thaliana]
                   169892
Seq. No.
                   LIB3234-091-P1-K1-E10
Seq. ID
Method
                   BLASTX
```

Seq. ID



```
521
BLAST score
                  2.0e-53
E value
                  108
Match length
                  91
% identity
NCBI Description photosystem II protein D2 [Chlamydomonas reinhardtii]
                  169893
Seq. No.
                  LIB3234-091-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g3335171
NCBI GI
                  430
BLAST score
                  1.0e-42
E value
                  104
Match length
                   83
% identity
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
                   169894
Seq. No.
                  LIB3234-091-P1-K1-E12
Seq. ID
                  BLASTX
Method
                   g114654
NCBI GI
                   282
BLAST score
                   3.0e-25
E value
                   81
Match length
                   77
% identity
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
NCBI Description
                   >qi 67898 pir LWNTA H+-transporting ATP synthase (EC
                   3.6.1.34) lipid-binding protein - common tobacco
                   chloroplast >gi_11812 emb CAA77343 (Z00044) ATPase III
                   subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase
                   subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A
                   ATPase III, H translocating [Nicotiana sp.]
                   >gi_225272_prf__1211235G ATPase III [Nicotiana tabacum]
                   169895
Seq. No.
                   LIB3234-091-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g1699370
NCBI GI
BLAST score
                   259
                   1.0e-22
E value
Match length
                   83
                   58
% identity
                   (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9}
NCBI Description
                   [mice, liver, Peptide, 493 aa] [Mus sp.]
Seq. No.
                   169896
                   LIB3234-091-P1-K1-E8
Seq. ID
Method
                   BLASTN
                   g2358139
NCBI GI
                   351
BLAST score
                   0.0e+00
E value
                   367
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   169897
 Seq. No.
```

LIB3234-091-P1-K1-E9

Seq. ID

Method

BLASTX



```
BLASTX
Method
                  g1864017
NCBI GI
                  531
BLAST score
                  2.0e-54
E value
                  105
Match length
                  96
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                  169898
Seq. No.
                  LIB3234-091-P1-K1-F1
Seq. ID
                  BLASTX
Method
                  g881615
NCBI GI
                  639
BLAST score
                  4.0e-67
E value
                  123
Match length
                  100
% identity
                  (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 3096921 emb CAA18831.1 (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
                  169899
Seq. No.
                  LIB3234-091-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q114335
                   391
BLAST score
                   5.0e-38
E value
                   99
Match length
                  76
% identity
NCBI Description
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                  >gi 67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                   type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                   169900
Seq. No.
                   LIB3234-091-P1-K1-F2
Seq. ID
                   BLASTN
Method
                   g4589434
NCBI GI
BLAST score
                   141
                   2.0e-73
E value
Match length
                   370
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNJ7, complete sequence
Seq. No.
                   169901
                   LIB3234-091-P1-K1-F4
Seq. ID
                   BLASTN
Method
                   g3298610
NCBI GI
                   349
BLAST score
                   0.0e + 00
E value
Match length
                   373
                   99
% identity
                  Arabidopsis thaliana BAC T2H3
NCBI Description
                   169902
Seq. No.
                   LIB3234-091-P1-K1-F5
```



NCBI GI g2828296 BLAST score 72 3.0e-05 E value Match length 172 % identity 48 (AL021687) RNase L inhibitor [Arabidopsis thaliana] NCBI Description Seq. No. 169903 LIB3234-091-P1-K1-F6 Seq. ID BLASTN Method g3327867 NCBI GI BLAST score 299 E value 1.0e-167 370 Match length 96 % identity Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein NCBI Description 7, complete cds Seq. No. 169904 Seq. ID LIB3234-091-P1-K1-F8 BLASTX g3668082 210 8.0e-17 71

Method NCBI GI BLAST score E value Match length 58 % identity

(AC004667) putative DAL1 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 169905

LIB3234-091-P1-K1-F9 Seq. ID

BLASTX Method q1107501 NCBI GI 404 BLAST score 1.0e-39 E value 99 Match length 82 % identity

(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) NCBI Description

Match to gb X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

169906 Seq. No.

Seq. ID LIB3234-091-P1-K1-G10

Method BLASTX g1065515 NCBI GI 242 BLAST score 2.0e-20 E value 117 Match length 44 % identity

(U40420) weak similarity to procollagen alpha chain 1(V) NCBI Description

chain [Caenorhabditis elegans]

169907 Seq. No.

LIB3234-091-P1-K1-G11 Seq. ID

Method BLASTN g3758832 NCBI GI

42 BLAST score



```
E value
                  2.0e-14
                  70
Match length
% identity
                  90
                  Medicago truncatula mRNA for MtN6 gene
NCBI Description
                  169908
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q4510360
BLAST score
                  259
                  1.0e-144
E value
Match length
                  324
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                  sequence, complete sequence
                  169909
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  q3746057
BLAST score
                   41
                   9.0e-14
E value
Match length
                   141
% identity
                   82
                  Arabidopsis thaliana chromosome II BAC T16B12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169910
Seq. No.
Seq. ID
                  LIB3234-091-P1-K1-G6
Method
                   BLASTN
                   q4589408
NCBI GI
                   156
BLAST score
                   1.0e-82
E value
Match length
                   186
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F14A1, complete sequence
                   169911
Seq. No.
                   LIB3234-091-P1-K1-G8
Seq. ID
                   BLASTX
Method
                   g1109699
NCBI GI
BLAST score
                   582
                   2.0e-60
E value
                   118
Match length
                   94
% identity
                  (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
                   169912
Seq. No.
```

Seq. ID LIB3234-091-P1-K1-H10

Method BLASTX
NCBI GI g1171642
BLAST score 244
E value 7.0e-28
Match length 66
% identity 100

NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK



>gi_481206_pir__S38326 protein kinase - Arabidopsis
thaliana >gi_166809 (L07248) protein kinase [Arabidopsis
thaliana]

 Seq. No.
 169913

 Seq. ID
 LIB3234-091-P1-K1-H11

 Method
 BLASTX

 NCBI GI
 g2739373

BLAST score 212 E value 5.0e-17 Match length 114 % identity 39

NCBI Description (AC002505) putative flavonol 3-o-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 169914

Seq. ID LIB3234-091-P1-K1-H12

Method BLASTN
NCBI GI 94220634
BLAST score 347
E value 0.0e+00
Match length 371
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9H21, complete sequence [Arabidopsis thaliana]

Seq. No. 169915

Seq. ID LIB3234-091-P1-K1-H2

Method BLASTN
NCBI GI g4454587
BLAST score 344
E value 0.0e+00
Match length 372
% identity 98

NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 169916

Seq. ID LIB3234-091-P1-K1-H3

Method BLASTN
NCBI GI g3540210
BLAST score 289
E value 1.0e-162
Match length 337
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 169917

Seq. ID LIB3234-091-P1-K1-H4

Method BLASTX
NCBI GI g3024450
BLAST score 234
E value 4.0e-20
Match length 47
% identity 98

NCBI Description PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47



PROTEIN) >gi_2143323_emb_CAA73765_ (Y13328) 51kDa chlorophyll a protein [Populus deltoides]

169918 Seq. No. Seq. ID LIB3234-091-P1-K1-H5 Method BLASTN g2143322 NCBI GI BLAST score 36 7.0e-11 E value 48 Match length 94 % identity NCBI Description P.deltoides chloroplast DNA for psbB operon 169919 Seq. No. LIB3234-091-P1-K1-H8 Seq. ID Method BLASTX NCBI GI g1550740 BLAST score 562 E value 4.0e-58 109 Match length 97 % identity (Y07961) GDP-associated inhibitor [Arabidopsis thaliana] NCBI Description 169920 Seq. No. Seq. ID LIB3234-091-P1-K1-H9 Method BLASTN NCBI GI g4063756 BLAST score 245 1.0e-135 E value Match length 274 97 % identity Arabidopsis thaliana chromosome II BAC T9F8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 169921 LIB3234-092-P1-K1-A10 Seq. ID Method BLASTX NCBI GI g4200165 BLAST score 575 E value 1.0e-59 Match length 123 % identity 89 (Y16262) neutral invertase [Daucus carota] NCBI Description 169922 Seq. No. LIB3234-092-P1-K1-A11 Seq. ID BLASTN Method g4159703 NCBI GI BLAST score 180 1.0e-96 E value 347 Match length % identity 88 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K5F14, complete sequence

Seq. No. 169923

Seq. ID LIB3234-092-P1-K1-A12

BLAST score

E value

1.0e-46



```
BLASTX
Method
                  g1402904
NCBI GI
                  365
BLAST score
                  6.0e-35
E value
Match length
                  72
                  96
% identity
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
                  169924
Seq. No.
                  LIB3234-092-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g4567293
NCBI GI
                  419
BLAST score
                  3.0e-41
E value
                  123
Match length
                   72
% identity
                   (AC006918) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  169925
                  LIB3234-092-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2760326
BLAST score
                   249
                   2.0e-21
E value
                   122
Match length
                   45
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.
                   169926
Seq. ID
                   LIB3234-092-P1-K1-A5
                   BLASTN
Method
                   q4678291
NCBI GI
                   341
BLAST score
E value
                   0.0e+00
                   372
Match length
% identity
                   97
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
NCBI Description
                   (ESSA project)
Seq. No.
                   169927
                   LIB3234-092-P1-K1-A8
Seq. ID
Method
                   BLASTN
                   q4309864
NCBI GI
BLAST score
                   357
                   0.0e+00
E value
                   357
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC F27C21 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169928
Seq. No.
                   LIB3234-092-P1-K1-A9
Seq. ID
                   BLASTN
Method
                   g4309864
NCBI GI
                   96
```



244 Match length % identity Arabidopsis thaliana chromosome II BAC F27C21 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 169929 Seq. No. LIB3234-092-P1-K1-B10 Seq. ID BLASTX Method g3776029 NCBI GI BLAST score 624 2.0e-65 E value 123 Match length 99 % identity (AJ010476) RNA helicase [Arabidopsis thaliana] NCBI Description 169930 Seq. No. Seq. ID LIB3234-092-P1-K1-B11 Method BLASTN g3212846 NCBI GI BLAST score 367 0.0e + 00E value 367 Match length 100 % identity Arabidopsis thaliana chromosome II BAC F6E13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 169931 Seq. No. Seq. ID LIB3234-092-P1-K1-B12 Method BLASTX NCBI GI q2829892 582 BLAST score 2.0e-60 E value 117 Match length % identity (AC002311) putative pectinesterase [Arabidopsis thaliana] NCBI Description 169932 Seq. No. LIB3234-092-P1-K1-B2 Seq. ID Method BLASTX NCBI GI g3808062 BLAST score 149 1.0e-09 E value Match length 62 % identity 45 (AB019195) PV100 [Cucurbita maxima] NCBI Description 169933 Seq. No. LIB3234-092-P1-K1-B3 Seq. ID BLASTX Method g1203832 NCBI GI 224 BLAST score 2.0e-18 E value

Match length 79 % identity 57

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. ID



```
169934
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-B4
                  BLASTX
Method
NCBI GI
                  g4585882
BLAST score
                   489
                   2.0e-49
E value
                   94
Match length
                   99
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  169935
Seq. No.
                  LIB3234-092-P1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3947733
BLAST score
                   147
                   2.0e-09
E value
Match length
                   103
% identity
                   30
                  (AJ009719) NL25 [Solanum tuberosum]
NCBI Description
                   169936
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-B7
Method
                  BLASTN
NCBI GI
                   g4159712
                   43
BLAST score
                   5.0e-15
E value
                   55
Match length
% identity
                   95
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
                   169937
Seq. No.
Seq. ID
                   LIB3234-092-P1-K1-B9
                   BLASTN
Method
NCBI GI
                   q3510343
BLAST score
                   53
                   7.0e-21
E value
Match length
                   166
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169938
                   LIB3234-092-P1-K1-C1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3510343
BLAST score
                   53
E value
                   6.0e-21
                   200
Match length
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJC20, complete sequence [Arabidopsis thaliana]
                   169939
Seq. No.
```

23115

LIB3234-092-P1-K1-C12



BLASTX Method NCBI GI q2494264 293 BLAST score 2.0e-26 E value Match length 123 48 % identity HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 NCBI Description >qi 1651837 dbj BAA16764 (D90900) elongation factor EF-G [Synechocystis sp.] 169940 Seq. No. Seq. ID LIB3234-092-P1-K1-C2 Method BLASTX NCBI GI g1523796 362 BLAST score 1.0e-34 E value Match length 103 % identity 61 NCBI Description (X97864) cytochrome P450 [Arabidopsis thaliana]

169941 Seq. No.

LIB3234-092-P1-K1-C3 Seq. ID

BLASTX Method NCBI GI g1532169 465 BLAST score 1.0e-46 E value 122 Match length 79 % identity

NCBI Description (U63815) similar to a E. coli hypothetical protein F402

encoded by GenBank Accession Number S47768 [Arabidopsis

thaliana]

169942 Seq. No.

LIB3234-092-P1-K1-C6 Seq. ID

BLASTN Method NCBI GI g2924652 280 BLAST score 1.0e-156 E value Match length 371 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K9L2, complete sequence [Arabidopsis thaliana]

Seq. No. 169943

LIB3234-092-P1-K1-C7 Seq. ID

BLASTX Method g2129639 NCBI GI BLAST score 436 3.0e-43 E value Match length 85 100 % identity

luminal binding protein (BiP) - Arabidopsis thaliana NCBI Description

 $>gi_1303695_dbj_BAA12348_$ (D84414) luminal binding protein

(BiP) [Arabidopsis thaliana]

169944 Seq. No.

LIB3234-092-P1-K1-C8 Seq. ID

NCBI GI

BLAST score



```
BLASTN
Method
                   g4006885
NCBI GI
                   323
BLAST score
                   0.0e + 00
E value
                   357
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   169945
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-C9
                  BLASTN
Method
                   g3128136
NCBI GI
BLAST score
                   174
                   4.0e-93
E value
                   258
Match length
                   92
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K1F13, complete sequence [Arabidopsis thaliana]
                   169946
Seq. No.
                   LIB3234-092-P1-K1-D1
Seq. ID
                   BLASTX
Method
                   g4314363
NCBI GI
                   453
BLAST score
                   3.0e-45
E value
                   99
Match length
                   83
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169947
Seq. No.
                   LIB3234-092-P1-K1-D10
Seq. ID
                   BLASTN
Method
                   q3128166
NCBI GI
BLAST score
                   135
                   8.0e-70
E value
                   290
Match length
                   94
% identity
                   Arabidopsis thaliana chromosome II BAC F4I1 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169948
Seq. No.
                   LIB3234-092-P1-K1-D12
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4159709
                   99
BLAST score
E value
                   6.0e-49
Match length
                   103
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MLN21, complete sequence
                   169949
Seq. No.
                   LIB3234-092-P1-K1-D2
Seq. ID
                   BLASTX
Method
```

23117

g4406787



```
1.0e-54
E value
                  103
Match length
                  100
% identity
NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]
                  169950
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-D7
                  BLASTN
Method
                  g3873174
NCBI GI
                  341
BLAST score
E value
                  0.0e + 00
                  365
Match length
                  98
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  169951
Seq. No.
                  LIB3234-092-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4115362
                   467
BLAST score
                   6.0e-47
E value
                  121
Match length
                   70
% identity
NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]
                   169952
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-D9
Method
                  BLASTX
NCBI GI
                   q4115362
                   198
BLAST score
E value
                   2.0e-15
                   75
Match length
% identity
                  (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169953
Seq. No.
                   LIB3234-092-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454482
BLAST score
                   326
                   2.0e-30
E value
                   112
Match length
% identity
                   64
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   169954
Seq. No.
                   LIB3234-092-P1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2894574
                   566
BLAST score
                   2.0e-58
E value
Match length
                   108
                   100
% identity
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
NCBI Description
```

[Arabidopsis thaliana]

>gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1



```
169955
Seq. No.
                  LIB3234-092-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1402904
                  286
BLAST score
                  1.0e-25
E value
Match length
                  110
% identity
                  59
                 (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                  169956
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-E3
Method
                  BLASTX
                  g127041
NCBI GI
                  644
BLAST score
                  1.0e-67
E value
                  122
Match length
% identity
                  100
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 81647 pir JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
                  169957
Seq. No.
                  LIB3234-092-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170317
BLAST score
                  634
                   2.0e-66
E value
                  124
Match length
                   100
% identity
                  3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (HMG-COA
NCBI Description
                   REDUCTASE 2) (HMGR2) >gi_388558 (L19262)
                   3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis
                   thaliana] >gi 2262168 (AC002329)
                   3-hydroxy-3-methylglutaryl-CoA reductase (HMG2 protein)
                   [Arabidopsis thaliana]
                   169958
Seq. No.
                  LIB3234-092-P1-K1-E6
Seq. ID
                  BLASTX
Method
                   g1170317
NCBI GI
                   296
BLAST score
                   5.0e-44
E value
                   120
Match length
                   81
% identity
                   3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (HMG-COA
NCBI Description
                   REDUCTASE 2) (HMGR2) >gi_388558 (L19262)
                   3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis
                   thaliana] >gi_2262168 (AC002329)
                   3-hydroxy-3-methylglutaryl-CoA reductase (HMG2 protein)
                   [Arabidopsis thaliana]
```

Seq. No. 169959

Seq. ID LIB3234-092-P1-K1-E7



```
BLASTN
Method
                  g4406752
NCBI GI
                  275
BLAST score
                  1.0e-153
E value
                  349
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F19B11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  169960
Seq. No.
                  LIB3234-092-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g4585977
NCBI GI
                  329
BLAST score
                   9.0e-31
E value
                   91
Match length
                   66
% identity
                  (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   169961
Seq. No.
                  LIB3234-092-P1-K1-E9
Seq. ID
                  BLASTN
Method
                   g3176694
NCBI GI
                   359
BLAST score
                   0.0e + 00
E value
                   359
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   169962
Seq. No.
                   LIB3234-092-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   q1402914
NCBI GI
BLAST score
                   586
                   7.0e-61
E value
                   116
Match length
% identity
                   100
                   (X98318) peroxidase [Arabidopsis thaliana]
NCBI Description
                   169963
Seq. No.
                   LIB3234-092-P1-K1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4454004
BLAST score
                   62
                   3.0e-26
E value
                   137
Match length
                   93
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
NCBI Description
                   (ESSAII project)
                   169964
Seq. No.
                   LIB3234-092-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g4314363
NCBI GI
                   182
BLAST score
```

4.0e-18

E value

NCBI GI

BLAST score



```
79
Match length
                  59
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  169965
Seq. No.
                  LIB3234-092-P1-K1-F5
Seq. ID
                  BLASTX
Method
                  g118926
NCBI GI
                  151
BLAST score
                  7.0e-10
E value
                  61
Match length
                  52
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi 227781 prf 1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
                  169966
Seq. No.
                  LIB3234-092-P1-K1-F6
Seq. ID
                  BLASTN
Method
                  g2760173
NCBI GI
                  343
BLAST score
                  0.0e + 00
E value
                   374
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH19, complete sequence [Arabidopsis thaliana]
                   169967
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-F7
                   BLASTN
Method
                   q4586098
NCBI GI
BLAST score
                   316
                   1.0e-178
E value
                   361
Match length
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
NCBI Description
                   (ESSA project)
Seq. No.
                   169968
                   LIB3234-092-P1-K1-F9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2244870
BLAST score
                   278
                   1.0e-155
E value
Match length
                   290
% identity
                   82
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   169969
Seq. No.
                   LIB3234-092-P1-K1-G1
Seq. ID
                   BLASTX
Method
```

23121

g2160151

NCBI GI

E value

BLAST score



```
2.0e-69
E value
                  122
Match length
                  100
% identity
                  (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                  (gb X77260). [Arabidopsis thaliana]
                  169970
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-G10
                  BLASTX
Method
                  q3882297
NCBI GI
                  327
BLAST score
                  2.0e-30
E value
                  125
Match length
% identity
                  (AB018331) KIAA0788 protein [Homo sapiens]
NCBI Description
                  169971
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-G12
                   BLASTN
Method
                   g4249393
NCBI GI
                   356
BLAST score
                   0.0e + 00
E value
                   376
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC T9J23 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   169972
Seq. No.
Seq. ID
                   LIB3234-092-P1-K1-G2
Method
                   BLASTX
                   q133959
NCBI GI
                   413
BLAST score
                   1.0e-40
E value
                   89
Match length
% identity
                   92
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_81526_pir__A30833
NCBI Description
                   ribosomal protein S4 - spinach chloroplast >gi_343377
                   (M16878) ribosomal protein S4 [Spinacia oleracea]
                   >gi 225464 prf 1303355A ribosomal protein S4 [Spinacia
                   oleracea]
                   169973
Seq. No.
                   LIB3234-092-P1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4063734
                   515
BLAST score
                   1.0e-52
E value
                   121
Match length
                   82
% identity
                   (AC006259) putative P450 [Arabidopsis thaliana]
NCBI Description
                   1.69974
Seq. No.
                   LIB3234-092-P1-K1-G4
Seq. ID
                   BLASTX
Method
```

23122

g2244906

1.0e-35



```
103
Match length
                  72
% identity
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  169975
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-G5
                  BLASTN
Method
                  g2245031
NCBI GI
BLAST score
                  201
                  1.0e-109
E value
                  241
Match length
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  169976
Seq. No.
                  LIB3234-092-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3445209
                  388
BLAST score
                  1.0e-37
E value
                   91
Match length
                   75 -
% identity
                   (AC004786) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana]
                   169977
Seq. No.
                  LIB3234-092-P1-K1-G7
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4589414
                   358
BLAST score
                   0.0e + 00
E value
                   366
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K14B15, complete sequence
                   169978
Seq. No.
Seq. ID
                   LIB3234-092-P1-K1-G8
                   BLASTN
Method
NCBI GI
                   g2924653
BLAST score
                   318
                   1.0e-179
E value
Match length
                   330
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169979
```

Seq. ID LIB3234-092-P1-K1-H1

Method BLASTN
NCBI GI g2264307
BLAST score 345
E value 0.0e+00
Match length 366
% identity 98



% identity

NCBI Description

```
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MED24, complete sequence [Arabidopsis thaliana]
                   169980
Seq. No.
Seq. ID
                  LIB3234-092-P1-K1-H10
                   BLASTN
Method
                   q4512656
NCBI GI
BLAST score
                   193
                   1.0e-104
E value
                   350
Match length
                   93
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
                   169981
Seq. No.
                   LIB3234-092-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2623962
BLAST score
                   365
                   1.0e-59
E value
                   125
Match length
% identity
                   86
                   (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                   graveolens]
                   169982
Seq. No.
                   LIB3234-092-P1-K1-H12
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4757662
BLAST score
                   338
                   0.0e + 00
E value
Match length
                   373
                   97
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F10B6 from
NCBI Description
                   chromosome I, complete sequence
                   169983
Seq. No.
                   LIB3234-092-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924258
BLAST score
                   57
                   3.0e-13
E value
                   75
Match length
% identity
                   56
                   (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
NCBI Description
                   169984
Seq. No.
                   LIB3234-092-P1-K1-H3
Seq. ID
                   BLASTN
Method
                   g3449321
NCBI GI
                   177
BLAST score
                   7.0e-95
E value
                   342
Match length
```

MTG10, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Method

NCBI GI

BLASTX

g1705463



```
169985
Seq. No.
                  LIB3234-092-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3128142
BLAST score
                  326
                  0.0e + 00
E value
                   358
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQN23, complete sequence [Arabidopsis thaliana]
                  169986
Seq. No.
                  LIB3234-092-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4406809
BLAST score
                   142
E value
                   8.0e-09
                   68
Match length
% identity
                   49
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                   169987
Seq. No.
                   LIB3234-092-P1-K1-H8
Seq. ID
Method
                   BLASTX
                   q3600039
NCBI GI
BLAST score
                   299
                   2.0e-27
E value
                   89
Match length
% identity
                   71
                   (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                   protein (GB:D14061) [Arabidopsis thaliana]
                   169988
Seq. No.
                   LIB3234-093-P1-K1-A1
Seq. ID
                   BLASTN
Method
                   g3047088
NCBI GI
                   191
BLAST score
                   1.0e-103
E value
Match length
                   409
% identity
                   100
                  Arabidopsis thaliana BAC T26D22
NCBI Description
                   169989
Seq. No.
                   LIB3234-093-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497539
                   546
BLAST score
                   4.0e-56
E value
                   130
Match length
                   83
% identity
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703
NCBI Description
                   (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
                   169990
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-A11
```



626 BLAST score E value 2.0e-65 133 Match length % identity 89 BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >qi 2129547 pir S71201 NCBI Description biotin sythase - Arabidopsis thaliana >qi 1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi 1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi 1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi 2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi 1589016 prf 2209438A biotin synthase [Arabidopsis thaliana] 169991 Seq. No. LIB3234-093-P1-K1-A2 Seq. ID Method BLASTN NCBI GI q4490717 BLAST score 58 E value 6.0e-24 Match length 102 95 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA NCBI Description project) Seq. No. 169992 LIB3234-093-P1-K1-A4 Seq. ID BLASTX Method NCBI GI g4337196 BLAST score 166 E value 1.0e-22 83 Match length 73 % identity (AC006403) putative serine/threonine receptor kinase NCBI Description [Arabidopsis thaliana] 169993 Seq. No. Seq. ID LIB3234-093-P1-K1-A5 BLASTN Method NCBI GI q2351073 BLAST score 164 4.0e-87 E value Match length 378 93 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MYJ24, complete sequence [Arabidopsis thaliana] 169994 Seq. No. LIB3234-093-P1-K1-A6 Seq. ID Method BLASTX NCBI GI q4006897 BLAST score 467 7.0e-47E value 99 Match length 95

% identity

(Z99708) globulin-like protein [Arabidopsis thaliana] NCBI Description

169995 Seq. No.

Seq. ID

Method

BLASTN



```
LIB3234-093-P1-K1-A9
Seq. ID
                  BLASTN
Method
                  g2924257
NCBI GI
                  217
BLAST score
                  1.0e-119
E value
                  350
Match length
                  45
% identity
NCBI Description Tobacco chloroplast genome DNA
                  169996
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-B1
                  BLASTN
Method
                  g4558586
NCBI GI
BLAST score
                   320
                   1.0e-180
E value
                   336
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome 1 BAC T518 sequence,
NCBI Description
                   complete sequence
                   169997
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-B10
                   BLASTX
Method
NCBI GI
                   g543632
BLAST score
                   553
                   6.0e-57
E value
                   134
Match length
                   72
% identity
                   aldehyde reductase (EC 1.1.1.21), NADPH-dependent -
NCBI Description
                   bromegrass >gi_167113 (L12042) aldose reductase-related
                   protein [Bromus inermis]
                   169998
Seq. No.
                   LIB3234-093-P1-K1-B11
Seq. ID
Method
                   BLASTN
                   g4199934
NCBI GI
                   265
BLAST score
                   1.0e-147
E value
                   384
Match length
% identity
                   92
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   169999
Seq. No.
                   LIB3234-093-P1-K1-B12
Seq. ID
                   BLASTN
Method
                   g4159708
NCBI GI
                   325
BLAST score
                   0.0e+00
E value
                   347
Match length
                   100
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MKP6, complete sequence
                   170000
 Seq. No.
                   LIB3234-093-P1-K1-B4
```

Method

NCBI GI

BLAST score

BLASTN g3894156

269



```
g2760172
NCBI GI
BLAST score
                  140
                   7.0e-73
E value
                   317
Match length
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
                   170001
Seq. No.
                  LIB3234-093-P1-K1-B5
Seq. ID
                  BLASTN
Method
                   g1497986
NCBI GI
                   297
BLAST score
                   1.0e-166
E value
                   387
Match length
% identity
                  Arabidopsis thaliana SCARECROW (SCARECROW1) gene, complete
NCBI Description
                   cds
                   170002
Seq. No.
                   LIB3234-093-P1-K1-B7
Seq. ID
                   BLASTX
Method
                   q2129579
NCBI GI
BLAST score
                   746
                   1.0e-79
E value
                   136
Match length
                   97
% identity
                   Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                   Dwarf1 [Arabidopsis thaliana]
                   170003
Seq. No.
                   LIB3234-093-P1-K1-B8
Seq. ID
                   BLASTN
Method
                   q4159704
NCBI GI
BLAST score
                   87
                   8.0e-42
E value
                   99
Match length
                   97
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MCB17, complete sequence
                   170004
Seq. No.
                   LIB3234-093-P1-K1-B9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2109292
                   366
BLAST score
                   0.0e+00
E value
                   386
Match length
                   99
% identity
                   Arabidopsis thaliana serine/threonine protein kinase mRNA,
NCBI Description
                   complete cds
                   170005
Seq. No.
                   LIB3234-093-P1-K1-C1
Seq. ID
```



```
1.0e-150
E value
                  348
Match length
                  81
% identity
                  Arabidopsis thaliana chromosome II BAC T16F16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170006
Seq. No.
                  LIB3234-093-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g1903357
NCBI GI
                  300
BLAST score
                  3.0e-27
E value
                  95
Match length
                   60
% identity
                   (AC000104) Strong similarity to Arabidopsis 2A6
NCBI Description
                   (gb_X83096). [Arabidopsis thaliana]
                  170007
Seq. No.
                  LIB3234-093-P1-K1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3269280
BLAST score
                  277
                  1.0e-154
E value
                  396
Match length
                  84
% identity
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
NCBI Description
                   (ESSAII project)
                   170008
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-C2
Method
                  BLASTX
                   g3935181
NCBI GI
                   366
BLAST score
E value
                   5.0e-35
                   85
Match length
                   79
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                   170009
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   q4159708
BLAST score
                   35
                   2.0e-10
E value
                   47
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MKP6, complete sequence
                   170010
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-C5
                   BLASTN
Method
NCBI GI
                   g3702731
BLAST score
                   128
```

1.0e-65

507

68

E value Match length

% identity



```
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
                  170011
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-C6
                  BLASTX
Method
                  q1350768
NCBI GI
BLAST score
                  450
E value
                  7.0e-45
                  107
Match length
                  85
% identity
                  60S RIBOSOMAL PROTEIN L7A
NCBI Description
                  170012
Seq. No.
                  LIB3234-093-P1-K1-C7
Seq. ID
                  BLASTN
Method
                  g3449315
NCBI GI
BLAST score
                   349
                  0.0e+00
E value
Match length
                   404
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K23L20, complete sequence [Arabidopsis thaliana]
                   170013
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-C8
                  BLASTX
Method
                   g82223
NCBI GI
BLAST score
                   55
E value
                   8.0e-11
Match length
                   58
                   72
% identity
                   hypothetical protein 70B - common tobacco chloroplast
NCBI Description
                   >gi 11878 emb CAA77391 (Z00044) hypothetical protein
                   [Nicotiana tabacum] >gi 1223681 emb CAA77402 (Z00044)
                   hypothetical protein [Nicotiana tabacum]
                   >gi 225250 prf 1211235CJ ORF 70B [Nicotiana tabacum]
                   170014
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-C9
                   BLASTX
Method
NCBI GI
                   g4091806
BLAST score
                   180
                   3.0e-13
E value
Match length
                   134
% identity
                   37
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
NCBI Description
                   170015
Seq. No.
                   LIB3234-093-P1-K1-D1
Seq. ID
Method
                   BLASTX
                   g2959370
NCBI GI
BLAST score
                   169
                   6.0e-12
E value
                   79
Match length
% identity
                   35
                   (AL022117) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
```

NCBI Description



```
170016
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-D10
                  BLASTX
Method
                  g1174846
NCBI GI
                  372
BLAST score
                  1.0e-35
E value
                  65
Match length
                  100
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3)
                  >qi 1076425 pir S43782 ubiquitin-conjugating enzyme UBC3 -
                  Arabidopsis thaliana >gi_431262 (L19352) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  170017
Seq. No.
                  LIB3234-093-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  g4337178
NCBI GI
BLAST score
                  444
E value
                  4.0e-44
                  85
Match length
                  100
% identity
NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]
                  170018
Seq. No.
                  LIB3234-093-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3292827
NCBI GI
BLAST score
                   444
E value
                   4.0e-44
Match length
                  102
                   78
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  170019
Seq. No.
                  LIB3234-093-P1-K1-D5
Seq. ID
                   BLASTN
                                                                , سي
Method
                   q16559
NCBI GI
BLAST score
                   177
                   7.0e-95
E value
Match length
                   231
                   95
% identity
NCBI Description A.thaliana gene for tRNA-Ala (P-2-L)
Seq. No.
                   170020
                   LIB3234-093-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g398963
BLAST score
                   169
                   6.0e-12
E value
                   82
Match length
% identity
                   46
```

23131

4-COUMARATE--COA LIGASE 1 (4CL) >gi 100413 pir A39827

(M62755) 4-coumarate--CoA ligase [Solanum tuberosum]

4-coumarate--CoA ligase (EC 6.2.1.12) 1 - potato >gi_169574



```
170021
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-D9
                  BLASTN
Method
NCBI GI
                  g4512656
                  153
BLAST score
                  1.0e-80
E value
Match length
                  346
                  84
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  170022
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-E1
                  BLASTN
Method
                  g2264321
NCBI GI
                  118
BLAST score
                  1.0e-59
E value
                  278
Match length
                   91
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXM12, complete sequence [Arabidopsis thaliana]
                  170023
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-E11
                  BLASTN
Method
NCBI GI
                   q4584387
                   \bar{1}51
BLAST score
                   2.0e-79
E value
                   397
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
NCBI Description
                   (ESSA project)
                   170024
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-E12
                   BLASTX
Method
NCBI GI
                   q3643609
BLAST score
                   632
                   3.0e-66
E value
Match length
                   132
                   87
% identity
                  (AC005395) putative Cys3His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   170025
                   LIB3234-093-P1-K1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2264321
BLAST score
                   328
E value
                   0.0e + 00
                   405
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXM12, complete sequence [Arabidopsis thaliana]
                   170026
Seq. No.
```

LIB3234-093-P1-K1-E5

Seq. ID

NCBI GI



Method

BLASTN

```
NCBI GI
                  g3449330
                  188
BLAST score
                  1.0e-101
E value
                  373
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDJ14, complete sequence [Arabidopsis thaliana]
                  170027
Seq. No.
                  LIB3234-093-P1-K1-E6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3449330
BLAST score
                  168
                  2.0e-89
E value
                  381
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDJ14, complete sequence [Arabidopsis thaliana]
                  170028
Seq. No.
                  LIB3234-093-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  q4220474
NCBI GI
BLAST score
                  344
                  2.0e-32
E value
                   95
Match length
                  78
% identity
                   (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
                   170029
Seq. No.
                   LIB3234-093-P1-K1-E8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3702730
BLAST score
                   78
                   9.0e - 36
E value
                   292
Match length
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAB16, complete sequence [Arabidopsis thaliana]
                   170030
Seq. No.
                   LIB3234-093-P1-K1-E9
Seq. ID
Method
                   BLASTX
                   q4406766
NCBI GI
                   540
BLAST score
                   2.0e-55
E value
                   100
Match length
                   99
% identity
                   (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                   thaliana]
                   170031
Seq. No.
                   LIB3234-093-P1-K1-F6
Seq. ID
                   BLASTN
Method
```

g2760173

NCBI GI BLAST score



```
107
BLAST score
                   4.0e-53
E value
                   199
Match length
                   88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYH19, complete sequence [Arabidopsis thaliana]
                   170032
Seq. No.
                   LIB3234-093-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4406766
NCBI GI
BLAST score
                   517
                   1.0e-52
E value
                   98
Match length
% identity
                   97
                   (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   170033
Seq. ID
                   LIB3234-093-P1-K1-G1
                   BLASTN
Method
                   g2760168
NCBI GI
                   74
BLAST score
                   2.0e-33
E value
                   254
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MEE6, complete sequence [Arabidopsis thaliana]
                   170034
Seq. No.
                   LIB3234-093-P1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3128199
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
                   77
Match length
                   47
% identity
                   (AC004521) putative proteinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   170035
                   LIB3234-093-P1-K1-G12
Seq. ID
                   BLASTX
Method
                   g2129739
NCBI GI
                   447
BLAST score
                   2.0e-44
E value
                   89
Match length
                   99
% identity
                   shaggy-like kinase etha - Arabidopsis thaliana
NCBI Description
                   >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha
                    [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947)
                   shaggy-like kinase etha [Arabidopsis thaliana]
                   170036
 Seq. No.
                   LIB3234-093-P1-K1-G2
Seq. ID
                   BLASTN
Method
```

23134

g4581138



E value 1.0e-143 Match length 384 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 170037

Seq. ID LIB3234-093-P1-K1-G4

Method BLASTN
NCBI GI g3869069
BLAST score 289
E value 1.0e-162
Match length 293
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 170038

Seq. ID LIB3234-093-P1-K1-G6

Method BLASTN
NCBI GI g3335170
BLAST score 299
E value 1.0e-167
Match length 358
% identity 96

NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,

complete cds

Seq. No. 170039

Seq. ID LIB3234-093-P1-K1-G7

Method BLASTX
NCBI GI g1710530
BLAST score 630
E value 6.0e-66
Match length 113
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256

ribosomal protein L27a - Arabidopsis thaliana

>gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No. 170040

Seq. ID LIB3234-093-P1-K1-G8

Method BLASTX
NCBI GI g1345973
BLAST score 684
E value 2.0e-72
Match length 128
% identity 98

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid



desaturase [Arabidopsis thaliana]

```
170041
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g585922
BLAST score
                  542
                  1.0e-55
E value
Match length
                  114
                  93
% identity
NCBI Description DNA-DIRECTED RNA POLYMERASE BETA" CHAIN
                  170042
Seq. No.
                  LIB3234-093-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g1169515
NCBI GI
                  612
BLAST score
                  7.0e-64
E value
Match length
                  117
% identity
                  98
                  EM-LIKE PROTEIN GEA1 >gi 2119768 pir S34819 embryonic
NCBI Description
                  abundant protein Em1 - Arabidopsis thaliana
                  >qi 298070 emb CAA77509 (Z11158) Em protein [Arabidopsis
                  thaliana] >gi 298072_emb CAA77979 (Z11921) Em protein
                  homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1
                  protein [Arabidopsis thaliana]
                  170043
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-H10
Method
                  BLASTN
                  q4512656
NCBI GI
                   110
BLAST score
                   6.0e-55
E value
                   222
Match length
% identity
                   91
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
                   170044
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-H12
                   BLASTN
Method
NCBI GI
                   g4454022
BLAST score
                   358
                   0.0e + 00
E value
Match length
                   402
% identity
                   98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                   (ESSAII project)
Seq. No.
                   170045
                   LIB3234-093-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352345
                   176
BLAST score
                   5.0e-51
E value
Match length
                   118
                   91
% identity
```

BLAST score

E value

645 1.0e-67



```
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_18765_emb_CAA40182_ (X56856) eEF-1a [Glycine max]
                  170046
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-H4
                  BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                  648
                  4.0e-68
E value
                  135
Match length
                  93
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  170047
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-H5
                  BLASTN
Method
                  g3128142
NCBI GI
BLAST score
                  79
E value
                  2.0e-36
                  139
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQN23, complete sequence [Arabidopsis thaliana]
                  170048
Seq. No.
                  LIB3234-093-P1-K1-H6
Seq. ID
                  BLASTN
Method
                  g3449330
NCBI GI
BLAST score
                   404
E value
                  0.0e + 00
                   412
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDJ14, complete sequence [Arabidopsis thaliana]
                   170049
Seq. No.
Seq. ID
                  LIB3234-093-P1-K1-H7
Method
                   BLASTX
                   q137465
NCBI GI
BLAST score
                   537
                   4.0e-55
E value
                   108
Match length
% identity
                   99
                  VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
NCBI Description
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886
                   H+-transporting ATPase (EC 3.6.1.35) 57K chain -
                   Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding
                   subunit of vacuolar ATPase [Arabidopsis thaliana]
                   170050
Seq. No.
Seq. ID
                   LIB3234-093-P1-K1-H8
Method
                   BLASTX
                   q3335169
NCBI GI
```

E value

Match length

% identity



122 Match length 99 % identity (AF067857) embryo-specific protein 1 [Arabidopsis thaliana] NCBI Description >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] 170051 Seq. No. LIB3234-094-P1-K1-A1 Seq. ID BLASTN Method g2351073 NCBI GI 356 BLAST score 0.0e + 00E value 373 Match length 99 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MYJ24, complete sequence [Arabidopsis thaliana] 170052 Seq. No. Seq. ID LIB3234-094-P1-K1-A10 Method BLASTN q2264321 NCBI GI 137 BLAST score 6.0e-71 E value 181 Match length 96 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MXM12, complete sequence [Arabidopsis thaliana] 170053 Seq. No. Seq. ID LIB3234-094-P1-K1-A2 Method BLASTX NCBI GI q2791834 490 BLAST score 1.0e-49 E value Match length 107 % identity 92 (AF041463) elongation factor 1-alpha [Manihot esculenta] NCBI Description 170054 Seq. No. Seq. ID LIB3234-094-P1-K1-A3 BLASTN Method NCBI GI q4056429 BLAST score 317 1.0e-178 E value 337 Match length % identity 99 Arabidopsis thaliana chromosome 1 BAC F508 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 170055 LIB3234-094-P1-K1-A6 Seq. ID Method BLASTX NCBI GI g2252840 400 BLAST score

23138

5.0e-39

125



60

Match length

% identity

```
(AF013293) contains regions of similarity to Haemophilus
NCBI Description
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
                  170056
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-A7
                  BLASTX
Method
                  q2244906
NCBI GI
                  360
BLAST score
                  2.0e-34
E value
                  101
Match length
                  71
% identity
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  170057
Seq. No.
                  LIB3234-094-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159709
BLAST score
                  88
E value
                  8.0e-42
                  302
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLN21, complete sequence
                  170058
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-A9
                  BLASTN
Method
NCBI GI
                  q3366536
BLAST score
                  89
                  2.0e-42
E value
                  379
Match length
                  99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T25N2O,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  170059
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  g266693
BLAST score
                  248
                   3.0e-21
E value
Match length
                  99
                   52
% identity
                  OLEOSIN >gi 282875 pir S22538 oleosin - Arabidopsis
NCBI Description
                   thaliana >gi 16405 emb CAA44225 (X62353) oleosin
                   [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                  170060
Seq. No.
                  LIB3234-094-P1-K1-B11
Seq. ID
                  BLASTX
Method
                  g3894194
NCBI GI
BLAST score
                  50
                  9.0e-16
E value
```



```
(AC005662) putative strictosidine synthase [Arabidopsis
NCBI Description
                  thaliana]
                  170061
Seq. No.
                  LIB3234-094-P1-K1-B3
Seq. ID
                  BLASTN
Method
                   q4581138
NCBI GI
BLAST score
                   95
                   6.0e-46
E value
                   380
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
NCBI Description
                   sequence, complete sequence
                   170062
Seq. No.
Seq. ID
                   LIB3234-094-P1-K1-B4
                   BLASTN
Method
                   q4581138
NCBI GI
BLAST score
                   38
                   4.0e-12
E value
                   154
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F1011 genomic
NCBI Description
                   sequence, complete sequence
                   170063
Seq. No.
                   LIB3234-094-P1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4220535
BLAST score
                   463
                   2.0e-46
E value
                   90
Match length
                   100
% identity
                   (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                   thaliana]
                   170064
Seq. No.
                   LIB3234-094-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q114330
BLAST score
                   227
                   5.0e-19
E value
                   48
Match length
                   92
 % identity
                   PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                   >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                   type 1, plasma membrane - Arabidopsis thaliana >gi_166746
                   (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                   thaliana]
                   170065
 Seq. No.
                   LIB3234-094-P1-K1-B8
 Seq. ID
                   BLASTX
 Method
                   g2129639
NCBI GI
                   487
BLAST score
```

3.0e-49

101

E value

Match length

NCBI GI BLAST score

E value

Match length

316 3.0e-29

106



```
% identity
                  luminal binding protein (BiP) - Arabidopsis thaliana
NCBI Description
                  >gi 1303695 dbj BAA12348 (D84414) luminal binding protein
                   (BiP) [Arabidopsis thaliana]
                  170066
Seq. No.
                  LIB3234-094-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  g3157949
NCBI GI
                  196
BLAST score
                  4.0e-15
E value
                  71
Match length
                  49
% identity
                  (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                  precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185
                  and gb AA605362 come from this gene. [Arabidopsis thaliana]
                  170067
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-C10
Method
                  BLASTN
                   g3367500
NCBI GI
BLAST score
                   93
                   2.0e-45
E value
                   97
Match length
                   99
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                   TO: 93489, complete sequence [Arabidopsis thaliana]
                   170068
Seq. No.
Seq. ID
                   LIB3234-094-P1-K1-C11
Method
                   BLASTX
                   g2827143
NCBI GI
                   327
BLAST score
                   2.0e-30
E value
Match length
                   58
                   100
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   170069
Seq. ID
                   LIB3234-094-P1-K1-C12
Method
                   BLASTN
                   q4757407
NCBI GI
BLAST score
                   113
E value
                   1.0e-56
Match length
                   263
% identity
                   94
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQD19, complete sequence
                   170070
Seq. No.
                   LIB3234-094-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g136739
```



```
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  170071
Seq. No.
                  LIB3234-094-P1-K1-C3
Seq. ID
                  BLASTN
Method
                  g4159712
NCBI GI
                  98
BLAST score
                  5.0e-48
E value
                  184
Match length
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
                  170072
Seq. No.
                  LIB3234-094-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g114974
NCBI GI
                   211
BLAST score
                   7.0e-17
E value
                   60
Match length
                   65
% identity
                  NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                  >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21)
                  precursor (clone TRE361) - white clover
                   >gi 21955 emb CAA40058.1_ (X56734) beta-glucosidase
                   [Trifolium repens]
                   170073
Seq. No.
                   LIB3234-094-P1-K1-C6
Seq. ID
Method
                   BLASTX
                   g3249096
NCBI GI
BLAST score
                   103
                   3.0e-04
E value
                   126
Match length
% identity
                   12
                   (AC003114) Match to mRNA for importin alpha-like protein 4
NCBI Description
                   (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440,
                   gb N37503, gb N37498 and gb T42198 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   170074
                   LIB3234-094-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   g1170503
NCBI GI
BLAST score
                   469
                   4.0e-47
E value
                   90
Match length
```

% identity

91



[Arabidopsis thaliana]

```
170075
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-C8
Method
                  BLASTN
                  q4589437
NCBI GI
                  269
BLAST score
E value
                  1.0e-150
                  361
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPN9, complete sequence
                  170076
Seq. No.
                  LIB3234-094-P1-K1-D1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3860242
BLAST score
                  319
E value
                  1.0e-179
                  378
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome I BAC T13M11 genomic
NCBI Description
                  sequence, complete sequence
                  170077
Seq. No.
                  LIB3234-094-P1-K1-D12
Seq. ID
                  BLASTN
Method
                   q4468103
NCBI GI
BLAST score
                   236
E value
                   1.0e-130
Match length
                   374
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
NCBI Description
                   (ESSA project)
                   170078
Seq. No.
                  LIB3234-094-P1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g112682
                   550
BLAST score
                   1.0e-56
E value
Match length
                   123
                   84
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   170079
Seq. No.
                   LIB3234-094-P1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q112682
BLAST score
                   229
E value
                   9.0e-51
                   116
Match length
```

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsīs thaliana >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis tha $\overline{\text{liana}}$ >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] 170080 Seq. No. Seq. ID LIB3234-094-P1-K1-D4 BLASTN Method g3212846 NCBI GI 353 BLAST score 0.0e + 00E value 373 Match length 99 % identity Arabidopsis thaliana chromosome II BAC F6E13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 170081 Seq. No. Seq. ID LIB3234-094-P1-K1-D7 BLASTN Method NCBI GI g2760172 320 BLAST score 1.0e-180 E value 336 Match length 99 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MUB3, complete sequence [Arabidopsis thaliana] 170082 Seq. No. Seq. ID LIB3234-094-P1-K1-D8 Method BLASTX q3738288 593 1.0e-61

NCBI GI BLAST score E value Match length 120 % identity

(AC005309) auxin-responsive GH3-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 170083

LIB3234-094-P1-K1-E10 Seq. ID

Method BLASTN NCBI GI q4584841 BLAST score 60 4.0e-25 E value Match length 438 49 % identity

Genomic sequence for Arabidopsis thaliana BAC T23E23, NCBI Description

complete sequence

170084 Seq. No.

LIB3234-094-P1-K1-E11 Seq. ID

Method BLASTN q4519183 NCBI GI BLAST score 319 1.0e-179 E value 380 Match length



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15C23, complete sequence
                  170085
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-E3
                  BLASTN
Method
NCBI GI
                  g16472
BLAST score
                  317
E value
                  1.0e-178
                  365
Match length
                  46
% identity
                  A.thaliana rRNA repeat unit, most frequent IGR type
NCBI Description
                  170086
Seq. No.
                  LIB3234-094-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  375
E value
                  4.0e-36
                  96
Match length
                  70
% identity
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
NCBI Description
Seq. No.
                  170087
Seq. ID
                  LIB3234-094-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  g3540210
BLAST score
                   321
E value
                   0.0e + 00
Match length
                   361
                   97
% identity
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170088
                  LIB3234-094-P1-K1-E7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4159707
BLAST score
                  79
                   2.0e-36
E value
Match length
                   251
                   86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJK13, complete sequence
                   170089
Seq. No.
                   LIB3234-094-P1-K1-E8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16472
                   256
BLAST score
                   1.0e-142
E value
Match length
                   287
                   46
% identity
```

A.thaliana rRNA repeat unit, most frequent IGR type

23145

170090

NCBI Description

Seq. No.



```
LIB3234-094-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1402914
                  434
BLAST score
                  5.0e-43
E value
Match length
                  118
                  75
% identity
NCBI Description (X98318) peroxidase [Arabidopsis thaliana]
                  170091
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-F5
                  BLASTN
Method
                  g4455229
NCBI GI
BLAST score
                  274
                  1.0e-153
E value
                   359
Match length
                   94
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
NCBI Description
                   (ESSAII project)
                   170092
Seq. No.
                  LIB3234-094-P1-K1-F6
Seq. ID
                  BLASTN
Method
                   g16404
NCBI GI
BLAST score
                   97
E value
                   3.0e-47
                   121
Match length
                   95
% identity
                  A.thaliana gene for oleosin >gi 2477486 gb_I57068_I57068
NCBI Description
                   Sequence 1 from patent US
                   170093
Seq. No.
                   LIB3234-094-P1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3150415
BLAST score
                   561
                   6.0e-58
E value
Match length
                   123
                   81
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   170094
Seq. No.
                   LIB3234-094-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   q3150415
NCBI GI
                   99
BLAST score
                   1.0e-29
E value
Match length
                   116
                   61
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
```

LIB3234-094-P1-K1-G1

Seq. No.

Seq. ID



```
BLASTN
Method
                  g16450
NCBI GI
                  82
BLAST score
                  2.0e-38
E value
Match length
                  194
% identity
                  87
NCBI Description A.thaliana rab18 gene
Seq. No.
                  170096
                  LIB3234-094-P1-K1-G11
Seq. ID
Method
                  BLASTN
                  q4589446
NCBI GI
                  55
BLAST score
                  2.0e-22
E value
Match length
                  87
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  T12B11, complete sequence
Seq. No.
                  170097
Seq. ID
                  LIB3234-094-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q4314363
BLAST score
                  486
                  4.0e-49
E value
Match length
                  103
                  85
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  170098
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-G2
                  BLASTX
Method
                  g125576
NCBI GI
                  146
BLAST score
                  3.0e-09
E value
                  62
Match length
                  81
% identity
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC
                   2.7.1.19) precursor - Arabidopsis thaliana
                   >gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate
                   kinase [Arabidopsis thaliana]
                  170099
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-G5
                   BLASTX
Method
                   q2462834
NCBI GI
                   390
BLAST score
                   7.0e-38
E value
                   104
Match length
                   69
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   170100
                   LIB3234-094-P1-K1-G6
Seq. ID
```

BLASTX

q4336436

Method NCBI GI



```
388
BLAST score
                  1.0e-37
E value
Match length
                  99
                  71
% identity
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
                  170101
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-G7
                  BLASTX
Method
                  q4336436
NCBI GI
                  381
BLAST score
                  8.0e-37
E value
                  119
Match length
                  62
% identity
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
                  170102
Seq. No.
                  LIB3234-094-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g16245
NCBI GI
                   608
BLAST score
                   2.0e-63
E value
                   126
Match length
                   96
% identity
                   (X51514) precursor acetolactate synthase (670 AA)
NCBI Description
                   [Arabidopsis thaliana]
                   170103
Seq. No.
Seq. ID
                   LIB3234-094-P1-K1-H11
Method
                   BLASTX
                   q3915961
NCBI GI
                   507
BLAST score
                   1.0e-51
E value
                   114
Match length
                   88
% identity
                   HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                   >qi 2924274 emb CAA77427 (Z00044) Ycf2 protein [Nicotiana
                   tabacum] >gi 2924285 emb CAA77438 (Z00044) hypothetical
                   protein [Nicotiana tabacum]
                   170104
Seq. No.
                   LIB3234-094-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   q4454476
NCBI GI
BLAST score
                   198
                   2.0e-15
E value
Match length
                   52
                   75
% identity
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   170105
Seq. No.
                   LIB3234-094-P1-K1-H2
Seq. ID
Method
                   BLASTX
                   g3617741
NCBI GI
                   647
BLAST score
                   5.0e-68
E value
```

23148

124

Match length

% identity

NCBI Description



```
% identity
                   (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
                   170106
Seq. No.
                  LIB3234-094-P1-K1-H3
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2264306
                   52
BLAST score
                   3.0e-20
E value
                   60
Match length
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
                   170107
Seq. No.
Seq. ID
                  LIB3234-094-P1-K1-H4
                   BLASTX
Method
NCBI GI
                   q2815905
                   255
BLAST score
                   5.0e-22
E value
                   86
Match length
                   60
% identity
                   (AF043734) Pros45 proteosome subunit homolog [Drosophila
NCBI Description
                   melanogaster]
Seq. No.
                   170108
Seq. ID
                   LIB3234-094-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   g4757406
BLAST score
                   357
                   0.0e + 00
E value
Match length
                   373
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPF21, complete sequence
                   170109
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-A1
Method
                   BLASTN
                   g4096078
NCBI GI
BLAST score
                   318
                   1.0e-179
E value
Match length
                   354
                   97
% identity
                   Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170110
Seq. No.
                   LIB3234-095-P1-K1-A10
Seq. ID
Method
                   BLASTX
                   g2462931
NCBI GI
BLAST score
                   646
E value
                   6.0e-68
                   124
Match length
                   100
```

(Z83833) UDP-glucose:sterol glucosyltransferase



[Arabidopsis thaliana]

```
170111
Seq. No.
                  LIB3234-095-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135858
BLAST score
                   436
                   3.0e-43
E value
                  124
Match length
                   71
% identity
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
```

>qi 99760 pir S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi 16182 emb CAA45114 (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi 166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

```
Seq. No.
                   170112
                   LIB3234-095-P1-K1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3510343
BLAST score
                   318
                   1.0e-179
E value
Match length
                   356
```

99

% identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJC20, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   170113
                   LIB3234-095-P1-K1-A6
Seq. ID
                   BLASTX
Method
                   q135858
NCBI GI
BLAST score
                   238
                   3.0e-20
E value
```

63 Match length 76 % identity

TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) NCBI Description

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi 166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

170114 Seq. No.

LIB3234-095-P1-K1-A8 Seq. ID

Method BLASTX g4309731 NCBI GI BLAST score 306 4.0e-28 E value Match length 71 83 % identity

(AC006439) hypothetical protein [Arabidopsis thaliana] NCBI Description

170115 Seq. No.

LIB3234-095-P1-K1-B1 Seq. ID

Seq. ID



```
BLASTX
Method
                  q3033375
NCBI GI
BLAST score
                  458
                  7.0e-46
E value
                  122
Match length
                  68
% identity
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  170116
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  g266693
BLAST score
                  467
                  6.0e-47
E value
                  116
Match length
                  83
% identity
                  OLEOSIN >gi 282875_pir S22538 oleosin - Arabidopsis
NCBI Description
                  thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin
                   [Arabidopsis thaliana] >gi 4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                  170117
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-B11
                  BLASTX
Method
                  g2129653
NCBI GI
                   638
BLAST score
                   6.0e-67
E value
                   123
Match length
                   100
% identity
                  myosin heavy chain MYA2 - Arabidopsis thaliana
NCBI Description
                   >gi 499047 emb_CAA84066 (Z34293) myosin [Arabidopsis
                   thaliana]
Seq. No.
                   170118
                   LIB3234-095-P1-K1-B3
Seq. ID
                   BLASTX
Method
                   q585922
NCBI GI
BLAST score
                   345
E value
                   1.0e-32
                   118
Match length
% identity
                   60
                  DNA-DIRECTED RNA POLYMERASE BETA" CHAIN
NCBI Description
                   170119
Seq. No.
                   LIB3234-095-P1-K1-B4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4376087
BLAST score
                   331
                   0.0e + 00
E value
Match length
                   347
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   170120
Seq. No.
                   LIB3234-095-P1-K1-B5
```

NCBI GI

g544424



```
BLASTX
Method
NCBI GI
                  g2388582
                  95
BLAST score
                  2.0e-59
E value
                  121
Match length
% identity
                  (ACO00098) Contains similarity to Rattus O-GlcNAc
NCBI Description
                  transferase (gb U76557). [Arabidopsis thaliana]
                  170121
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-B6
                  BLASTX
Method
                  g2160151
NCBI GI
BLAST score
                  447
                  1.0e-44
E value
                  106
Match length
                  83
% identity
                  (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                   (gb X77260). [Arabidopsis thaliana]
                  170122
Seq. No.
                  LIB3234-095-P1-K1-B8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4454004
BLAST score
                  42
E value
                  2.0e-14
                  134
Match length
                   87
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                   (ESSAII project)
                   170123
Seq. No.
                  LIB3234-095-P1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2851581
BLAST score
                   538
                   3.0e-55
E value
Match length
                   124
                   86
% identity
NCBI Description
                   DNA-DIRECTED RNA POLYMERASE BETA CHAIN
                   >gi 2196464_emb_CAA74024 (Y13690) DNA-dependent RNA
                   polymerase subunit beta [Arabidopsis thaliana]
Seq. No.
                   170124
                   LIB3234-095-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510348
BLAST score
                   519
                   5.0e-53
E value
Match length
                   106
                   94
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                   170125
Seq. No.
                   LIB3234-095-P1-K1-C11
Seq. ID
Method
                   BLASTX
```



```
441
BLAST score
                  7.0e-44
E value
                  85
Match length
                  100
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir__S30147
NCBI Description
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                  [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                  170126
Seq. No.
                  LIB3234-095-P1-K1-C12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4757407
                  113
BLAST score
                  1.0e-56
E value
                  226
Match length
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQD19, complete sequence
                  170127
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-C2
                  BLASTX
Method
                   g131336
NCBI GI
                   236
BLAST score
                   7.0e-20
E value
Match length
                   50
                   92
% identity
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715_pir_ F2NT0P
NCBI Description
                   photosystem II phosphoprotein psbH - common tobacco
                   chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
                   >gi 225225_prf__1211235BG photosystem II 10kD
                   phosphoprotein [Nicotiana tabacum]
                   170128
Seq. No.
                   LIB3234-095-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1906826
BLAST score
                   347
                   7.0e-33
E value
Match length
                   117
% identity
                   61
                  (Y11827) heat shock protein [Arabidopsis thaliana]
NCBI Description
                   170129
Seq. No.
                   LIB3234-095-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   g4581168
NCBI GI
BLAST score
                   235
                   1.0e-19
E value
```

(AC006220) hypothetical protein [Arabidopsis thaliana]

114

43

Match length % identity

NCBI Description

NCBI GI BLAST score

E value

Match length



```
170130
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  q135858
BLAST score
                  252
                  1.0e-21
E value
                  51
Match length
                  100
% identity
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >qi 99760 pir S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi 16182_emb CAA45114_ (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                   thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                   [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast
                   intrinsic protein alpha [Arabidopsis Thaliana]
Seq. No.
                   170131
Seq. ID
                  LIB3234-095-P1-K1-C8
Method
                  BLASTN
NCBI GI
                   q4519187
BLAST score
                   351
                   0.0e+00
E value
                   371
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K1G2, complete sequence
                   170132
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-C9
Method
                   BLASTN
                   q3805755
NCBI GI
                   297
BLAST score
                   1.0e-166
E value
Match length
                   337
                   81
% identity
                   Arabidopsis thaliana chromosome II BAC T25N22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170133
Seq. ID
                   LIB3234-095-P1-K1-D10
Method
                   BLASTN
                   q2264317
NCBI GI
                   204
BLAST score
E value
                   1.0e-111
                   374
Match length
                   47
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUG13, complete sequence [Arabidopsis thaliana]
                   170134
Seq. No.
                   LIB3234-095-P1-K1-D11
Seq. ID
                   BLASTN
Method
```

23154

g2264317

102 4.0e-50



```
45
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170135
                  LIB3234-095-P1-K1-D12
Seq. ID
Method
                  BLASTN
                  g4467094
NCBI GI
BLAST score
                  286
                  1.0e-160
E value
                  377
Match length
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
NCBI Description
                  (ESSA project)
Seq. No.
                  170136
                  LIB3234-095-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  g1255951
NCBI GI
BLAST score
                  501
E value
                  6.0e-51
Match length
                  120
                  78
% identity
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                  170137
Seq. No.
                  LIB3234-095-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  g2499236
NCBI GI
                  286
BLAST score
E value
                  1.0e-25
                  77
Match length
                  81
% identity
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST
NCBI Description
                  >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis
                  thaliana]
                  170138
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-D4
                  BLASTN
Method
                  q2392762
NCBI GI
BLAST score
                   62
                   2.0e-26
E value
Match length
                   145
                   73
% identity
                  Arabidopsis thaliana BAC T32N15 from chromsome III near 54
NCBI Description
                  cM, complete sequence
                   170139
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q82207
BLAST score
                   623
                   3.0e-65
E value
Match length
                   124
                   96
% identity
```

23155

NCBI Description hypothetical protein 1708 - common tobacco chloroplast



63

[Vitis vinifera]

% identity

NCBI Description

```
170140
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-D8
                   BLASTN
Method
                   g3046856
NCBI GI
                   333
BLAST score
                   0.0e+00
E value
                   368
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                   MXI22, complete sequence [Arabidopsis thaliana]
                   170141
Seq. No.
                   LIB3234-095-P1-K1-D9
Seq. ID
                   BLASTX
Method
                   g115484
NCBI GI
                   168
BLAST score
                   7.0e-12
E value
                   123
Match length
% identity
                   38
                   CALMODULIN 1 >gi 71684 pir MCPZDC calmodulin - carrot
NCBI Description
                   >gi_478632_pir__S22971_calmodulin - trumpet lily
>gi_541839_pir__S40301_calmodulin - Red bryony
                   >qi 2129970 pir S70768 calmodulin CAM81 - garden petunia
                   >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota]
>gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium
                   longiflorum] >gi 169207 (M80836) calmodulin [Petunia
                   hybrida] >gi 308900 (L18912) calmodulin [Lilium
                   longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin
                    [Malus domestica] >gi_535444 (U13882) calmodulin [Pisum
                   sativum] >gi 445602 prf 1909349A calmodulin [Daucus
                   carota]
                   170142
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1174779
BLAST score
                   51
E value
                    2.0e-47
Match length
                   117
                    86
% identity
                   TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 166894
NCBI Description
                    (M81620) tryptophan synthase beta-subunit [Arabidopsis
                    thaliana] >qi 4490703 emb CAB38837.1 (AL035680) tryptophan
                    synthase beta-subunit (TSB2) [Arabidopsis thaliana]
                    170143
Seq. No.
                   LIB3234-095-P1-K1-E10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2564114
BLAST score
                    252
                    1.0e-21
E value
Match length
                    81
```

(AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase

NCBI Description

thaliana]



```
170144
Seq. No.
                  LIB3234-095-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3894156
BLAST score
                  138
                  1.0e-71
E value
Match length
                  330
% identity
                  95
                  Arabidopsis thaliana chromosome II BAC T16F16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170145
                  LIB3234-095-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q465602
BLAST score
                  223
                  3.0e-18
E value
Match length
                  84
                  55
% identity
                  HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION
NCBI Description
                  >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490
                   (AE000306) orf, hypothetical protein [Escherichia coli]
                  >gi 744200 prf 2014253BL yeiN gene [Escherichia coli]
                  170146
Seq. No.
                  LIB3234-095-P1-K1-E3
Seq. ID
Method
                  BLASTN
                  g3510345
NCBI GI
                  61
BLAST score
                  1.0e-25
E value
                  141
Match length
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170147
Seq. ID
                  LIB3234-095-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  q3264778
BLAST score
                   416
E value
                   6.0e-41
Match length
                   93
% identity
                   84
                  (AF072536) H-protein promoter binding factor-1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   170148
                  LIB3234-095-P1-K1-E6
Seq. ID
Method
                   BLASTX
                   g2708750
NCBI GI
BLAST score
                   214
                   3.0e-17
E value
Match length
                   109
% identity
                   49
```

(AC003952) putative physical impedence protein [Arabidopsis

Seq. ID

Method

BLASTX



```
170149
Seq. No.
                  LIB3234-095-P1-K1-E8
Seq. ID
                  BLASTN
Method
                  g2244870
NCBI GI
BLAST score
                  262
                  1.0e-145
E value
                  369
Match length
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  170150
Seq. No.
                  LIB3234-095-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g1592677
NCBI GI
                  180
BLAST score
                   3.0e-13
E value
                   38
Match length
                   95
% identity
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                   170151
Seq. No.
                   LIB3234-095-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   g2500376
NCBI GI
                   407
BLAST score
                   4.0e-40
E value
                   79
Match length
                   97
% identity
                  60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb_AAD14494_
NCBI Description
                   (AC005508) 23552 [Arabidopsis thaliana]
                   170152
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-F12
Method
                   BLASTX
                   g4455313
NCBI GI
                   409
BLAST score
                   4.0e-40
E value
                   127
Match length
% identity
                   (AL035528) fatty acid elongase-like protein (cer2-like)
NCBI Description
                   [Arabidopsis thaliana]
                   170153
Seq. No.
Seq. ID
                   LIB3234-095-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g4454587
                   25
BLAST score
                   1.0e-04
E value
Match length
                   64
                   77
% identity
                   Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
                   170154
Seq. No.
                   LIB3234-095-P1-K1-F3
```

Method

NCBI GI

BLAST score



```
g4336436
NCBI GI
                  265
BLAST score
                  3.0e-23
E value
                  98
Match length
                  54
% identity
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
NCBI Description
                  170155
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-F5
                  BLASTN
Method
                  g4512690
NCBI GI
BLAST score
                  318
                  1.0e-179
E value
                  326
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
NCBI Description
                  sequence, complete sequence
                  170156
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-F6
Method
                  BLASTX
                  g99737
NCBI GI
                  641
BLAST score
                  3.0e-67
E value
                  127
Match length
                   98
% identity
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                  Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                  170157
Seq. No.
                  LIB3234-095-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   q2947060
NCBI GI
BLAST score
                   479
                   2.0e-48
E value
Match length
                   99
                   83
% identity
NCBI Description
                  (AC002521) putative membrane protein [Arabidopsis thaliana]
Seq. No.
                   170158
                   LIB3234-095-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4033469
BLAST score
                   399
                   6.0e-39
E value
Match length
                   75
% identity
                   58
                   ARGININE/SERINE-RICH SPLICING FACTOR RSP41
NCBI Description
                   >gi_1707370_emb_CAA67799_ (X99436) splicing factor
                   [Arabidopsis thaliana]
                   170159
Seq. No.
                   LIB3234-095-P1-K1-G1
Seq. ID
```

23159

BLASTX

109

q1703200



1.0e-23 E value 108 Match length 57 % identity PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase NCBI Description [Arabidopsis thaliana] >gi 642130 dbj BAA08214 (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana] 170160 Seq. No. LIB3234-095-P1-K1-G11 Seq. ID BLASTN Method g3702735 NCBI GI BLAST score 349 0.0e+00E value 383 Match length 57 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MQL5, complete sequence [Arabidopsis thaliana] 170161 Seq. No. LIB3234-095-P1-K1-G12 Seq. ID BLASTX Method NCBI GI g1628622 BLAST score 435 E value 3.0e-4388 Match length % identity (U72631) flavonol synthase [Arabidopsis thaliana] NCBI Description >gi 1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi 1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >qi 1805309 (U84260) flavonol synthase [Arabidopsis thaliana] Seq. No. 170162 LIB3234-095-P1-K1-G2 Seq. ID BLASTX Method g3033400 NCBI GI BLAST score 437 E value 2.0e-43 120 Match length % identity (AC004238) putative Ser/Thr protein kinase [Arabidopsis NCBI Description thaliana] Seq. No. 170163 LIB3234-095-P1-K1-G3 Seq. ID Method BLASTN NCBI GI g3702736 BLAST score 146

8.0e-77 E value 154 Match length % identity 99

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MRI1, complete sequence [Arabidopsis thaliana]

170164 Seq. No.

NCBI GI



```
LIB3234-095-P1-K1-G4
Seq. ID
                  BLASTN
Method
                  g3406034
NCBI GI
BLAST score
                  366
                  0.0e+00
E value
                  386
Match length
                  99
% identity
                  BAC F18A17 from chromosome V containing TINY at 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  170165
Seq. No.
                  LIB3234-095-P1-K1-G6
Seq. ID
                  BLASTN
Method
                  g3367500
NCBI GI
                  126
BLAST score
                  2.0e-64
E value
                  293
Match length
                  98
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
                  170166
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-G7
                  BLASTN
Method
NCBI GI
                  g3608126
                  40
BLAST score
                  4.0e-13
E value
                  116
Match length
                  92
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170167
Seq. No.
Seq. ID
                  LIB3234-095-P1-K1-G8
Method
                  BLASTX
                  g3738306
NCBI GI
                  465
BLAST score
                  1.0e-46
E value
                  121
Match length
% identity
                  69
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  170168
Seq. No.
                  LIB3234-095-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2832644
BLAST score
                  266
                  1.0e-24
E value
Match length
                   83
                   74
% identity
                  (AL021710) teosinte branched1 - like protein [Arabidopsis
NCBI Description
                   thaliana]
                  170169
Seq. No.
                  LIB3234-095-P1-K1-H11
Seq. ID
Method
                  BLASTN
```

23161

g4582444



BLAST score 78
E value 4.0e-36
Match length 162
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC T9H9 genomic

sequence, complete sequence

Seq. No. 170170

Seq. ID LIB3234-095-P1-K1-H12

Method BLASTX
NCBI GI g3004564
BLAST score 178
E value 5.0e-13
Match length 105
% identity 39

NCBI Description (AC003673) putative receptor Ser/Thr protein kinase

[Arabidopsis thaliana]

Seq. No. 170171

Seq. ID LIB3234-095-P1-K1-H2

Method BLASTX
NCBI GI 94335735
BLAST score 659
E value 2.0e-69
Match length 122
% identity 99

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 170172

Seq. ID LIB3234-095-P1-K1-H3

Method BLASTX
NCBI GI g2130149
BLAST score 637
E value 7.0e-67
Match length 124
% identity 99

NCBI Description translation elongation factor eEF-1 alpha chain - maize

(fragment)

Seq. No. 170173

Seq. ID LIB3234-095-P1-K1-H4

Method BLASTN
NCBI GI g4159712
BLAST score 198
E value 1.0e-107
Match length 238
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 170174

Seg. ID LIB3234-095-P1-K1-H5

Method BLASTN
NCBI GI g3980374
BLAST score 138
E value 1.0e-71
Match length 174



```
95
% identity
                  Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170175
Seq. No.
                  LIB3234-095-P1-K1-H6
Seq. ID
                  BLASTN
Method
                  q4589432
NCBI GI
BLAST score
                  94
                  1.0e-45
E value
Match length
                  151
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MMJ24, complete sequence
                  170176
Seq. No.
                  LIB3234-095-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  g2739388
NCBI GI
BLAST score
                  162
E value
                  2.0e-36
Match length
                  92
                  77
% identity
                   (AC002505) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  170177
Seq. No.
                  LIB3234-096-P1-K1-A11
Seq. ID
                  BLASTN
Method
                  g3135250
NCBI GI
BLAST score
                  191
                  1.0e-103
E value
                  329
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F27F23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170178
Seq. No.
                  LIB3234-096-P1-K1-A12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4699904
BLAST score
                  136
E value
                   6.0e-71
Match length
                  136
                   64
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,
                   complete sequence
                   170179
Seq. No.
                  LIB3234-096-P1-K1-A3
Seq. ID
Method
                   BLASTN
                   q4558586
NCBI GI
BLAST score
                   358
                   0.0e+00
E value
Match length
                   383
                   98
% identity
```

NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence,



complete sequence

```
170180
Seq. No.
Seq. ID
                  LIB3234-096-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  192
                  4.0e-47
E value
Match length
                  122
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir_ S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  170181
Seq. No.
                  LIB3234-096-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449331
                  372
BLAST score
                  0.0e + 00
E value
                  376
Match length
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC17, complete sequence [Arabidopsis thaliana]
                  170182
Seq. No.
Seq. ID
                  LIB3234-096-P1-K1-A9
Method
                  BLASTX
                   q1067224
NCBI GI
                   288
BLAST score
E value
                   6.0e-26
                   120
Match length
% identity
                   46
                   (Z67999) serine palmitoyltransferase 2 [Schizosaccharomyces
NCBI Description
                  pombe]
                   170183
Seq. No.
Seq. ID
                   LIB3234-096-P1-K1-B1
                   BLASTN
Method
NCBI GI
                   q4314374
BLAST score
                   165
                   5.0e-88
E value
Match length
                   181
% identity
                   98
                   Arabidopsis thaliana chromosome II BAC F10A12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170184
                   LIB3234-096-P1-K1-B10
Seq. ID
Method
                   BLASTX
                   g1864017
NCBI GI
                   548
BLAST score
                   2.0e-56
E value
                   109
Match length
```

97

% identity



```
170185
Seq. No.
                  LIB3234-096-P1-K1-B11
Seq. ID
                  BLASTN
Method
                  g4199934
NCBI GI
                  277
BLAST score
                  1.0e-154
E value
                  360
Match length
                  93
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  170186
Seq. No.
Seq. ID
                  LIB3234-096-P1-K1-B12
                  BLASTN
Method
                  g4314374
NCBI GI
                  351
BLAST score
                  0.0e+00
E value
                  374
Match length
% identity
                  11
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170187
Seq. No.
                  LIB3234-096-P1-K1-B3
Seq. ID
                  BLASTX
Method
                   g3335169
NCBI GI
                   365
BLAST score
                   5.0e-35
E value
Match length
                   111
                   63
% identity
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                   >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                   protein 1 (ATS1) [Arabidopsis thaliana]
                   170188
Seq. No.
                   LIB3234-096-P1-K1-B4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4263753
BLAST score
                   125
E value
                   6.0e-64
                   303
Match length
% identity
                   99
                   Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   170189
Seq. No.
                   LIB3234-096-P1-K1-B5
Seq. ID
Method
                   BLASTN
                   g2924505
NCBI GI
                   155
BLAST score
                   9.0e-82
E value
                   360
Match length
                   91
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
NCBI Description
```

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

23165

(ESSAII project)



170190

LIB3234-096-P1-K1-B6

Seq. No.

Seq. ID

```
Method
                  BLASTX
                  g2341033
NCBI GI
BLAST score
                  645
                  9.0e-68
E value
                  127
Match length
                  99
% identity
                   (AC000104) Similar to Babesia aldo-keto reductase
NCBI Description
                   (gb M93122). [Arabidopsis thaliana]
                  170191
Seq. No.
Seq. ID
                  LIB3234-096-P1-K1-B7
Method
                  BLASTX
                   g4581045
NCBI GI
                   575
BLAST score
                   1.0e-59
E value
                   127
Match length
                   87
% identity
                   (AF134324) chlorophyll a-binding protein PsbC [Populus
NCBI Description
                  deltoides]
                   170192
Seq. No.
Seq. ID
                   LIB3234-096-P1-K1-B8
                   BLASTX
Method
                   g82051
NCBI GI
                   302
BLAST score
                   1.0e-27
E value
                   113
Match length
% identity
                   55
                   lipid body-associated membrane protein - carrot
NCBI Description
                   >gi 259453 bbs 117620 (S47635) lipid body membrane
                   protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                   180 aa] [Daucus carota]
                   170193
Seq. No.
                   LIB3234-096-P1-K1-B9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2656027
                   376
BLAST score
E value
                   0.0e + 00
                   380
Match length
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJH22
                   170194
Seq. No.
                   LIB3234-096-P1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4704730
BLAST score
                   166
E value
                   1.0e-11
                   55
Match length
                   60
% identity
NCBI Description (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]
```



```
170195
Seq. No.
Seq. ID
                   LIB3234-096-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3152587
                   488
BLAST score
                   2.0e-49
E value
Match length
                   111
% identity
                   81
NCBI Description
```

NCBI Description (AC002986) Similar to CREB-binding protein homolog gb U88570 from D. melanogaster and contains similarity to

callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

 Seq. No.
 170196

 Seq. ID
 LIB3234-096-P1-K1-C3

 Method
 BLASTX

 NCBI GI
 g4204299

 BLAST score
 574

BLAST score 574
E value 2.0e-59
Match length 113
% identity 99

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 170197

Seq. ID LIB3234-096-P1-K1-C4

Method BLASTX
NCBI GI g1419090
BLAST score 270
E value 8.0e-24
Match length 69
% identity 75

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 170198

Seq. ID LIB3234-096-P1-K1-C6

Method BLASTX
NCBI GI g3928758
BLAST score 548
E value 2.0e-56
Match length 121
% identity 91

NCBI Description (AB007987) Lipoic acid synthase [Arabidopsis thaliana]

>gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid

synthase [Arabidopsis thaliana]

Seq. No. 170199

Seq. ID LIB3234-096-P1-K1-C7

Method BLASTX
NCBI GI g1765899
BLAST score 498
E value 1.0e-50
Match length 119
% identity 83

NCBI Description (Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244

(U86700) EGF receptor like protein [Arabidopsis thaliana]

Seq. ID



Seq. No.

170200

```
LIB3234-096-P1-K1-C9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2952432
                  173
BLAST score
                  1.0e-92
E value
                  317
Match length
                  89
% identity
                  Arabidopsis thaliana putative ubiquitin activating enzyme
NCBI Description
                  E1 (ECR1) mRNA, complete cds
                  170201
Seq. No.
                  LIB3234-096-P1-K1-D1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3805755
                  117
BLAST score
                  3.0e-59
E value
                  149
Match length
                   95
% identity
                  Arabidopsis thaliana chromosome II BAC T25N22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  170202
Seq. No.
                  LIB3234-096-P1-K1-D10
Seq. ID
                  BLASTX
Method
                   g1526424
NCBI GI
                   466
BLAST score
                   8.0e-47
E value
                   106
Match length
                   88
% identity
                  (D64140) LEA protein in group 3 [Arabidopsis thaliana]
NCBI Description
                   170203
Seq. No.
Seq. ID
                  LIB3234-096-P1-K1-D11
                   BLASTX
Method
                   q225282
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
                   120
Match length
                   56
% identity
NCBI Description RNA polymerase beta [Nicotiana tabacum]
                   170204
Seq. No.
                   LIB3234-096-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129642
BLAST score
                   642
                   2.0e-67
E value
Match length
                   118
% identity
                   98
                   major latex protein type 3 - Arabidopsis thaliana
NCBI Description
                   >gi 1107495 emb CAA63027_ (X91961) major latex protein
                   type3 [Arabidopsis thaliana]
Seq. No.
                   170205
```

23168

LIB3234-096-P1-K1-D2



```
BLASTX
Method
                  g118926
NCBI GI
                  377
BLAST score
                  2.0e-36
E value
                  125
Match length
                  56
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi 227781_prf_ 1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
                  170206
Seq. No.
                  LIB3234-096-P1-K1-D3
Seq. ID
Method
                  BLASTX
                   g4678285
NCBI GI
                   181
BLAST score
                   2.0e-13
E value
                   124
Match length
% identity
                   37
                  (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
                   170207
Seq. No.
                   LIB3234-096-P1-K1-D5
Seq. ID
                   BLASTN
Method
                   g4263540
NCBI GI
                   323
BLAST score
                   0.0e+00
E value
                   335
Match length
                   85
% identity
                  Arabidopsis thaliana chromosome II BAC T6A13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170208
Seq. No.
                   LIB3234-096-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g3132475
NCBI GI
                   471
BLAST score
                   2.0e-47
E value
                   108
Match length
% identity
                   (AC003096) similar to proline-rich protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   170209
                   LIB3234-096-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   g166570
NCBI GI
                   214
BLAST score
E value
                   3.0e-17
Match length
                   100
                   46
% identity
                  (L04173) glycine rich protein [Arabidopsis thal_ana]
NCBI Description
```

170210

LIB3234-096-P1-K1-D8

Seq. No.

Seq. ID



```
BLASTX
Method
                  g4091806
NCBI GI
BLAST score
                  175
                  1.0e-12
E value
                  120
Match length
                  38
% identity
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]
                  170211
Seq. No.
                  LIB3234-096-P1-K1-D9
Seq. ID
                  BLASTN
Method
                  g1419473
NCBI GI
                  71
BLAST score
                  1.0e-31
E value
                  135
Match length
                  88
% identity
NCBI Description A.thaliana chloroplast ndhA gene
                   170212
Seq. No.
                  LIB3234-096-P1-K1-E1
Seq. ID
                  BLASTX
Method
                   g2119353
NCBI GI
                   261
BLAST score
                   4.0e-23
E value
                   74
Match length
                   76
% identity
NCBI Description calmodulin - moss (Physcomitrella patens)
                   170213
Seq. No.
Seq. ID
                   LIB3234-096-P1-K1-E10
Method
                   BLASTX
                   q425194
NCBI GI
                   493
BLAST score
                   6.0e-50
E value
Match length
                   126
                   78
% identity
                   (L26243) heat shock protein [Spinacia oleracea] >gi_2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                   oleracea]
                   170214
Seq. No.
                   LIB3234-096-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   q2062164
NCBI GI
BLAST score
                   87
                   2.4e-02
E value
                   122
Match length
 % identity
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   170215
 Seq. No.
                   LIB3234-096-P1-K1-E12
 Seq. ID
                   BLASTN
 Method
                   g3063690
 NCBI GI
                   84
 BLAST score
```

2.0e-39

E value



136 Match length 90 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 NCBI Description

(ESSAII project)

170216 Seq. No.

LIB3234-096-P1-K1-E2 Seq. ID

BLASTN Method NCBI GI q4691223 379 BLAST score 0.0e+00E value 383 Match length 100 % identity

Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 NCBI Description

(ESSA project)

170217 Seq. No.

LIB3234-096-P1-K1-E3 Seq. ID

Method BLASTN q4309683 NCBI GI BLAST score 352 E value 0.0e + 00372 Match length 99 % identity

Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

170218 Seq. No.

Seq. ID LIB3234-096-P1-K1-E4

BLASTX Method NCBI GI g4115943 496 BLAST score 3.0e-50 E value 98 Match length 91 % identity

(AF118223) contains similarity to eukaryotic protein kinase NCBI Description

domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4)

[Arabidopsis thaliana]

170219 Seq. No.

Seq. ID LIB3234-096-P1-K1-E6

BLASTX Method NCBI GI q4455337 BLAST score 631 4.0e-66 E value 127 Match length % identity

(AL035525) pectinesterase-like protein [Arabidopsis NCBI Description

thaliana]

170220 Seq. No.

LIB3234-096-P1-K1-E7 Seq. ID

Method BLASTX NCBI GI q585744 BLAST score 1445.0e-09 E value



Match length 29 % identity 100

NCBI Description PHOTOSYSTEM II REACTION CENTRE T PROTEIN

Seq. No. 170221

Seq. ID LIB3234-096-P1-K1-E8

Method BLASTN
NCBI GI g3341671
BLAST score 309
E value 1.0e-173
Match length 373
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F16B22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170222

Seq. ID LIB3234-096-P1-K1-E9

Method BLASTX
NCBI GI g4583542
BLAST score 273
E value 4.0e-24
Match length 117
% identity 56

NCBI Description (Y16847) 16 kDa polypeptide of oxygen-evolving complex

[Arabidopsis thaliana]

Seq. No. 170223

Seq. ID LIB3234-096-P1-K1-F1

Method BLASTX
NCBI GI g118926
BLAST score 363
E value 1.0e-34
Match length 119
% identity 62

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR

>gi_320600_pir__E45509 desiccation-related protein (clone PCCl3-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781 prf 1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 170224

Seq. ID LIB3234-096-P1-K1-F11

Method BLASTN
NCBI GI g2696018
BLAST score 382
E value 0.0e+00
Match length 382
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 170225

Seq. ID LIB3234-096-P1-K1-F2

Method BLASTN
NCBI GI g3128140
BLAST score 296

% identity



```
1.0e-166
E value
                  361
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE4, complete sequence [Arabidopsis thaliana]
                  170226
Seq. No.
                  LIB3234-096-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g3298542
NCBI GI
BLAST score
                  323
                  5.0e-30
E value
Match length
                   61
                   98
% identity
NCBI Description
                   (AC004681) putative cellulose synthase [Arabidopsis
                  thaliana]
                   170227
Seq. No.
                  LIB3234-096-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2264303
BLAST score
                   349
                   0.0e + 00
E value
                   353
Match length
% identity
                   89
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBB18, complete sequence [Arabidopsis thaliana]
                   170228
Seq. No.
                   LIB3234-096-P1-K1-F6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3047088
                   302
BLAST score
                   1.0e-169
E value
                   354
Match length
                   99
% identity
NCBI Description Arabidopsis thaliana BAC T26D22
                   170229
Seq. No.
                   LIB3234-096-P1-K1-F8
Seq. ID
                   BLASTN
Method
                   q3176694
NCBI GI
                   352
BLAST score
                   0.0e + 00
E value
                   373
Match length
% identity
                   Arabidopsis thaliana chromosome I BAC T14N5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170230
Seq. No.
Seq. ID
                   LIB3234-096-P1-K1-G1
                   BLASTN
Method
                   q4325340
NCBI GI
BLAST score
                   216
E value
                   1.0e-118
Match length
                   363
```

Seq. ID



```
NCBI Description Arabidopsis thaliana BAC T1J1
                  170231
Seq. No.
                  LIB3234-096-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244747
                  227
BLAST score
                  1.0e-125
E value
Match length
                  239
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  170232
Seq. No.
                  LIB3234-096-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g166570
BLAST score
                  174
                   1.0e-12
E value
                  31
Match length
% identity
                  100
                  (L04173) glycine rich protein [Arabidopsis thaliana].
NCBI Description
Seq. No.
                   170233
                   LIB3234-096-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q633890
BLAST score
                   278
                   1.0e-24
E value
Match length
                   89
                   62
% identity
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
                   170234
Seq. No.
Seq. ID
                   LIB3234-096-P1-K1-G6
Method
                   BLASTN
                   g4415905
NCBI GI
BLAST score
                   60
                   4.0e-25
E value
                   120
Match length
% identity
                   72
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170235
Seq. No.
                   LIB3234-096-P1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2245032
BLAST score
                   213
                   4.0e-17
E value
                   95
Match length
                   47
% identity
NCBI Description
                  (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
Seq. No.
                   170236
```

23174

LIB3234-096-P1-K1-G9

BLAST score

E value



```
BLASTN
Method
                  q3695372
NCBI GI
                  126
BLAST score
                  2.0e-64
E value
Match length
                  264
% identity
                  70
NCBI Description Arabidopsis thaliana BAC F1104
                  170237
Seq. No.
                  LIB3234-096-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q4510348
NCBI GI
BLAST score
                  211
                  7.0e-17
E value
Match length
                  58
                  66
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  170238
Seq. No.
                  LIB3234-096-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4507857
BLAST score
                  352
                  2.0e-33
E value
                  125
Match length
                  59
% identity
                  Herpes virus-associated ubiquitin-specific protease
NCBI Description
                  >gi 2501460 sp Q93009 UBPH HUMAN PROBABLE UBIQUITIN
                  CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE
                   HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP)
                   (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED
                   UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952 emb_CAA96580
                   (Z72499) herpesvirus associated ubiquitin-specific protease
                   (HAUSP) [Homo sapiens]
                   170239
Seq. No.
                  LIB3234-096-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   g4220451
NCBI GI
                   270
BLAST score
                   8.0e-24
E value
                   124
Match length
                   18
% identity
                  (AC006216) Identical to gb AF054906 myrosinase-binding
NCBI Description
                   protein homolog from Arabidopsis thaliana. ESTs gb F15276
                   and gb_F15275 come from this gene. [Arabidopsis thaliana]
                   170240
Seq. No.
                   LIB3234-096-P1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3550519
                   354
```

Match length 102 63 % identity NCBI Description (AJ007630) oxygenase [Nicotiana tabacum]

1.0e-33

Seq. ID Method



```
170241
Seq. No.
Seq. ID
                  LIB3234-096-P1-K1-H7
                  BLASTX
Method
NCBI GI
                  g2459430
                  606
BLAST score
                  3.0e-63
E value
                  113
Match length
                  100
% identity
NCBI Description (AC002332) putative CUC2 protein [Arabidopsis thaliana]
                  170242
Seq. No.
                  LIB3234-096-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  g2947062
NCBI GI
BLAST score
                  147
                  2.0e-09
E value
                  98
Match length
                  40
% identity
                  (AC002521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170243
                  LIB3234-096-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g132863
NCBI GI
                  415
BLAST score
                  8.0e-41
E value
                  76
Match length
                  99
% identity
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
NCBI Description
                  >gi 12214 emb CAA46568 (X65615) ribosomal protein L2
                   [Sinapis alba]
                   170244
Seq. No.
                  LIB3234-097-P1-K1-A10
Seq. ID
                  BLASTN
Method
                   g3869062
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
                   341
Match length
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K11I1, complete sequence [Arabidopsis thaliana]
                   170245
Seq. No.
Seq. ID
                   LIB3234-097-P1-K1-A6
Method
                   BLASTN
                   g2618677
NCBI GI
BLAST score
                   246
                   1.0e-136
E value
Match length
                   389
% identity
                   96
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   170246
Seq. No.
```

23176

LIB3234-097-P1-K1-A8

BLASTX



```
NCBI GI
                  g1708194
BLAST score
                  168
                  8.0e-12
E value
                  125
Match length
                  16
% identity
                  HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1)
NCBI Description
                  (VCAF) (CFF) >gi_644882_dbj_BAA08258_ (D45419) HCF
                  [Mesocricetus auratus]
                  170247
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-A9
Method
                  BLASTX
                  q1076393
NCBI GI
                  500
BLAST score
                  9.0e-51
E value
                  103
Match length
                  99
% identity
                  RCI14A protein - Arabidopsis thaliana
NCBI Description
                  >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis
                  thaliana]
Seq. No.
                  170248
Seq. ID
                  LIB3234-097-P1-K1-B11
                  BLASTN
Method
                  q4218109
NCBI GI
                  375
BLAST score
                  0.0e + 00
E value
Match length
                  399
                   98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16
                   (ESSAII project)
                  170249
Seq. No.
                  LIB3234-097-P1-K1-B3
Seq. ID
Method
                  BLASTX
                  q3860272
NCBI GI
                   676
BLAST score
                   2.0e-71
E value
                   136
Match length
                   99
% identity
                   (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4314399 gb_AAD15609_ (AC006232) putative skd1
                   protein [Arabidopsis thaliana]
                   170250
Seq. No.
                   LIB3234-097-P1-K1-B4
Seq. ID
                   BLASTN
Method
                   g3985949
NCBI GI
                   287
BLAST score
                   1.0e-160
E value
                   394
Match length
                   93
% identity
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOB24, complete sequence [Arabidopsis thaliana]

Seq. No. 170251

Seq. ID LIB3234-097-P1-K1-B6

E value

Match length

5.0e-11

73



```
BLASTX
Method
                  g2244760
NCBI GI
BLAST score
                  634
                  2.0e-66
E value
Match length
                  134
% identity
                  91
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.
                  170252
                  LIB3234-097-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539422
BLAST score
                  379
                  1.0e-36
E value
Match length
                  126
% identity
                  61
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                  170253
                  LIB3234-097-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1107482
BLAST score
                  344
E value
                  0.0e+00
Match length
                  395
                  97
% identity
NCBI Description A.thaliana mRNA for 30S ribosomal protein S13
                  170254
Seq. No.
                  LIB3234-097-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4199934
                  274
BLAST score
                  1.0e-153
E value
                  363
Match length
                  94
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
                  170255
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g4263543
BLAST score
                  153
                  1.0e-10
E value
                  62
Match length
% identity
                  56
                  (AC006250) putative Athila retroelement ORF1 protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  170256
                  LIB3234-097-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076758
BLAST score
                  156
```

NCBI Description



```
% identity
                  heat-shock protein precursor - rye >gi_2130093 pir S65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi 556673_emb_CAA82945_ (Z30243) heat-shock protein
                  [Secale cereale]
                  170257
Seq. No.
                  LIB3234-097-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1518540
                  301
BLAST score
                  2.0e-27
E value
                  87
Match length
                  74
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  170258
Seq. No.
                  LIB3234-097-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2911044
BLAST score
                  294
                  6.0e-29
E value
Match length
                  89
                  78
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170259
                  LIB3234-097-P1-K1-C5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4589419
BLAST score
                  188
E value
                  1.0e-101
                  249
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2I5, complete sequence
                  170260
Seq. No.
                  LIB3234-097-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  q4105782
NCBI GI
BLAST score
                  149
                  1.0e-09
E value
                  32
Match length
% identity
                  94
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]
Seq. No.
                  170261
                  LIB3234-097-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g2583135
NCBI GI
BLAST score
                  386
E value
                  2.0e-37
                  72
Match length
                  97
% identity
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
```

23179

>gi 3822216 (AF074948) FIL [Arabidopsis thaliana]

% identity

NCBI Description

96

(ESSA project)



>gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs
protein [Arabidopsis thaliana]

170262 Seq. No. LIB3234-097-P1-K1-C8 Seq. ID Method BLASTX g4678323 NCBI GI BLAST score 532 E value 2.0e-54 Match length 134 % identity 84 (AL049658) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 170263 LIB3234-097-P1-K1-D11 Seq. ID Method BLASTX NCBI GI g4204298 BLAST score 498 E value 2.0e-50 Match length 133 77 % identity NCBI Description (AC003027) lcl prt seq No definition line found [Arabidopsis thaliana] Seq. No. 170264 LIB3234-097-P1-K1-D12 Seq. ID Method BLASTN NCBI GI g2264367 207 BLAST score 1.0e-113 E value 338 Match length % identity 95 Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, NCBI Description complete sequence [Arabidopsis thaliana] 170265 Seq. No. LIB3234-097-P1-K1-D3 Seq. ID BLASTXMethod NCBI GI g3335169 573 BLAST score 3.0e-59 E value 132 Match length 77 % identity (AF067857) embryo-specific protein 1 [Arabidopsis thaliana] NCBI Description >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] 170266 Seq. No. Seq. ID LIB3234-097-P1-K1-D6 BLASTN Method NCBI GI g4835223 BLAST score 323 0.0e+00E value Match length 412

23180

Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3

Seq. ID

Method



170267

```
Seq. No.
                  LIB3234-097-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3183185
BLAST score
                  156
                  2.0e-10
E value
                  45
Match length
% identity
                  67
                  GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG
NCBI Description
                  >gi 2224766 emb CAB09712 (Z97025) product highly similar
                  to elongation factor EF-G [Bacillus subtilis]
                  >gi 2633848 emb CAB13350_ (Z99111) similar to GTP-binding
                  elongation factor [Bacillus subtilis]
                  170268
Seq. No.
                  LIB3234-097-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g3080402
NCBI GI
                  605
BLAST score
                  5.0e-63
E value
Match length
                  126
% identity
                  93
                  (AL022603) putative NADPH quinone oxidoreductase
NCBI Description
                   [Arabidopsis thaliana] >gi 4455266_emb_CAB36802.1_
                   (AL035527) putative NADPH quinone oxidoreductase
                   [Arabidopsis thaliana]
                  170269
Seq. No.
                  LIB3234-097-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130149
                  382
BLAST score
                  2.0e-37
E value
                  79
Match length
                   91
% identity
                  translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                   (fragment)
                  170270
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-E10
                  BLASTX
Method
                  g2829275
NCBI GI
BLAST score
                  159
                   9.0e-11
E value
                   47
Match length
                   72
% identity
                  (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                   thaliana] >gi_3513740 (AF080118) contains similarity to
                   nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                   301.12) [Arabidopsis thaliana] >gi_4539375 emb CAB40069.1
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                   [Arabidopsis thaliana]
                   170271
Seq. No.
```

23181

LIB3234-097-P1-K1-E11

BLASTX

% identity

96



```
g3935151
NCBI GI
                  725
BLAST score
                  4.0e-77
E value
                  134
Match length
% identity
                  99
NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]
                  170272
Seq. No.
                  LIB3234-097-P1-K1-E12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4757414
                   362
BLAST score
                  0.0e+00
E value
                  402
Match length
                   98
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
                   170273
Seq. No.
                   LIB3234-097-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2924257
                   40
BLAST score
                   4.0e-13
E value
                   190
Match length
                   43
% identity
NCBI Description Tobacco chloroplast genome DNA
                   170274
Seq. No.
                   LIB3234-097-P1-K1-E4
Seq. ID
                   BLASTX
Method
                   g2529665
NCBI GI
                   489
BLAST score
                   2.0e-49
E value
                   123
Match length
                   80
% identity
                   (ACO02535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                   thaliana]
                   170275
Seq. No.
                   LIB3234-097-P1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2529721
BLAST score
                   152
                   6.0e-10
E value
                   82
Match length
                   38
% identity
NCBI Description (AF001891) unknown [Homo sapiens]
                   170276
Seq. No.
Seq. ID
                   LIB3234-097-P1-K1-E7
                   BLASTN
Method
                   q3426033
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   332
```



```
Arabidopsis thaliana chromosome II BAC F12C20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170277
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  341
E value
                  0.0e + 00
Match length
                  381
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  170278
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1572819
BLAST score
                  148
E value
                  2.0e-09
Match length
                  113
% identity
NCBI Description
                  (U70855) similar to the RAS gene family [Caenorhabditis
```

elegans]

Seq. No. 170279 Seq. ID LIB3234-097-P1-K1-F10

Method BLASTX NCBI GI g2499236

BLAST score 521 3.0e-53E value Match length 121 % identity 88

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST NCBI Description >gi 1419474 emb CAA66944 (X98298) ndhA [Arabidopsis

thaliana]

170280 Seq. No.

Seq. ID LIB3234-097-P1-K1-F12

BLASTX Method g3914239 NCBI GI BLAST score 666 3.0e-70E value Match length 134 96 % identity

PROTEIN PHOSPHATASE 2C ABI2 (PP2C) NCBI Description

>gi_1945140 emb CAA70163 (Y08966) ABI2 protein phosphatase

2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162

(Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]

>gi 2564213 emb CAA72538 (Y11840) ABI2 [Arabidopsis

thaliana]

170281 Seq. No.

Seq. ID LIB3234-097-P1-K1-F2

Method BLASTX q1419390 NCBI GI BLAST score 589

E value

Match length % identity

1.0e-37 131

63



```
4.0e-61
E value
                  133
Match length
                  86
% identity
                  (X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis
NCBI Description
                  thaliana]
                  170282
Seq. No.
                  LIB3234-097-P1-K1-F5
Seq. ID
Method
                  BLASTN
                  g3738275
NCBI GI
BLAST score
                  320
                  1.0e-180
E value
                  403
Match length
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  170283
Seq. No.
                  LIB3234-097-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q207905
BLAST score
                  231
                  3.0e-19
E value
                  134
Match length
                  37
% identity
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
                  170284
Seq. No.
                  LIB3234-097-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  g2146774
NCBI GI
BLAST score
                   317
                   3.0e-29
E value
                  85
Match length
                  78
% identity
                  serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis
NCBI Description
                   thaliana >gi 905391 (U30298) serine acetyltransferase
                   [Arabidopsis thaliana]
                   170285
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-G1
                  BLASTX
Method
NCBI GI
                   g4510348
BLAST score
                   47
                   3.0e-54
E value
                   128
Match length
                   79
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   170286
Seq. No.
Seq. ID
                   LIB3234-097-P1-K1-G3
                   BLASTX
Method
                   q419789
NCBI GI
BLAST score
                   59
```

NCBI Description



```
NCBI Description hypothetical protein - potato
                  170287
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  150
                  1.0e-78
E value
Match length
                  343
% identity
                  83
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  170288
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-G8
Method
                  BLASTX
                  g3176690
NCBI GI
BLAST score
                  568
                  9.0e-59
E value
                  120
Match length
% identity
                  94
                  (AC003671) Similar to ubiquitin ligase gb D63905 from S.
NCBI Description
                  cerevisiae. EST gb R65295 comes from this gene.
                  [Arabidopsis thaliana]
                  170289
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-G9
                  BLASTX
Method
                  g3738257
NCBI GI
BLAST score
                  447
E value
                  2.0e-44
Match length
                  100
                  88
% identity
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                  170290
Seq. No.
                  LIB3234-097-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589420
                  291
BLAST score
E value
                  1.0e-163
Match length
                  311
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3G17, complete sequence
                  170291
Seq. No.
Seq. ID
                  LIB3234-097-P1-K1-H10
                  BLASTX
Method
NCBI GI
                  g2129641
BLAST score
                  618
E value
                  1.0e-64
Match length
                  113
% identity
                  100
```

major latex protein type 1 - Arabidopsis thaliana
>gi 1107493 emb CAA63026 (X91960) major latex protein



typel [Arabidopsis thaliana]

Seq. No. 170292 Seq. ID LIB3234-097-P1-K1-H12 Method BLASTN NCBI GI g4589445 182 BLAST score E value 6.0e-98 Match length 248 95 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence 170293 Seq. No. Seq. ID LIB3234-097-P1-K1-H4 Method BLASTX NCBI GI g2262167 BLAST score 191 E value 4.0e-15 71 Match length % identity 62 NCBI Description (AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana] Seq. No. 170294 Seq. ID LIB3234-097-P1-K1-H7 Method BLASTX NCBI GI g4589536 BLAST score 175 1.0e-12 E value Match length 40 % identity 62 NCBI Description (AB023163) KIAA0946 protein [Homo sapiens] 170295 Seq. No. Seq. ID LIB3234-097-P1-K1-H8 Method BLASTN NCBI GI g3449334 BLAST score 116 E value 2.0e-58 Match length 367 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana] Seq. No. 170296 LIB3234-097-P1-K1-H9 Seq. ID Method BLASTX NCBI GI q3540196 BLAST score 601 E value 1.0e-62 Match length 125 95 % identity NCBI Description (AC004260) Putative amp-binding protein [Arabidopsis thaliana]

23186

170297

Seq. No.



```
LIB3234-098-P1-K1-A1
Seq. ID
Method
                  BLASTX
                  g131378
NCBI GI
BLAST score
                  220
                  6.0e-18
E value
                  43
Match length -
                  100
% identity
                  PHOTOSYSTEM II REACTION CENTRE N PROTEIN
NCBI Description
                  >gi_2924272_emb_CAA77424 (Z00044) PSII N-protein
                  [Nicotiana tabacum]
                  170298
Seq. No.
Seq. ID
                  LIB3234-098-P1-K1-A10
                  BLASTX
Method
                  g384341
NCBI GI
                  197
BLAST score
                  3.0e-15
E value
                  99
Match length
                  42
% identity
NCBI Description major storage protein [Theobroma cacao]
                  170299
Seq. No.
                  LIB3234-098-P1-K1-A11
Seq. ID
Method
                  BLASTX
                  g3983125
NCBI GI
                  471
BLAST score
                  2.0e-47
E value
                  117
Match length
% identity
                  79
NCBI Description (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  170300
                  LIB3234-098-P1-K1-A12
Seq. ID
Method
                  BLASTN
                  g3128137
NCBI GI
                  246
BLAST score
                  1.0e-136
E value
Match length
                  366
% identity.
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170301
                  LIB3234-098-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3128137
BLAST score
                  267
E value
                  1.0e-148
                  382
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9I9, complete sequence [Arabidopsis thaliana]
```

23187

170302

BLASTX

LIB3234-098-P1-K1-A5

Seq. No. Seq. ID

Method



```
NCBI GI
                  q1929056
                  464
BLAST score
                  1.0e-46
E value
                  98
Match length
                  90
% identity
                  (Y12090) putative 3,4-dihydroxy-2-butanone kinase
NCBI Description
                   [Lycopersicon esculentum]
                  170303
Seq. No.
                  LIB3234-098-P1-K1-A7
Seq. ID
Method
                  BLASTN
```

NCBI GI g4512656 81 BLAST score 1.0e-37 E value Match length 145 % identity 81

Arabidopsis thaliana chromosome II BAC F7D19 genomic NCBI Description

sequence, complete sequence

170304 Seq. No.

LIB3234-098-P1-K1-A8 Seq. ID

Method BLASTX NCBI GI g2499236 BLAST score 388 1.0e-37 E value Match length 92 85 % identity

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST NCBI Description

>qi 1419474 emb CAA66944 (X98298) ndhA [Arabidopsis

thaliana]

170305 Seq. No.

LIB3234-098-P1-K1-A9 Seq. ID

BLASTX Method NCBI GI g462147 BLAST score 60 2.0e-53 E value Match length 125 % identity 87

GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) NCBI Description

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi 541866 pir S41808 glucose-6-phosphate isomerase

(EC 5.3.1.9) - Arabidopsis thaliana

>gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate

isomerase [Arabidopsis thaliana]

170306 Seq. No.

Seq. ID LIB3234-098-P1-K1-B1

BLASTX Method q1432083 NCBI GI 471 BLAST score 2.0e-47 E value 102 Match length 91 % identity

(U60981) homolog to Skplp, an evolutionarily conserved NCBI Description

kinetochore protein in budding yeast [Arabidopsis thaliana] >qi 3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]



>gi 3719209 (U97020) UIP1 [Arabidopsis thaliana]

```
170307
Seq. No.
                  LIB3234-098-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2088725
BLAST score
                  199
                  2.0e-15
E value
                  92
Match length
                  43
% identity
                  (AF003140) weak similarity to the drosophila hyperplastic
NCBI Description
                  disc protein (GB:L14644) [Caenorhabditis elegans]
                  170308
Seq. No.
                  LIB3234-098-P1-K1-B4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4732165
                  114
BLAST score
                  3.0e-57
E value
Match length
                  311
                  90
% identity
NCBI Description Arabidopsis thaliana BAC F14G16
Seq. No.
                  170309
                  LIB3234-098-P1-K1-B8
Seq. ID
                  BLASTN
Method
                  a4662628
NCBI GI
BLAST score
                   71
E value
                  8.0e-32
                  223
Match length
                   91
% identity
                  Arabidopsis thaliana chromosome II BAC F27010 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                   170310
                   LIB3234-098-P1-K1-C1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4586098
                   311
BLAST score
                   1.0e-175
E value
                   355
Match length
% identity
                   97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
NCBI Description
                   (ESSA project)
Seq. No.
                   170311
                   LIB3234-098-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g633890
NCBI GI
BLAST score
                   288
                   6.0e-26
E value
                   89
Match length
                   64
% identity
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
```

23189

170312

Seq. No.



LIB3234-098-P1-K1-C12 Seq. ID

Method BLASTX NCBI GI q2780225 BLAST score 253 E value 8.0e-22 Match length 103 % identity 50

NCBI Description (AJ223281) alpha-hydroxynitrile lyase [Manihot esculenta]

Seq. No. 170313

LIB3234-098-P1-K1-C2 Seq. ID

Method BLASTN NCBI GI g4096078 BLAST score 87 E value 3.0e-41 Match length 209 % identity 86

NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170314

Seq. ID LIB3234-098-P1-K1-C3

Method BLASTX NCBI GI q112682 BLAST score 561 E value 6.0e-58 Match length 104 % identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 170315

Seq. ID LIB3234-098-P1-K1-C4

Method BLASTN NCBI GI q2618600 BLAST score 77 E value 3.0e-35 Match length 369 96 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDC12, complete sequence [Arabidopsis thaliana]

Seq. No. 170316

Seq. ID LIB3234-098-P1-K1-C5

BLASTN Method NCBI GI q3335331 BLAST score 208 E value 1.0e-113 Match length 254 % identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,

complete sequence [Arabidopsis thaliana]

170317 Seq. No.



```
Seq. ID
                   LIB3234-098-P1-K1-C6
Method
                  BLASTX
NCBI GI
                   q3522956
BLAST score
                   243
                   1.0e-20
E value
Match length
                   72
                   69
% identity
NCBI Description
                   (AC004411) putative pectinacetylesterase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   170318
Seq. ID
                  LIB3234-098-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  q2914688
BLAST score
                  152
                   4.0e-80
E value
                  200
Match length
                   94
% identity
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170319
Seq. No.
Seq. ID
                  LIB3234-098-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q3242723
BLAST score
                   108
E value
                   2.0e-17
Match length
                   108
% identity
                   50
NCBI Description
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
                   thaliana]
                   170320
Seq. No.
                  LIB3234-098-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4589445
BLAST score
                   61
E value
                   1.0e-25
Match length
                  113
                   88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWL2, complete sequence
                   170321
Seq. No.
Seq. ID
                  LIB3234-098-P1-K1-D5
Method
                  BLASTN
NCBI GI
                   q4757392
BLAST score
                  110
                   5.0e-55
E value
Match length
                  245
                   97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
```

Seq. No. 170322

Seq. ID LIB3234-098-P1-K1-D6

Method BLASTN



```
g3510347
NCBI GI
BLAST score
                   251
                  1.0e-139
E value
                  310
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  170323
Seq. No.
                  LIB3234-098-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2996096
BLAST score
                  391
                  5.0e-38
E value
                  106
Match length
                  75
% identity
                  (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                  alpha [Oryza sativa]
                  170324
Seq. No.
                  LIB3234-098-P1-K1-D9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2244788
BLAST score
                  228
E value
                  1.0e-125
Match length
                  332
% identity
                  92
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  170325
                  LIB3234-098-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4415928
BLAST score
                  158
E value
                   1.0e-83
Match length
                   322
                   95
% identity
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170326
Seq. ID
                  LIB3234-098-P1-K1-E10
Method
                  BLASTN
NCBI GI
                   q2564049
BLAST score
                  139
E value
                   1.0e-72
Match length
                   171
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170327
```

Seq. ID LIB3234-098-P1-K1-E2

Method BLASTN NCBI GI g4757406 BLAST score 213



E value 1.0e-116 Match length 245 97 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPF21, complete sequence 170328 Seq. No. LIB3234-098-P1-K1-E3 Seq. ID Method BLASTX NCBI GI g3242709 BLAST score 219 E value 8.0e-18 Match length 114 % identity 43 (AC003040) putative guanine nucleotide-binding protein NCBI Description [Arabidopsis thaliana] 170329 Seq. No. LIB3234-098-P1-K1-E4 Seq. ID Method BLASTX NCBI GI q4038040 BLAST score 292 E value 2.0e-26 Match length 77 77 % identity (AC005936) proteinase inhibitor II [Arabidopsis thaliana] NCBI Description Seq. No. 170330 LIB3234-098-P1-K1-E5 Seq. ID Method BLASTX NCBI GI q4455371 BLAST score 389 E value 9.0e-38 Match length 109 % identity 75 NCBI Description (AL035524) putative protein [Arabidopsis thaliana] Seq. No. 170331 LIB3234-098-P1-K1-E6 Seq. ID BLASTX Method NCBI GI g3128195 BLAST score 76 E value 1.0e-29 75 Match length % identity 95 NCBI Description [Arabidopsis thaliana] >gi 3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

(AC004521) putative phosphoribosyl pyrophosphate synthetase

Seq. No. 170332

Seq. ID LIB3234-098-P1-K1-E7

Method BLASTN NCBI GI g4757414 BLAST score 319 E value 1.0e-179 Match length 375



% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 170333

Seq. ID LIB3234-098-P1-K1-E8

Method BLASTN
NCBI GI g4558656
BLAST score 90
E value 5.0e-43
Match length 101
% identity 33

NCBI Description Arabidopsis thaliana chromosome II BAC T10F5 genomic

sequence, complete sequence

Seq. No. 170334

Seq. ID LIB3234-098-P1-K1-E9

Method BLASTN
NCBI GI g2583106
BLAST score 245
E value 1.0e-135
Match length 359
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170335

Seq. ID LIB3234-098-P1-K1-F1

Method BLASTX
NCBI GI g116392
BLAST score 541
E value 1.0e-55
Match length 106
% identity 97

NCBI Description CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE)

>gi_66543_pir__SYMUCN naringenin-chalcone synthase (EC

2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308)

chalcone synthase [Arabidopsis thaliana]

Seq. No. 170336

Seq. ID LIB3234-098-P1-K1-F10

Method BLASTN
NCBI GI g4581103
BLAST score 223
E value 1.0e-122
Match length 344
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T24I21 genomic

sequence, complete sequence

Seq. No. 170337

Seq. ID LIB3234-098-P1-K1-F11

Method BLASTX
NCBI GI g228403
BLAST score 513
E value 2.0e-52
Match length 116

Match length

% identity

121

49



```
% identity
NCBI Description glycolate oxidase [Lens culinaris]
                  170338
Seq. No.
                  LIB3234-098-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046853
BLAST score
                  47
E value
                  2.0e-17
Match length
                  94
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170339
                  LIB3234-098-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827621
BLAST score
                  294
E value
                  1.0e-26
Match length
                  118
                  50
% identity
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                  170340
                  LIB3234-098-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1071912
BLAST score
                  395
E value
                  1.0e-38
Match length
                  83
% identity
                  cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis
NCBI Description
                  thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine
                  synthase [Arabidopsis thaliana]
                  170341
Seq. No.
Seq. ID
                  LIB3234-098-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g4206197
                  77
BLAST score
                  2.0e-43
E value
Match length
                  116
                  83
% identity
NCBI Description
                  (AF071527) putative pre-mRNA splicing factor [Arabidopsis
                  thaliana]
                  170342
Seq. No.
Seq. ID
                  LIB3234-098-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  g4468804
BLAST score
                  311
E value
                  1.0e-28
```

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

% identity

82



```
Seq. No.
                  170343
                  LIB3234-098-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1071912
BLAST score
                  426
                  2.0e-47
E value
Match length
                  118
                  89
% identity
                  cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis
NCBI Description
                  thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine
                  synthase [Arabidopsis thaliana]
                  170344
Seq. No.
                  LIB3234-098-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3128189
BLAST score
                  280
                  3.0e-25
E value
                  85
Match length
                  69
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170345
                  LIB3234-098-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1502428
BLAST score
                  394
E value
                  2.0e-38
Match length
                  78
                  100
% identity
                  (U62330) phosphate transporter [Arabidopsis thaliana]
NCBI Description
                  >gi 2258116 dbj BAA21503 (D86591) inorganic phosphate
                  transporter [Arabidopsis thaliana]
                  >gi_2258118 dbj BAA21504 (D86608) inorganic phosphate
                   transporter [Arabidopsis thaliana]
Seq. No.
                  170346
Seq. ID
                  LIB3234-098-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  q267055
                   357
BLAST score
E value
                   6.0e-34
Match length
                  78
                   95
% identity
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   >gi_66572_pir__YUMU sucrose synthase (EC 2.4.1.13)
                  Arabidopsis thaliana >gi_16526_emb_CAA43303_ (X60987)
                   sucrose synthase [Arabidopsis thaliana]
Seq. No.
                   170347
                  LIB3234-098-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4589062
BLAST score
                   311
E value
                   1.0e-28
Match length
                   67
```



NCBI Description (AF120146) myo-inositol 1-phosphate synthase [Triticum aestivum] >gi_4589064_gb_AAD26331.1_AF120147_1 (AF120147) myo-inositol 1-phosphate synthase [Triticum aestivum]

>gi_4589066_gb_AAD26332.1_AF120148_1 (AF120148)

myo-inositol 1-phosphate synthase [Triticum aestivum]

Seq. No. 170348

Seq. ID LIB3234-098-P1-K1-G6

Method BLASTN
NCBI GI g4757403
BLAST score 71
E value 5.0e-32
Match length 117
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJL12, complete sequence

Seq. No. 170349

Seq. ID LIB3234-098-P1-K1-G7

Method BLASTN
NCBI GI g3348076
BLAST score 102
E value 3.0e-50
Match length 102

NCBI Description Arabidopsis thaliana isochorismate synthase mRNA, complete

cds

100

Seq. No. 170350

% identity

Seq. ID LIB3234-098-P1-K1-G9

Method BLASTX
NCBI GI g3024358
BLAST score 464
E value 1.0e-46
Match length 124

% identity 73

NCBI Description PHENYLALANINE AMMONIA-LYASE G4 >gi 1374783 dbj BAA07861

(D43803) phenylalanine ammonia-lyase [Populus

kitakamiensis]

Seq. No. 170351

Seq. ID LIB3234-098-P1-K1-H1

Method BLASTN
NCBI GI g2828186
BLAST score 58
E value 2.0e-24
Match length 102

% identity 90 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 170352

Seq. ID LIB3234-098-P1-K1-H10

Method BLASTX
NCBI GI g2511590
BLAST score 387
E value 1.0e-37



```
Match length
                  84
                  94
% identity
                  (Y13692) multicatalytic endopeptidase complex, proteasome
NCBI Description
                  component, beta subunit [Arabidopsis thaliana] >gi_3421111
                  (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis
                  thaliana]
Seq. No.
                  170353
                  LIB3234-098-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928862
                  145
BLAST score
                  4.0e-09
E value
Match length
                  126
% identity
                  39
                  (AF089710) disease resistance protein RPP8 [Arabidopsis
NCBI Description
                  thaliana]
                  170354
Seq. No.
                  LIB3234-098-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2623962
                  339
BLAST score
                  6.0e-32
E value
                  70
Match length
                  93
% identity
                  (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                  graveolens]
                  170355
Seq. No.
                  LIB3234-098-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159707
BLAST score
                  241
E value
                  1.0e-133
Match length
                  378
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJK13, complete sequence
Seq. No.
                  170356
Seq. ID
                  LIB3234-098-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  q3510338
BLAST score
                  278
                   1.0e-155
E value
Match length
                  360
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21I16, complete sequence [Arabidopsis thaliana]
```

Seq. No. 170357

Seq. ID LIB3234-098-P1-K1-H7

Method BLASTX
NCBI GI g3075394
BLAST score 111
E value 6.0e-43



Match length 93 % identity 99

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi 3559809 emb_CAA09311_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No. 170358

Seq. ID LIB3234-098-P1-K1-H8

Method BLASTN
NCBI GI g1209632
BLAST score 198
E value 1.0e-107
Match length 258
% identity 95

NCBI Description Arabidopsis thaliana pattern-formation (GNOM) gene,

complete cds

Seq. No. 170359

Seq. ID LIB3234-098-P1-K1-H9

Method BLASTX
NCBI GI g400846
BLAST score 143
E value 6.0e-09
Match length 49
% identity 19

NCBI Description MAJOR PRION PROTEIN HOMOLOG PRECURSOR (PR-LP)

(ACETYLCHOLINE RECEPTOR-INDUCING ACTIVITY) (ARIA) (65-21 PROTEIN) >gi_422698_pir_A46280 prion protein - chicken

>gi_212611 (M95404) prion protein [Gallus gallus]

Seq. No. 170360

Seq. ID LIB3234-100-P1-K1-A1

Method BLASTN
NCBI GI g2656028
BLAST score 51
E value 4.0e-20

E value 4.0e-20 Match length 146 % identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 170361

Seq. ID LIB3234-100-P1-K1-A6

Method BLASTX
NCBI GI g2244897
BLAST score 644
E value 1.0e-67
Match length 126
% identity 98

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 170362

Seq. ID LIB3234-100-P1-K1-A8

Method BLASTX
NCBI GI g2262167
BLAST score 557
E value 2.0e-57



```
Match length
                  124
                  90
% identity
                  (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  170363
                  LIB3234-100-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  g4584255
NCBI GI
                  293
BLAST score
                  1.0e-26
E value
Match length
                  93
                  61
% identity
                  (Y18471) SINA1p [Vitis vinifera]
NCBI Description
Seq. No.
                  170364
                  LIB3234-100-P1-K1-B1
Seq. ID
Method
                  BLASTN
                   g4263694
NCBI GI
                   303
BLAST score
                   1.0e-170
E value
                   358
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170365
Seq. No.
                   LIB3234-100-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   g4586052
NCBI GI
                   45
BLAST score
                   4.0e-49
E value
                   119
Match length
                   82
% identity
                  (AC007020) unknown protein [Arabidopsis thaliana]
NCBI Description
                   170366
Seq. No.
                   LIB3234-100-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   q1542941
NCBI GI
                   180
BLAST score
                   2.0e-13
E value
Match length
                   47
                   85
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                   170367
Seq. No.
                   LIB3234-100-P1-K1-B4
Seq. ID
Method
                   BLASTX
                   q1351135
NCBI GI
                   630
BLAST score
                   6.0e-66
E value
Match length
                   132
                   93
 % identity
                   SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   >gi_436792_emb_CAA50317_ (X70990) sucrose synthase
```

[Arabidopsis thaliana]



Seq. No. 170368

Seq. ID LIB3234-100-P1-K1-B6

Method BLASTX
NCBI GI g131286
BLAST score 395
E value 1.0e-38
Match length 99
% identity 79

NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN PRECURSOR (P6

PROTEIN) (CP43) >gi_2144937_pir__F2SP44 photosystem II chlorophyll a-binding protein psbC - spinach chloroplast >gi_12281_emb_CAA25864_ (X01724) 44 kd reaction-centre protein [Spinacia oleracea] >gi_343362 (M36833) 44 kD

chlorophyll a apoprotein [Spinacia oleracea]

Seq. No. 170369

Seq. ID LIB3234-100-P1-K1-B7

Method BLASTX
NCBI GI g2499535
BLAST score 438
E value 2.0e-43
Match length 128
% identity 69

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 170370

Seq. ID LIB3234-100-P1-K1-B8

Method BLASTX
NCBI GI g4455341
BLAST score 320
E value 1.0e-29
Match length 101
% identity 68

NCBI Description (AL035522) O-methyltransferase-like protein [Arabidopsis

thaliana]

Seq. No. 170371

Seq. ID LIB3234-100-P1-K1-B9

Method BLASTX
NCBI GI g462147
BLAST score 699
E value 4.0e-74
Match length 133
% identity 99

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase

(EC 5.3.1.9) - Arabidopsis thaliana

>gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 170372

Seq. ID LIB3234-100-P1-K1-C4

Method BLASTN



NCBI GI g4159708 BLAST score 362 E value 0.0e+00 Match length 394 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence

Seq. No. 170373

Seq. ID LIB3234-100-P1-K1-C8

Method BLASTN
NCBI GI g4432811
BLAST score 277
E value 1.0e-154
Match length 379
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F16D14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170374

Seq. ID LIB3234-100-P1-K1-D1

Method BLASTN
NCBI GI g4734003
BLAST score 283
E value 1.0e-158
Match length 370
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F3L12 genomic

sequence, complete sequence

Seq. No. 170375

Seq. ID LIB3234-100-P1-K1-D11

Method BLASTN
NCBI GI g2264303
BLAST score 23
E value 5.0e-03
Match length 101

Match length 101 % identity 64

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBB18, complete sequence [Arabidopsis thaliana]

Seq. No. 170376

Seq. ID LIB3234-100-P1-K1-D12

Method BLASTN
NCBI GI g3805755
BLAST score 262
E value 1.0e-145
Match length 360
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T25N22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170377

Seq. ID LIB3234-100-P1-K1-D2

Method BLASTX NCBI GI g1345973 BLAST score 471



E value 2.0e-47 Match length 105 % identity 82

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 170378

Seq. ID LIB3234-100-P1-K1-D3

Method BLASTN
NCBI GI g3108025
BLAST score 125
E value 7.0e-64
Match length 318
% identity 97

NCBI Description Arabidopsis thaliana chromosome 1 BAC T13D8, complete

sequence [Arabidopsis thaliana]

Seq. No. 170379

Seq. ID LIB3234-100-P1-K1-D8

Method BLASTN
NCBI GI g4584519
BLAST score 156
E value 1.0e-82
Match length 210
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18

(ESSA project)

Seq. No. 170380

Seq. ID LIB3234-100-P1-K1-E10

Method BLASTX
NCBI GI g267069
BLAST score 540
E value 2.0e-55
Match length 100
% identity 100

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 170381

Seq. ID LIB3234-100-P1-K1-E2

Method BLASTN
NCBI GI g3980374
BLAST score 394
E value 0.0e+00
Match length 402
% identity 40

NCBI Description Arabidopsis thaliana chromosome II BAC F16P2 genomic



sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                    170382
Seq. ID
                    LIB3234-100-P1-K1-E3
Method
                    BLASTN
NCBI GI
                    g3980374
BLAST score
                    201
E value
                    1.0e-109
Match length
                    328
% identity
                    50
                    Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    170383
Seq. No.
                    LIB3234-100-P1-K1-E6
Seq. ID
Method
                    BLASTN
NCBI GI
                    q3449322
BLAST score
                    282
E value
                    1.0e-157
Match length
                    306
% identity
                    63
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MXC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                    170384
                    LIB3234-100-P1-K1-F11
Seq. ID
Method
                    BLASTN
NCBI GI
                    q4159706
BLAST score
                    321
                    0.0e+00
E value
Match length
                    362
                    100
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                    MGL6, complete sequence
Seq. No.
                    170385
Seq. ID
                    LIB3234-100-P1-K1-F12
Method
                    BLASTX
NCBI GI
                    g2252634
BLAST score
                    184
E value
                    1.0e-13
Match length
                    59
% identity
NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    170386
Seq. ID
                    LIB3234-100-P1-K1-F4
Method
                    BLASTX
NCBI GI
                    g131372
BLAST score
                    161
E value
                    6.0e-11
Match length
                    34
                    100
% identity
                    PHOTOSYSTEM II REACTION CENTRE M PROTEIN
NCBI Description
                    >gi_72719_pir__F2RZM photosystem II protein psbM - rice
chloroplast >gi_11969_emb_CAA33984 (X15901) PSII low MW
protein [Oryza sativa] >gi_2924261_emb_CAA77413 (Z00044)
```



PSII M-protein [Nicotiana tabacum] >gi 226687 prf 1603356M photosystem II low MW protein [Oryza sativa]

Seq. No. 170387

LIB3234-100-P1-K1-F6 Seq. ID

Method BLASTN NCBI GI q3335170 BLAST score 83 E value 5.0e-39 Match length 228 % identity 92

NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,

complete cds

Seq. No. 170388

Seq. ID LIB3234-100-P1-K1-F8

Method BLASTX NCBI GI q3335169 BLAST score 414 E value 9.0e-41 Match length 83 92 % identity

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

170389 Seq. No.

Seq. ID LIB3234-100-P1-K1-G10

Method BLASTX NCBI GI g137580 BLAST score 168 E value 8.0e-12 Match length 126 % identity 32

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)

> >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi 167375 (M16891) vicilin precursor

[Gossypium hirsutum]

170390 Seq. No.

Seq. ID LIB3234-100-P1-K1-G6

BLASTX Method NCBI GI g1076366 BLAST score 548 E value 2.0e-56 Match length 106

% identity 97

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis

thaliana >gi 460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186)

cyclophilin [Arabidopsis thaliana]

>gi 1091580 prf 2021266A peptidyl-Pro cis-trans isomerase

[Arabidopsis thaliana]

Seq. No. 170391

Seq. ID LIB3234-100-P1-K1-H1

Method BLASTX

Seq. No.

Seq. ID

170396

LIB35-001-Q1-E1-C8



```
NCBI GI
                  q3421094
BLAST score
                  496
E value
                  3.0e-50
Match length
                  103
% identity
                  94
NCBI Description
                  (AF043527) 20S proteasome subunit PAF2 [Arabidopsis
                  thaliana]
                  170392
Seq. No.
Seq. ID
                  LIB35-001-Q1-E1-A2
                  BLASTX
Method
NCBI GI
                  g1717957
                  97
BLAST score
                  2.0e-09
E value
Match length
                  90
                  49
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT
NCBI Description
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)
                  >gi_100923_pir__A41607 ubiquinol--cytochrome-c reductase
                   (EC 1.10.2.2) iron-sulfur protein precursor - maize
                  >gi_168607 (M77224) Rieske Fe-S protein [Zea mays]
                  170393
Seq. No.
                  LIB35-001-Q1-E1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2245031
                  401
BLAST score
E value
                  0.0e + 00
Match length
                  409
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  170394
                  LIB35-001-Q1-E1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3150396
BLAST score
                  49
                  2.0e-18
E value
Match length
                  77
                  91
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T27E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170395
Seq. ID
                  LIB35-001-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                  g4335755
BLAST score
                  217
E value
                  1.0e-17
Match length
                  102
% identity
                   55
                  (AC006284) putative hydroxyproline-rich glycoprotein
NCBI Description
                   [Arabidopsis thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  q3123279
BLAST score
                  381
E value
                  9.0e-37
Match length
                  78
                  91
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S26 >gi 2651298 (AC002336) putative
                  ribosomal protein S26 [Arabidopsis thaliana]
                  170397
Seq. No.
Seq. ID
                  LIB35-001-Q1-E1-D8
Method
                  BLASTN
                  g531828
NCBI GI
BLAST score
                  33
E value
                  2.0e-09
Match length
                  81
% identity
                  85
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  170398
Seq. ID
                  LIB35-001-Q1-E1-E4
Method
                  BLASTX
NCBI GI
                  g4827253
BLAST score
                  591
E value
                  2.0e-61
Match length
                  126
% identity
                  90
NCBI Description (AB027002) plastidic aldolase [Nicotiana paniculata]
Seq. No.
                  170399
Seq. ID
                  LIB35-001-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  g3241923
BLAST score
                  59
E value
                  2.0e-24
Match length
                  95
                  91
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170400
Seq. ID
                  LIB35-001-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g2961285
BLAST score
                  382
E value
                  3.0e-37
Match length
                  72
                  97
% identity
NCBI Description
                  (Y16848) cinnamyl alcohol dehydrogenase-like protein,
                  subunit b [Arabidopsis thaliana]
Seq. No.
                  170401
Seq. ID
                  LIB35-001-Q1-E1-F1
```

Method BLASTX NCBI GI g4185511 BLAST score 440 E value 9.0e-44



```
Match length
                  85
                  100
% identity
NCBI Description
                  (AF102822) actin depolymerizing factor 4 [Arabidopsis
                  thaliana]
                  170402
Seq. No.
Seq. ID
                  LIB35-001-Q1-E1-H1
Method
                  BLASTX
                  g4559396
NCBI GI
BLAST score
                  131
E value
                  5.0e-39
Match length
                  104
% identity
                  88
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170403
                  LIB35-002-Q1-E1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q544424
BLAST score
                  305
E value
                  4.0e-28
Match length
                  70
                  86
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                   [Arabidopsis thaliana] >gi 166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >gi_4567224_gb_AAD23639.1 AC007119 5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                  170404
Seq. ID
                  LIB35-002-Q1-E1-E9
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  148
E value
                  1.0e-77
Match length
                  350
                  43
% identity
NCBI Description Tobacco chloroplast genome DNA
                  170405
Seq. No.
Seq. ID
                  LIB35-002-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  q131398
                   339
BLAST score
E value
                   6.0e-32
Match length
                  98
```

% identity 73
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400



come from this gene. [Arabidopsis

Seq. No. 170406 LIB35-002-Q1-E1-G1 Seq. ID Method BLASTX NCBI GI q131398 BLAST score 451 E value 5.0e-45 107 Match length % identity 86 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis Seq. No. 170407 Seq. ID LIB35-003-Q1-E1-A11 Method BLASTN NCBI GI g2264318 BLAST score 166 E value 2.0e-88 Match length 336 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MUP24, complete sequence [Arabidopsis thaliana] Seq. No. 170408 LIB35-003-Q1-E1-B10 Seq. ID Method BLASTX NCBI GI q2689631 BLAST score 183 E value 1.0e-13 Match length 59 % identity NCBI Description (AF022389) ADP-ribosylation factor [Vigna unquiculata] Seq. No. 170409 Seq. ID LIB35-003-Q1-E1-B4 Method BLASTN NCBI GI q4096078 BLAST score 203 E value 1.0e-110 Match length 385 % identity 100 NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 170410

Seq. ID LIB35-003-Q1-E1-D3

Method BLASTN NCBI GI g4063730 BLAST score 136



9.0e-71 E value Match length 176 97 % identity

NCBI Description Arabidopsis thaliana BAC F21J6 from chromosome V,

containing KNAT3 and mapping near 60.5 cM, complete

sequence [Arabidopsis thaliana]

170411 Seq. No.

Seq. ID LIB35-003-Q1-E1-E6

Method BLASTN NCBI GI g3193311 BLAST score 305 E value 1.0e-171 Match length 324 98 % identity

NCBI Description Arabidopsis thaliana BAC F6N15

170412 Seq. No.

LIB35-004-Q1-E1-E2 Seq. ID

Method BLASTX NCBI GI g4581163 BLAST score 357 E value 4.0e-34 Match length 70 % identity 99

NCBI Description (AC006220) unknown protein [Arabidopsis thaliana]

170413 Seq. No.

Seq. ID LIB35-004-Q1-E1-F1

Method BLASTN NCBI GI g4220641 BLAST score 192 1.0e-104 E value Match length 346

83 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUL3, complete sequence [Arabidopsis thaliana]

Seq. No. 170414

Seq. ID LIB35-004-Q1-E1-G7

Method BLASTX NCBI GI g131398 BLAST score 191 E value 1.0e-14 Match length 87 % identity 51

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170415



```
LIB35-004-Q1-E1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   a267077
BLAST score
                   624
                   6.0e-72
E value
                   147
Match length
                   97
% identity
NCBI Description
                   TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5
                   chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5
                   tubulin [Arabidopsis thaliana]
Seq. No.
                   170416
                   LIB35-005-Q1-E1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346156
BLAST score
                   321
                   1.0e-29
E value
Match length
                   87
                   72
% identity
NCBI Description
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481943_pir__S40213 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                   >gi_437997_emb_CAA81079_ (Z25860) glycine
                   hydroxymethyltransferase [Flaveria pringlei]
Seq. No.
                   170417
                   LIB35-005-01-E1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131398
BLAST score
                   214
E value
                   1.0e-17
Match length
                   62
% identity
                   74
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi 3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                   come from this gene. [Arabidopsis
```

Seq. No. 170418 Seq. ID LIB35-005-Q1-E1-E5 Method BLASTX NCBI GI g115783 BLAST score 505 E value 2.0e-51

Match length 95 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]



```
Seq. No.
                  170419
Seq. ID
                  LIB35-005-Q1-E1-F10
Method
                  BLASTX
                  q4262182
NCBI GI
BLAST score
                  322
                  4.0e-50
E value
Match length
                  107
                  93
% identity
NCBI Description (AC005508) 44123 [Arabidopsis thaliana]
Seq. No.
                  170420
Seq. ID
                  LIB35-005-Q1-E1-H11
Method
                  BLASTN
NCBI GI
                  q4757678
BLAST score
                  254
                  1.0e-141
E value
Match length
                  282
                  98
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic
                  sequence, complete sequence
Seq. No.
                  170421
Seq. ID
                  LIB35-007-Q1-E1-A2
Method
                  BLASTX
NCBI GI
                  q1172969
BLAST score
                  548
E value
                  2.0e-56
Match length
                  112
% identity
                  97
NCBI Description 60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033
                  ribosomal protein L11.e - Arabidopsis thaliana
                  >gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16
                  [Arabidopsis thaliana]
Seq. No.
                  170422
                  LIB35-007-Q1-E1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  396
E value
                  1.0e-38
                  89
Match length
                  85
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  170423
Seq. No.
                  LIB35-007-Q1-E1-F10
```

Seq. ID

BLASTX Method NCBI GI g2529685 BLAST score 431 E value 1.0e-42

Match length 87



% identity 98

NCBI Description (AC002535) putative dimethyladenosine transferase

[Arabidopsis thaliana]

Seq. No. 170424

Seq. ID LIB35-007-Q1-E1-F3

Method BLASTX
NCBI GI g131398
BLAST score 411
E value 3.0e-40
Match length 105
% identity 81

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170425

Seq. ID LIB35-007-Q1-E1-G11

Method BLASTX
NCBI GI g4115925
BLAST score 469
E value 5.0e-47
Match length 143
% identity 51

NCBI Description (AF118222) contains similarity to RNA recognition motifs

(Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein

[Arabidopsis thaliana]

Seq. No. 170426

Seq. ID LIB35-007-Q1-E1-G9

Method BLASTX
NCBI GI g2618725
BLAST score 647
E value 6.0e-68
Match length 128
% identity 98

NCBI Description (U49074) IAA18 [Arabidopsis thaliana]

Seq. No. 170427

Seq. ID LIB35-007-Q1-E1-H2

Method BLASTX
NCBI GI 94240120
BLAST score 516
E value 1.0e-52
Match length 104
% identity 95

NCBI Description (AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No. 170428

Seq. ID LIB35-008-Q1-E1-A1



Method BLASTX NCBI GI a131398 BLAST score 327 E value 2.0e-30 Match length 68 99 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170429

Seq. ID LIB35-008-Q1-E1-A4

Method BLASTX NCBI GI q4455313 BLAST score 160 2.0e-11 E value Match length 60 % identity 57

NCBI Description (AL035528) fatty acid elongase-like protein (cer2-like)

[Arabidopsis thaliana]

Seq. No. 170430

LIB35-008-Q1-E1-B10 Seq. ID

Method BLASTX NCBI GI q3834319 BLAST score 712 E value 1.0e-75

Match length 139 % identity

NCBI Description (AC005679) Similar to gi_2244754 heat shock transcription

factor HSF30 homolog from Arabidopsis thaliana chromosome 4

contig gb Z97335. [Arabidopsis thaliana]

Seq. No. 170431

Seq. ID LIB35-008-Q1-E1-C5

Method BLASTX NCBI GI g115767 BLAST score 692 E value 4.0e-73 Match length 131 % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170432

Seq. ID LIB35-008-Q1-E1-D4



Method BLASTN
NCBI GI 94757390
BLAST score 120
E value 3.0e-61
Match length 120
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F24B18, complete sequence

Seq. No. 170433

Seq. ID LIB35-008-Q1-E1-D8

Method BLASTX
NCBI GI g131398
BLAST score 358
E value 4.0e-34
Match length 94

% identity 80

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170434

Seq. ID LIB35-008-Q1-E1-E1

Method BLASTX
NCBI GI g131372
BLAST score 150
E value 1.0e-09
Match length 33
% identity 97

NCBI Description PHOTOSYSTEM II REACTION CENTRE M PROTEIN

>gi_72719_pir__F2RZM photosystem II protein psbM - rice
chloroplast >gi_11969_emb_CAA33984_ (X15901) PSII low MW
protein [Oryza sativa] >gi_2924261_emb_CAA77413_ (Z00044)
PSII M-protein [Nicotiana tabacum] >gi_226687_prf__1603356M

photosystem II low MW protein [Oryza sativa]

Seq. No. 170435

Seq. ID LIB35-008-Q1-E1-E4

Method BLASTN
NCBI GI g16446
BLAST score 33
E value 3.0e-09
Match length 77
% identity 86

NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide

Seq. No. 170436

Seq. ID LIB35-008-Q1-E1-E8

Method BLASTN
NCBI GI g4567193
BLAST score 124



```
3.0e-63
E value
Match length
                  365
% identity...
                  98
NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic
                  sequence, complete sequence
                  170437
Seq. No.
Seq. ID
                  LIB35-008-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  q3869074
BLAST score
                  210
E value
                  1.0e-114
Match length
                  253
% identity
                  83
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMI9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170438
Seq. ID
                  LIB35-008-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  g2252823
BLAST score
                  278
E value
                  1.0e-155
Match length
                  322
% identity
                  97
NCBI Description Arabidopsis thaliana BAC IG005I10
Seq. No.
                  170439
Seq. ID
                  LIB35-008-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  g2583118
BLAST score
                  264
E value
                  5.0e-23
Match length
                  88
% identity
                  56
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  170440
Seq. ID
                  LIB35-008-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  g3980389
BLAST score
                  349
E value
                  4.0e-33
Match length
                  87
% identity
                  82
                 (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  170441
Seq. ID
                  LIB35-008-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  g16506
BLAST score
                  63
E value
                  9.0e-27
Match length
                  67
% identity
                  99
```

23216

NCBI Description Arabidopsis thaliana 18S rRNA gene



```
Seq. No.
                  170442
                  LIB35-009-Q1-E1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213583
BLAST score
                  369
                  3.0e-35
E value
Match length
                  119
% identity
                  67
                 (AC000348) T7N9.3 [Arabidopsis thaliana]
NCBI Description
                  170443
Seq. No.
                  LIB35-009-Q1-E1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3063472
                  524
BLAST score
                  2.0e-53
E value
                  98
Match length
                  99
% identity
NCBI Description (AC003981) F22013.34 [Arabidopsis thaliana]
                  170444
Seq. No.
                  LIB35-009-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741960
BLAST score
                  746
                  2.0e-79
E value
Match length
                  139
                  97
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
                  170445
Seq. No.
                  LIB35-009-Q1-E1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168529
BLAST score
                  177
E value
                  2.0e-47
Match length
                  109
% identity
                  94
NCBI Description SERINE/THREONINE-PROTEIN KINASE ASK1 >qi 541890 pir
                  probable serine/threonine-specific protein kinase (EC
                  2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi 166882
                   (M91548) serine/threonine kinase [Arabidopsis thaliana]
                  >gi 1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]
Seq. No.
                  170446
Seq. ID
                  LIB35-009-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  284
E value
                  9.0e-26
                  75
Match length
                  76
```

% identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding



protein (LHCP AB 65) [Arabidopsis thaliana]
>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170447

Seq. ID LIB35-009-Q1-E1-D3

Method BLASTX
NCBI GI g2213592
BLAST score 369
E value 2.0e-35
Match length 96
% identity 72

NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No. 170448

Seq. ID LIB35-009-Q1-E1-E4

Method BLASTN
NCBI GI g2262155
BLAST score 232
E value 1.0e-127
Match length 425
% identity 99

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 170449

Seq. ID LIB35-009-Q1-E1-F1

Method BLASTX
NCBI GI g3367568
BLAST score 322
E value 8.0e-30
Match length 99
% identity 62

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 170450

Seq. ID LIB35-009-Q1-E1-G1

Method BLASTX
NCBI GI 94063542
BLAST score 761
E value 3.0e-81
Match length 152
% identity 99

NCBI Description (AF035903) ATP synthase beta subunit [Cupaniopsis

anacardioides]

Seq. No. 170451

Seq. ID LIB35-009-Q1-E1-G4

Method BLASTX
NCBI GI g131398
BLAST score 272
E value 5.0e-24
Match length 104
% identity 56

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor



- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 170452

Seq. ID LIB35-009-Q1-E1-G7

Method BLASTX
NCBI GI g4755196
BLAST score 197
E value 4.0e-15
Match length 81
% identity 47

NCBI Description (AC007018) similar to the GDSL family of lipolytic enzymes

[Arabidopsis thaliana]

Seq. No. 170453

Seq. ID LIB35-010-Q1-E1-E3

Method BLASTX
NCBI GI g115783
BLAST score 222
E value 1.0e-18
Match length 57
% identity 77

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170454

Seq. ID LIB35-011-Q1-E1-A10

Method BLASTX
NCBI GI g2129777
BLAST score 47
E value 4.0e-10
Match length 59
% identity 71

NCBI Description Y49 protein - Arabidopsis thaliana >gi_928969_emb_CAA62033_

(X90385) Y49 [Arabidopsis thaliana] $>g\bar{i}$ 1020157 (\bar{U} 26937)

DNA-binding protein [Arabidopsis thaliana]

>gi_4581115_gb_AAD24605.1_AC005825_12 (AC005825) MYB-like
protein; very similar to GB:2129777 [Arabidopsis thaliana]

Seq. No. 170455

Seq. ID LIB35-011-Q1-E1-A6

Method BLASTX
NCBI GI g1174162
BLAST score 170
E value 5.0e-12
Match length 90
% identity 40

NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis

thaliana] >gi 3746915 (AF091106) E2

ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]



Seq. No. 170456
Seq. ID LIB35-011-Q1-E1-A7

Method BLASTN
NCBI GI g4115930
BLAST score 278
E value 1.0e-155
Match length 318

NCBI Description Arabidopsis thaliana BAC T4B21

Seq. No. 170457

% identity

Seq. ID LIB35-011-Q1-E1-B12

97

Method BLASTX
NCBI GI g131398
BLAST score 346
E value 1.0e-32
Match length 93
% identity 75

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170458

Seq. ID LIB35-011-Q1-E1-E8

Method BLASTX
NCBI GI g2827139
BLAST score 236
E value 6.0e-20
Match length 92
% identity 57

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 170459

Seq. ID LIB35-011-Q1-E1-F11

Method BLASTX
NCBI GI g3309086
BLAST score 310
E value 2.0e-28
Match length 65

% identity 91

NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis

thaliana]

Seq. No. 170460

Seq. ID LIB35-011-Q1-E1-F2

Method BLASTN NCBI GI g2618720

23220

% identity

NCBI Description

77



```
38
BLAST score
                  2.0e-12
E value
Match length
                  38
% identity
                  100
NCBI Description
                  Arabidopsis thaliana early auxin-induced (IAA16) mRNA,
                  complete cds
Seq. No.
                  170461
Seq. ID
                  LIB35-011-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  q4760343
BLAST score
                  161
                  4.0e-11
E value
Match length
                  81
                  41
% identity
NCBI Description
                  (AL049769) putative SNRNP SM-like protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  170462
Seq. ID
                  LIB35-011-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  g4309738
BLAST score
                  500
E value
                  9.0e-51
Match length
                  94
% identity
                  99
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]
                  170463
Seq. No.
Seq. ID
                  LIB35-011-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g1134882
BLAST score
                  257
E value
                  2.0e-22
Match length
                  96
% identity
                  55
NCBI Description (Z68291) cysteine protease [Pisum sativum]
Seq. No.
                  170464
Seq. ID
                  LIB35-011-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  g2981439
BLAST score
                  144
                   4.0e-09
E value
Match length
                  61
% identity
NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
Seq. No.
                  170465
Seq. ID
                  LIB35-011-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  g3153207
BLAST score
                  514
E value
                  2.0e-52
Match length
                  132
```

23221

(AF001949) ATHB-12 [Arabidopsis thaliana]



170466 Seq. No. LIB35-011-Q1-E1-H9 Seq. ID Method BLASTN g2494106 NCBI GI 67 BLAST score E value 1.0e-29 Match length 107 91 % identity Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, NCBI Description complete sequence [Arabidopsis thaliana] 170467 Seq. No. LIB35-012-Q1-E1-A5 Seq. ID Method BLASTX NCBI GI q2129549 336 BLAST score 1.0e-31 E value Match length 67 100 % identity calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -NCBI Description Arabidopsis thaliana >gi_2129551_pir__S71778 calcium-dependent protein kinase 19 - Arabidopsis thaliana >gi 836942 (U20624) calcium-dependent protein kinase [Arabidopsis thaliana] >gi 836948 (U20627) calcium-dependent protein kinase [Arabidopsis thaliana] 170468 Seq. No. Seq. ID LIB35-012-Q1-E1-B1 Method BLASTN NCBI GI q531832 33 BLAST score 3.0e-09 E value Match length 109 83 % identity NCBI Description Cloning vector pSport2, complete sequence 170469 Seq. No. LIB35-012-Q1-E1-C1 Seq. ID Method BLASTN NCBI GI g4467094 BLAST score 186 1.0e-100 E value 375 Match length % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project) 170470 Seq. No. LIB35-012-Q1-E1-E11 Seq. ID BLASTX Method NCBI GI g4544445

Method BLASTX
NCBI GI g4544445
BLAST score 389
E value 7.0e-38
Match length 76
% identity 97

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate



1-phosphotransferase [Arabidopsis thaliana]

```
170471
Seq. No.
                    LIB35-012-Q1-E1-E2
Seq. ID
Method
                    BLASTX
                    g3281848
NCBI GI
BLAST score
                    366
                    3.0e-35
E value
                    74
Match length
                    99
% identity
                    (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    170472
                    LIB35-012-Q1-E1-E7
Seq. ID
Method
                    BLASTN
NCBI GI
                    q16446
BLAST score
                     46
                     5.0e-17
E value
                    126
Match length
                     85
% identity
                   A.thaliana gene for photosystem II 10 kDa polypeptide
NCBI Description
                    170473
Seq. No.
                    LIB35-012-Q1-E1-F3
Seq. ID
Method
                    BLASTN
NCBI GI
                    g4589430
BLAST score
                     271
                     1.0e-151
E value
                     301
Match length
                     97
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                    MLD14, complete sequence
                     170474
Seq. No.
                    LIB35-012-Q1-E1-H6
Seq. ID
Method
                     BLASTX
NCBI GI
                     q3850570
BLAST score
                     312
                     1.0e-28
E value
                     85
Match length
                     78
% identity
NCBI Description
                    (AC005278) F15K9.6 [Arabidopsis thaliana]
                     170475
Seq. No.
                     LIB35-013-Q1-E1-B7
Seq. ID
                     BLASTX
Method
NCBI GI
                     q131398
BLAST score
                     58
E value
                     3.0e-15
Match length
                     62
                     82
% identity
NCBI Description
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                    >gi_72714_pir___F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
```

23223

>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb X55970. ESTs gb Z17693, gb N37616,



gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

170476 Seq. No. LIB35-013-Q1-E1-C8 Seq. ID Method BLASTN q3212846 NCBI GI BLAST score 128 E value 1.0e-65 Match length 387 % identity 98 Arabidopsis thaliana chromosome II BAC F6E13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 170477 Seq. No. LIB35-013-Q1-E1-D7 Seq. ID BLASTX Method g4262156 NCBI GI BLAST score 486 E value 5.0e-49125 Match length 79 % identity (AC005275) putative component of cytochrome B6-F complex NCBI Description [Arabidopsis thaliana] Seq. No. 170478 LIB35-013-01-E1-E7 Seq. ID Method BLASTX q531829 NCBI GI BLAST score 144 5.0e-09 E value Match length 78 44 % identity (U12390) beta galactosidase alpha peptide [cloning vector NCBI Description pSport1] 170479 Seq. No. LIB35-013-Q1-E1-H4 Seq. ID Method BLASTX NCBI GI g2829889 BLAST score 159 E value 1.0e-10 36 Match length 78 % identity NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana] 170480 Seq. No. Seq. ID LIB35-014-Q1-E1-A1 BLASTN Method NCBI GI g2828188 BLAST score 287 E value 1.0e-160 287 Match length

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

100

% identity



```
170481
Seq. No.
                   LIB35-014-Q1-E1-A2
Seq. ID
                   BLASTN
Method
                   g2924732
NCBI GI
BLAST score
                   142
                   4.0e-74
E value
                   179
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUA2, complete sequence [Arabidopsis thaliana]
                   170482
Seq. No.
                   LIB35-014-Q1-E1-A4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519183
                   159
BLAST score
E value
                   3.0e-84
                   297
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15C23, complete sequence
                   170483
Seq. No.
                   LIB35-014-Q1-E1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1350956
BLAST score
                   417
                   4.0e-41
E value
                   80
Match length
                   100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
                   170484
Seq. No.
                   LIB35-014-Q1-E1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131398
BLAST score
                   306
                   3.0e-33
E value
Match length
                   84
                   95
% identity
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                   gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                   come from this gene. [Arabidopsis
                   170485
Seq. No.
Seq. ID
                   LIB35-014-Q1-E1-G6
```

Method BLASTX
NCBI GI g131398
BLAST score 283
E value 2.0e-25



```
Match length
% identity
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                   gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                   come from this gene. [Arabidopsis
                   170486
Seq. No.
                   LIB35-014-Q1-E1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4165340
                   131
BLAST score
E value
                   1.0e-67
                   279
Match length
                   95
% identity
                   Arabidopsis thaliana chromosome I BAC F11M15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170487
Seq. No.
                   LIB35-015-Q1-E1-A2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4220640
BLAST score
                   405
                   0.0e + 00
E value
Match length
                   437
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170488
Seq. ID
                   LIB35-015-Q1-E1-A3
Method
                   BLASTX
NCBI GI
                   g1256424
BLAST score
                   279
E value
                   4.0e-25
Match length
                   60
% identity
                   92
                   (U51119) cysteine proteinase inhibitor [Brassica
NCBI Description
                   campestris]
Seq. No.
                   170489
Seq. ID
                   LIB35-015-Q1-E1-B5
Method
                   BLASTN
NCBI GI
                   q3659491
BLAST score
                   258
                   1.0e-143
E value
Match length
                   420
                   99
```

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

% identity

Seq. No.

170490

23226



```
LIB35-015-Q1-E1-D5
Seq. ID
                    BLASTX
Method
NCBI GI
                    q4220515
BLAST score
                    543
                    8.0e-56
E value
                    105
Match length
                    99
% identity
                    (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    170491
Seq. ID
                    LIB35-015-Q1-E1-E4
Method
                    BLASTX
NCBI GI
                    a131398
BLAST score
                    523
E value
                    2.0e-53
                    121
Match length
% identity
                    88
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                    >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                    - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                    >gi_3152571 (AC002986) Match to photosystem II 10kDa
                    polypeptide gb X55970. ESTs gb_Z17693, gb_N37616,
                    gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                    come from this gene. [Arabidopsis
Seq. No.
                    170492
                    LIB35-015-Q1-E1-E6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2677828
BLAST score
                    504
                    4.0e-51
E value
Match length
                    132
% identity
                    70
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
                    170493
Seq. No.
                    LIB35-015-Q1-E1-E7
Seq. ID
                    BLASTN
Method
                    g2252848
NCBI GI
BLAST score
                    212
                    1.0e-116
E value
Match length
                    215
                    100
% identity
NCBI Description Arabidopsis thaliana BAC TM018A10
                    170494
Seq. No.
Seq. ID
                    LIB35-015-Q1-E1-F3
                    BLASTN
Method
                    g4585952
NCBI GI
BLAST score
                    376
E value
                    0.0e + 00
                    421
Match length
% identity
                    100
```

23227

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,

complete sequence

Seq. ID

Method



```
170495
Seq. No.
                  LIB35-015-Q1-E1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757662
BLAST score
                   141
                   2.0e-73
E value
Match length
                   307
                   97
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
NCBI Description
                   chromosome I, complete sequence
Seq. No.
                   170496
                  LIB35-015-Q1-E1-H4
Seq. ID
Method
                   BLASTN
                   g4335744
NCBI GI
BLAST score
                   69
E value
                   2.0e-30
                   197
Match length
                   84
% identity
                   Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170497
Seq. No.
                   LIB35-016-Q1-E1-B6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3128143
BLAST score
                   81
                   6.0e-38
E value
                   165
Match length
                   87
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTI20, complete sequence [Arabidopsis thaliana]
                   170498
Seq. No.
Seq. ID
                   LIB35-016-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   q2443755
BLAST score
                   239
                   4.0e-20
E value
                   56
Match length
% identity
                  (AF020433) cyclophilin [Arabidopsis thaliana]
NCBI Description
                   170499
Seq. No.
Seq. ID
                   LIB35-016-Q1-E1-C3
Method
                   BLASTX
NCBI GI
                   g2979545
BLAST score
                   150
E value
                   1.0e-09
                   71
Match length
% identity
                  (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   170500
Seq. No.
```

23228

LIB35-016-Q1-E1-D9

BLASTX



```
g115767
NCBI GI
                  268
BLAST score
                  1.0e-30
E value
                  85
Match length
                  81
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  170501
Seq. No.
                  LIB35-016-Q1-E1-E6
Seq. ID
                  BLASTN
Method
                  g16446
NCBI GI
                  96
BLAST score
                  6.0e-47
E value
                  160
Match length
                  90
% identity
NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide
                  170502
Seq. No.
                  LIB35-016-Q1-E1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1495804
                  413
BLAST score
                  9.0e-41
E value
                  98
Match length
                  73
% identity
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]
                  170503
Seq. No.
                  LIB35-016-Q1-E1-F7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2494106
BLAST score
                  115
                   4.0e-58
E value
                  203
Match length
                   89
% identity
NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
                   complete sequence [Arabidopsis thaliana]
                   170504
Seq. No.
                   LIB35-016-Q1-E1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586021
BLAST score
                   361
                   1.0e-34
E value
                   89
Match length
                   80
% identity
                  (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 170505

Seq. ID LIB35-016-Q1-E1-G10



```
BLASTX
Method
                  g132677
NCBI GI
                  183
BLAST score
                  1.0e-25
E value
                  94
Match length
                  70
% identity
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
NCBI Description
                  >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor,
                  chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_
                  (Z11508) Plastid ribosomal protein CL15 [Arabidopsis
                  thaliana]
                  170506
Seq. No.
                  LIB35-016-Q1-E1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4583542
                  392
BLAST score
                  4.0e-38
E value
                  112
Match length
                  78
% identity
                  (Y16847) 16 kDa polypeptide of oxygen-evolving complex
NCBI Description
                  [Arabidopsis thaliana]
                  170507
Seq. No.
                  LIB35-016-Q1-E1-G7
Seq. ID
Method
                  BLASTN
                  g2689438
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
                  119
Match length
                  86
% identity
NCBI Description Arabidopsis thaliana BAC F2401 chromosome 1, complete
                  sequence [Arabidopsis thaliana]
                  170508
Seq. No.
Seq. ID
                  LIB35-016-Q1-E1-H4
Method
                  BLASTX
                  g1402912
NCBI GI
                  498
BLAST score
                   2.0e-50
E value
Match length
                  116
% identity
                   85
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]
                   170509
Seq. No.
Seq. ID
                  LIB35-017-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                   g2851508
BLAST score
                   486
E value
                   3.0e-49
                   97
Match length
% identity
                   93
                  60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
NCBI Description
```

ribosomal protein L21 (gb_L38826). ESTs

gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

E value



```
170510
Seq. No.
                  LIB35-017-Q1-E1-A11
Seq. ID
                  BLASTX
Method
                  q3386618
NCBI GI
                  377
BLAST score
                  3.0e - 36
E value
                  116
Match length
                  63
% identity
                  (AC004665) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170511
                  LIB35-017-Q1-E1-A3
Seq. ID
                  BLASTX
Method
                  g4741960
NCBI GI
BLAST score
                  490
                  2.0e-49
E value
Match length
                  115
                  83
% identity
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
                  170512
Seq. No.
                  LIB35-017-Q1-E1-B8
Seq. ID
Method
                  BLASTX
                  q417381
NCBI GI
                  237
BLAST score
                   6.0e-20
E value
Match length
                  96
                  53
% identity
                  NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) -
NCBI Description
                  Arabidopsis thaliana >gi 16400 emb CAA45041 (X63445)
                  nitrilase I [Arabidopsis thaliana]
                  170513
Seq. No.
                  LIB35-017-Q1-E1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q131398
BLAST score
                   417
                   4.0e-41
E value
                   90
Match length
                   94
% identity
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                   gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                   come from this gene. [Arabidopsis
                   170514
Seq. No.
Seq. ID
                   LIB35-017-Q1-E1-D1
                   BLASTN
Method
                   g3859658
NCBI GI
                   226
BLAST score
```

23231

1.0e-124



Match length 440 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 170515

Seq. ID LIB35-017-Q1-E1-D4

Method BLASTX
NCBI GI g115783
BLAST score 430
E value 6.0e-43
Match length 92
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170516

Seq. ID LIB35-017-Q1-E1-D8

Method BLASTX
NCBI GI g4468813
BLAST score 192
E value 9.0e-15
Match length 100
% identity 43

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 170517

Seq. ID LIB35-017-Q1-E1-E8

Method BLASTN
NCBI GI g3869072
BLAST score 48
E value 3.0e-18
Match length 82
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB24, complete sequence [Arabidopsis thaliana]

Seq. No. 170518

Seq. ID LIB35-017-Q1-E1-H3

Method BLASTN
NCBI GI g16446
BLAST score 34
E value 8.0e-10
Match length 142
% identity 81

NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide

Seq. No. 170519

Seq. ID LIB35-017-Q1-E1-H4

Method BLASTN
NCBI GI g2618605
BLAST score 214
E value 1.0e-117
Match length 338
% identity 99



```
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUK11, complete sequence [Arabidopsis thaliana]
                   170520
Seq. No.
                   LIB35-018-Q1-E1-A11
Seq. ID
Method
                   BLASTN
                   g4567259
NCBI GI
                   206
BLAST score
                   1.0e-112
E value
                   323
Match length
                   96
% identity
                   Arabidopsis thaliana chromosome II BAC F3K23 genomic
NCBI Description
                   sequence, complete sequence
                   170521
Seq. No.
                   LIB35-018-Q1-E1-B7
Seq. ID
Method
                   BLASTX
                   q418548
NCBI GI
                   164
BLAST score
                   3.0e-11
E value
                   73
Match length
                   47
% identity
                   HYPOTHETICAL 15.7 KD PROTEIN IN APHA-UVRA INTERGENIC REGION
NCBI Description
                   (O138) >gi_396391 (U00006) No definition line found
                   [Escherichia coli] >gi_1790491 (AE000479) orf, hypothetical
                   protein [Escherichia coli]
                   170522
Seq. No.
                   LIB35-018-Q1-E1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2809233
BLAST score
                   363
                   1.0e-34
E value
                   91
Match length
                   86
% identity
                   (AC002560) F21B7.2 [Arabidopsis thaliana]
NCBI Description
                   170523
Seq. No.
                   LIB35-018-Q1-E1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g131398
BLAST score
                   461
                    3.0e-46
E value
Match length
                   103
                   88
% identity
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
```

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170524

Seq. ID LIB35-018-Q1-E1-C4

BLAST score

Match length % identity

E value

248 4.0e-21

125

42



```
BLASTX
Method
                  g1097877
NCBI GI
                  612
BLAST score
                  9.0e-64
E value
                  128
Match length
                  92
% identity
                  aminolevulinate dehydratase [Lycopersicon esculentum]
NCBI Description
                  170525
Seq. No.
                  LIB35-018-Q1-E1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262232
                  455
BLAST score
                  2.0e-45
E value
                  116
Match length
                   82
% identity
                  (AC006200) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                   thaliana]
                   170526
Seq. No.
                  LIB35-018-Q1-E1-D4
Seq. ID
                  BLASTX
Method
                   g131397
NCBI GI
                   236
BLAST score
                   6.0e-20
E value
                   109
Match length
% identity
                   57
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                   SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi 81480 pir S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                   photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
Seq. No.
                   170527
                   LIB35-018-Q1-E1-D7
Seq. ID
                   BLASTX
Method
                   q115783
NCBI GI
                   490
BLAST score
E value
                   1.0e-49
                   96
Match length
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   170528
Seq. No.
Seq. ID
                   LIB35-018-Q1-E1-G4
Method
                   BLASTX
NCBI GI
                   g1749676
```

23234



```
(D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
NCBI Description
                   EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                   170529
                   LIB35-018-Q1-E1-G8
Seq. ID
Method
                   BLASTX
                   g595768
NCBI GI
                   142
BLAST score
                   7.0e-09
E value
                   47
Match length
                   62
% identity
                   (U13866) non-functional lacZ alpha peptide [Cloning vector]
NCBI Description
                   170530
Seq. No.
                   LIB35-018-Q1-E1-H1
Seq. ID
                   BLASTX
Method
                   g115783
NCBI GI
                   331
BLAST score
                   4.0e-31
E value
                   69
Match length
                   90
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b bind\overline{\text{ing protein}} (LHCP \overline{\text{AB}} 140) [Arabidopsis
                   thaliana]
                   170531
Seq. No.
                   LIB35-018-Q1-E1-H4
Seq. ID
                   BLASTN
Method
                   g2924733
NCBI GI
                   77
BLAST score
                   3.0e-35
E value
                   272
Match length
                   86
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170532
                   LIB35-019-Q1-E1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2146733
BLAST score
                   428
                   3.0e-42
E value
                   75
Match length
                   96
% identity
NCBI Description GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana
Seq. No.
                   170533
                   LIB35-019-Q1-E1-C3
Seq. ID
Method
                   BLASTX
                   q1169341
NCBI GI
BLAST score
                   324
E value
                   4.0e-30
                   116
Match length
                   32
% identity
                   DEHYDRIN XERO 2 (LOW-TEMPERATURE-INDUCED PROTEIN LTI30)
NCBI Description
                   >gi 2129571 pir S63689 dehydrin - Arabidopsis thaliana
```

NCBI GI

E value

BLAST score

g3135261

3.0e-73

693



>gi 633763 (U19536) dehydrin [Arabidopsis thaliana]

```
170534
Seq. No.
                    LIB35-019-Q1-E1-E3
Seq. ID
                    BLASTX
Method
NCBI GI
                    q4006934
                    443
BLAST score
                    4.0e-44
E value
                    84
Match length
                    100
% identity
                    (AJ012571) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                    170535
Seq. No.
                    LIB35-019-Q1-E1-E4
Seq. ID
                    BLASTN
Method
                    g3702315
NCBI GI
BLAST score
                    332
                    0.0e + 00
E value
                    340
Match length
                    99
% identity
                    Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    170536
Seq. No.
                    LIB35-019-Q1-E1-G3
Seq. ID
                    BLASTX
Method
                    q131398
NCBI GI
BLAST score
                    165
                    9.0e-12
E value
                    74
Match length
                    45
% identity
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                    >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                    - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                    >gi_3152571 (AC002986) Match to photosystem II 10kDa
                    polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                    gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                    come from this gene. [Arabidopsis
                    170537
Seq. No.
                    LIB35-019-Q1-E1-G6
Seq. ID
Method
                    BLASTN
NCBI GI
                    q732560
                     332
BLAST score
E value
                    0.0e + 00
Match length
                    339
% identity
                     99
NCBI Description A.thaliana H1-1C mRNA for histone H1-1 (partial)
                     170538
Seq. No.
                    LIB35-019-Q1-E1-G8
Seq. ID
Method
                    BLASTX
```



135 Match length 98 % identity (AC003058) putative 18.5 KDa class I heat shock protein NCBI Description [Arabidopsis thaliana] 170539 Seq. No. LIB35-019-Q1-E1-G9 Seq. ID BLASTN Method g2618602 NCBI GI BLAST score 176 2.0e-94 E value 256 Match length 92 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSJ1, complete sequence [Arabidopsis thaliana] 170540 Seq. No. LIB35-019-Q1-E1-H1 Seq. ID BLASTX Method g3378491 NCBI GI BLAST score 253 1.0e-21 E value 80 Match length 60 % identity (AJ007578) pRIB5 protein [Ribes nigrum] NCBI Description Seq. No. 170541 LIB35-019-Q1-E1-H10 Seq. ID Method BLASTN NCBI GI q4220645 BLAST score 120 7.0e-61 E value 397 Match length 99 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MYA6, complete sequence [Arabidopsis thaliana] 170542 Seq. No. LIB35-019-Q1-E1-H12 Seq. ID BLASTN Method NCBI GI q16446 BLAST score 111 6.0e-56 E value Match length 123 % identity NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide 170543 Seq. No.

Seq. ID LIB35-019-Q1-E1-H5

Method BLASTX
NCBI GI g2194127
BLAST score 402
E value 2.0e-39
Match length 106
% identity 69

NCBI Description (AC002062) Strong similarity to Arabidopsis receptor-like protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis

Seq. ID

Method



thaliana]

170544 Seq. No. LIB35-019-Q1-E1-H9 Seq. ID Method BLASTN g2618602 NCBI GI 263 BLAST score 1.0e-146 E value 393 Match length 96 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSJ1, complete sequence [Arabidopsis thaliana] 170545 Seq. No. LIB35-020-Q1-E1-D4 Seq. ID BLASTN Method q3869069 NCBI GI 123 BLAST score 1.0e-62 E value 271 Match length 90 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MEB5, complete sequence [Arabidopsis thaliana] 170546 Seq. No. LIB35-020-Q1-E1-E6 Seq. ID Method BLASTX g4581141 NCBI GI 155 BLAST score 2.0e-10 E value 85 Match length 46 % identity (AC006919) unknown protein [Arabidopsis thaliana] NCBI Description 170547 Seq. No. Seq. ID LIB35-020-Q1-E1-E9 Method BLASTN NCBI GI g437313 BLAST score 43 5.0e-15 E value Match length 43 % identity 59 NCBI Description Arabidopsis thaliana DNA sequence with repeats 170548 Seq. No. Seq. ID LIB35-020-Q1-E1-G12 Method BLASTN NCBI GI q2065012 155 BLAST score 6.0e-82 E value 215 Match length % identity 93 NCBI Description A.thaliana mRNA for cyclic phosphodiesterase 170549 Seq. No.

23238

LIB35-020-Q1-E1-G3

 ${\tt BLASTX}$



```
NCBI GI
                  g2341034
                  499
BLAST score
                  1.0e-50
E value
                  110
Match length
                  93
% identity
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
                  170550
Seq. No.
                  LIB35-021-Q1-E1-A7
Seq. ID
                  BLASTX
Method
                  g131398
NCBI GI
BLAST score
                  221
                  2.0e-18
E value
                  104
Match length
                  58
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >qi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                  come from this gene. [Arabidopsis
                  170551
Seq. No.
                  LIB35-021-Q1-E1-D4
Seq. ID
Method
                  BLASTN
                  g4519183
NCBI GI
                  88
BLAST score
                  8.0e-42
E value
Match length
                  298
                  80
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15C23, complete sequence
Seq. No.
                  170552
                  LIB35-021-Q1-E1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  58
                   1.0e-11
E value
                   97
Match length
                   45
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb CAA39441_ (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb X55970. ESTs gb Z17693, gb_N37616,
                   gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                   come from this gene. [Arabidopsis
```

Seq. No. 170553

Seq. ID LIB35-022-Q1-E1-B11

Method BLASTN

Method

NCBI GI

BLAST score



```
NCBI GI
                  g1946354
                  191
BLAST score
                  1.0e-103
E value
                   309
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                   sequence, complete sequence
                   170554
Seq. No.
                   LIB35-022-Q1-E1-B4
Seq. ID
                   BLASTX
Method
                   g3242721
NCBI GI
                   675
BLAST score
                   4.0e-71
E value
Match length
                   142
                   91
% identity
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
                   170555
Seq. No.
                   LIB35-022-Q1-E1-B9
Seq. ID
                   BLASTN
Method
                   g2264303
NCBI GI
                   218
BLAST score
                   1.0e-119
E value
                   266
Match length
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBB18, complete sequence [Arabidopsis thaliana]
                   170556
Seq. No.
                   LIB35-022-Q1-E1-C11
Seq. ID
                   BLASTN
Method
                   g4335744
NCBI GI
                   63
BLAST score
                   8.0e-27
E value
                   167
Match length
                   84
% identity
                   Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170557
 Seq. No.
                   LIB35-022-Q1-E1-C12
 Seq. ID
                   BLASTX
 Method
                   q4006853
 NCBI GI
                    703
 BLAST score
                    2.0e-74
 E value
 Match length
                    137
                    100
 % identity
                    (Z99707) cytochrome P450-like protein [Arabidopsis
 NCBI Description
                    thaliana]
                    170558
 Seq. No.
                    LIB35-022-Q1-E1-C7
 Seq. ID
```

BLASTN

245

g2341023



E value 1.0e-135 Match length 400 % identity 94

NCBI Description Sequence of BAC F19P19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 170559

Seq. ID LIB35-022-Q1-E1-E1

Method BLASTN
NCBI GI g4559375
BLAST score 123
E value 1.0e-62
Match length 296
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic

sequence, complete sequence

Seq. No. 170560

Seq. ID LIB35-022-Q1-E1-E10

Method BLASTX
NCBI GI g4741960
BLAST score 263
E value 5.0e-23
Match length 58
% identity 90

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 170561

Seq. ID LIB35-022-Q1-E1-E11

Method BLASTX
NCBI GI g3980400
BLAST score 307
E value 3.0e-28
Match length 100
% identity 58

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 170562

Seq. ID LIB35-022-Q1-E1-E12

Method BLASTX
NCBI GI g131398
BLAST score 406
E value 1.0e-39
Match length 106
% identity 77

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170563



```
LIB35-022-Q1-E1-E2
 Seq. ID
Method
                   BLASTN
                   g1769904
 NCBI GI
                   67
 BLAST score
                   2.0e-29
E value
Match length
                   119
                   89
 % identity
NCBI Description A.thaliana psbP gene
                   170564
 Seq. No.
                   LIB35-022-Q1-E1-F11
 Seq. ID
                   {\tt BLASTX}
Method
                   g3169182
NCBI GI
 BLAST score
                   327
                   2.0e-30
E value
Match length
                   69
                   91
 % identity
                   (AC004401) unknown protein [Arabidopsis thaliana]
NCBI Description
                   170565
 Seq. No.
                   LIB35-022-Q1-E1-F8
 Seq. ID
Method
                   BLASTN
                   g2459406
NCBI GI
                   40
BLAST score
                   1.0e-13
E value
Match length
                   112
 % identity
                   85
NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   170566
 Seq. No.
                   LIB35-022-Q1-E1-G10
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g4309683
                    43
 BLAST score
 E value
                    2.0e-15
 Match length
                    63
 % identity
                   Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
 NCBI Description
                    complete sequence [Arabidopsis thaliana]
 Seq. No.
                    170567
                    LIB35-022-Q1-E1-G4
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q3687221
 BLAST score
                    160
 E value
                    9.0e-85
 Match length
                    303
 % identity
                    96
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F6F22 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 170568
Seq. ID LIB35-022-Q1-E1-G6

Method BLASTN NCBI GI g3687221

BLAST score 112



3.0e-56 E value Match length 185 93 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

170569 Seq. No.

LIB35-022-Q1-E1-H7 Seq. ID

Method BLASTN NCBI GI g2494106 BLAST score 39 E value 1.0e-12 99 Match length 85 % identity

Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

170570 Seq. No.

LIB35-023-Q1-E1-C5 Seq. ID

BLASTX Method NCBI GI q115783 BLAST score 535 E value 8.0e-55 101 Match length 99 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thalianal

170571 Seq. No.

LIB35-023-Q1-E1-C6 Seq. ID

Method BLASTX NCBI GI q2493144 BLAST score 404 E value 2.0e-39 Match length 115 52 % identity

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

170572 Seq. No.

Seq. ID LIB35-023-Q1-E1-D1

Method BLASTX NCBI GI g123178 BLAST score 144 5.0e-09 E value Match length 62 52 % identity

NCBI Description HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi 99844 pir A39358 histidinol dehydrogenase (EC

1.1.1.23) precursor, chloroplast - cabbage >gi 167142 (M60466) histidinol dehydrogenase [Brassica oleracea]



170573 Seq. No.

LIB35-023-Q1-E1-D12 Seq. ID

BLASTX Method NCBI GI q4206198 BLAST score 407 3.0e-40E value 81 Match length

% identity NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

170574 Seq. No.

LIB35-023-Q1-E1-D2 Seq. ID

99

Method BLASTX g131398 NCBI GI BLAST score 362 1.0e-34 E value 92 Match length 83 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

> >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

170575 Seq. No.

LIB35-023-Q1-E1-E6 Seq. ID

Method BLASTX g3004547 NCBI GI BLAST score 609 2.0e-63 E value Match length 140 % identity 86

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

>gi 4185150 (AC005724) unknown protein [Arabidopsis

thaliana]

Seq. No. 170576

LIB35-023-Q1-E1-F5 Seq. ID

Method BLASTN NCBI GI q16506 BLAST score 101 E value 1.0e-49 Match length 229 % identity 88

NCBI Description Arabidopsis thaliana 18S rRNA gene

170577 Seq. No.

LIB35-024-Q1-E1-A6 Seq. ID

Method BLASTN NCBI GI g4581084 BLAST score 294 E value 1.0e-164



```
433
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  170578
                  LIB35-024-Q1-E1-A7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g16131
BLAST score
                  395
E value
                  0.0e+00
                  399
Match length
% identity
                  100
                  Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with
NCBI Description
                  18S rRNA fragment
                  170579
Seq. No.
                  LIB35-024-Q1-E1-C9
Seq. ID
                  BLASTX
Method
                  g2688824
NCBI GI
BLAST score
                  254
                  6.0e-22
E value
                  69
Match length
                  74
% identity
NCBI Description
                  (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
                  170580
Seq. No.
                  LIB35-024-Q1-E1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3128136
BLAST score
                  288
                  1.0e-161
E value
Match length
                  291
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1F13, complete sequence [Arabidopsis thaliana]
                  170581
Seq. No.
Seq. ID
                  LIB35-024-Q1-E1-H10
Method
                  BLASTN
NCBI GI
                  g4699904
BLAST score
                  373
E value
                  0.0e+00
Match length
                  404
% identity
                  100
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,
                  complete sequence
                  170582
Seq. No.
```

Seq. ID LIB35-025-Q1-E1-A2 Method BLASTN

NCBI GI g4741953 BLAST score 52

E value 2.0e-20 Match length 143 % identity 88



NCBI Description Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA, complete cds

Seq. No. 170583

Seq. ID LIB35-025-Q1-E1-A5

Method BLASTX
NCBI GI g1550738
BLAST score 275
E value 2.0e-24
Match length 88
% identity 65

NCBI Description (Y08061) endomembrane-associated protein [Arabidopsis

thaliana] >gi 2982443_emb_CAA18251_ (AL022224)

endomembrane-associated protein [Arabidopsis thaliana]

Seq. No. 170584

Seq. ID LIB35-025-Q1-E1-B8

Method BLASTX
NCBI GI g131398
BLAST score 80
E value 4.0e-18
Match length 63
% identity 86

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64065_gb_T417592 and gb_N65338_gb_N37466_and_gb_T4540

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170585

Seq. ID LIB35-025-Q1-E1-C10

Method BLASTN
NCBI GI g2160155
BLAST score 148
E value 1.0e-77
Match length 354
% identity 98

NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 170586

Seq. ID LIB35-025-Q1-E1-C3

Method BLASTN
NCBI GI g2739359
BLAST score 234
E value 1.0e-129
Match length 304
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T9J22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170587

Seq. ID LIB35-025-Q1-E1-D5



Method BLASTN
NCBI GI g3128136
BLAST score 143
E value 6.0e-75
Match length 168
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 170588

Seq. ID LIB35-025-Q1-E1-D8

Method BLASTX
NCBI GI g115767
BLAST score 496
E value 3.0e-50
Match length 117
% identity 85

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

 $>gi_16368_emb_CAA27540_ (X03907)$ chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170589

Seq. ID LIB35-025-Q1-E1-E1

Method BLASTX
NCBI GI g115767
BLAST score 587
E value 5.0e-61
Match length 113
% identity 98

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170590

Seq. ID LIB35-025-Q1-E1-E9

Method BLASTN
NCBI GI g2160132
BLAST score 154
E value 4.0e-81
Match length 372
% identity 98

NCBI Description Sequence of BAC F19K23 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 170591

Seq. ID _LIB35-025-Q1-E1-F10

Method BLASTN NCBI GI g3873174 BLAST score 300

NCBI Description



```
E value
                   1.0e-168
Match length
                   336
% identity
                   98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   170592
Seq. ID
                   LIB35-025-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                   q2230757
BLAST score
                   284
E value
                   2.0e-25
Match length
                   78
                   71
% identity
NCBI Description
                  (Y11969) dnaJ-like protein [Arabidopsis thaliana]
                   170593
Seq. No.
Seq. ID
                  LIB35-025-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                   q2564049
BLAST score
                  169
                   4.0e-90
E value
Match length
                   383
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170594
Seq. ID
                   LIB35-026-Q1-E1-B11
Method
                   BLASTX
NCBI GI
                   g4689108
BLAST score
                   212
E value
                   7.0e-17
Match length
                  84
% identity
                   48
NCBI Description
                 (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]
Seq. No.
                   170595
Seq. ID
                   LIB35-026-Q1-E1-B3
Method
                   BLASTX
NCBI GI
                   g531829
BLAST score
                   139
E value
                   1.0e-08
Match length
                   71
% identity
                   45
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
                   170596
Seq. No.
Seq. ID
                   LIB35-026-Q1-E1-E4
Method
                   BLASTX
NCBI GI
                   g1292710
BLAST score
                   580
                   5.0e-60
E value
Match length
                  114
% identity
                   59
```

(X97558) calmodulin-1 [Capsicum annuum]

Seq. ID Method



```
170597
Seq. No.
Seq. ID
                  LIB35-026-Q1-E1-F11
Method
                  BLASTX
                  q531829
NCBI GI
                  182
BLAST score
E value
                  1.0e-13
                  78
Match length
                  54
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                   170598
Seq. ID
                  LIB35-026-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   q4006827
BLAST score
                   567
                   2.0e-58
E value
Match length
                  110
                   100
% identity
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   170599
                   LIB35-026-Q1-E1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581162
BLAST score
                   254
E value
                   7.0e-22
                  73
Match length
                   58
% identity
                  (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                   thaliana]
                   170600
Seq. No.
                   LIB35-026-Q1-E1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4835246
BLAST score
                   729
                   1.0e-77
E value
Match length
                   142
                   99
% identity
                  (AL049862) putative disease resistance protein [Arabidopsis
NCBI Description
                   thaliana]
                   170601
Seq. No.
                   LIB35-026-Q1-E1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1542877
BLAST score
                   221
E value
                   5.0e-18
Match length
                   124
                   38
% identity
NCBI Description
                  (X95908) orf [Drosophila melanogaster]
                   170602
Seq. No.
```

LIB35-026-Q1-E1-G9

BLASTN



NCBI GI g3869072 BLAST score 274 E value 1.0e-153 Match length 367 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB24, complete sequence [Arabidopsis thaliana]

Seq. No. 170603

Seq. ID LIB35-026-Q1-E1-H11

Method BLASTX
NCBI GI 94725946
BLAST score 285
E value 2.0e-25
Match length 55
% identity 100

NCBI Description (AL049730) putative Phospholipase D [Arabidopsis thaliana]

Seq. No. 170604

Seq. ID LIB35-027-Q1-E1-B1

Method BLASTN
NCBI GI g16446
BLAST score 36
E value 7.0e-11
Match length 100

% identity 84

NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide

Seq. No. 170605

Seq. ID LIB35-027-Q1-E1-D5

Method BLASTN
NCBI GI g4159701
BLAST score 274
E value 1.0e-153
Match length 401
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence

Seq. No. 170606

Seq. ID LIB35-027-Q1-E1-D9

Method BLASTN
NCBI GI g3150395
BLAST score 212
E value 1.0e-116
Match length 228
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T9D9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170607

Seq. ID LIB35-027-Q1-E1-E2

Method BLASTN
NCBI GI g4371278
BLAST score 346
E value 0.0e+00
Match length 370

23250



% identity 98 NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana] 170608 Seq. No. LIB35-027-Q1-E1-F3 Seq. ID BLASTN Method g4220636 NCBI GI 32 BLAST score 1.0e-08 E value 68 Match length 88 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MFB16, complete sequence [Arabidopsis thaliana] 170609 Seq. No. Seq. ID LIB35-027-Q1-E1-F5 Method BLASTX q4585875 NCBI GI BLAST score 153 1.0e-56 E value 125 Match length % identity 84 (AC005850) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 170610 Seq. ID LIB35-028-Q1-E1-B2 Method BLASTX q3746062 NCBI GI BLAST score 451 6.0e-45 E value Match length 119 % identity 70 NCBI Description (AC005311) hypothetical protein [Arabidopsis thaliana] Seq. No. 170611 Seq. ID LIB35-028-Q1-E1-C3 Method BLASTX NCBI GI a131398 BLAST score 603 9.0e-63 E value Match length 121 98 % identity PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]

>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170612

LIB35-028-Q1-E1-D10 Seq. ID

BLASTX Method NCBI GI g115783

23251



```
BLAST score
                  535
                  8.0e-55
E value
Match length
                  101
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  170613
Seq. No.
                  LIB35-028-Q1-E1-E1
Seq. ID
Method
                  BLASTN
                  q4538895
NCBI GI
BLAST score
                  44
E value
                  2.0e-15
Match length
                  106
                  87
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8
                  (ESSA project)
Seq. No.
                  170614
                  LIB35-028-Q1-E1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512676
                  510
BLAST score
E value
                  7.0e-52
Match length
                  136
% identity
                  83
                 (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                  170615
Seq. No.
                  LIB35-028-Q1-E1-G9
Seq. ID
Method
                  BLASTX
                  g2088654
NCBI GI
BLAST score
                  318
E value
                  1.0e-29
Match length
                  90
                  73
% identity
                  (AF002109) 60S acidic ribosomal protein P0 isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  170616
                  LIB35-028-Q1-E1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618683
BLAST score
                  240
E value
                  1.0e-132
Match length
                  406
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic
```

Seq. No. 170617

Seq. ID LIB35-028-Q1-E1-H6

Method BLASTX NCBI GI g2244977 BLAST score 695

sequence, complete sequence [Arabidopsis thaliana]



2.0e-73 E value 143 Match length 91 % identity (Z97340) cysteine proteinase [Arabidopsis thaliana] NCBI Description 170618 Seq. No. LIB35-029-Q1-E1-B10 Seq. ID BLASTX Method g115767 NCBI GI BLAST score 563 3.0e-58 E value Match length 107 100 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] 170619 Seq. No. LIB35-029-Q1-E1-B2 Seq. ID Method BLASTX NCBI GI q1175014 488 BLAST score E value 3.0e-49109 Match length 87 % identity PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi 629543 pir S44085 NCBI Description plasma membrane intrinsic protein 2b - Arabidopsis thaliana >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic protein 2b [Arabidopsis thaliana] 170620 Seq. No. Seq. ID LIB35-029-Q1-E1-D1 Method BLASTN NCBI GI q4335744 BLAST score 42 E value 2.0e-14 42 Match length % identity 100 Arabidopsis thaliana chromosome II BAC T4M8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 170621 Seq. No. Seq. ID LIB35-029-Q1-E1-E11

Method BLASTN NCBI GI g3759176 39 BLAST score 1.0e-12 E value

Match length 39 100 % identity

NCBI Description Arabidopsis thaliana mRNA for 3-phosphoserine phosphatase,

complete cds

Seq. No. 170622

Match length

% identity

99



```
LIB35-029-Q1-E1-H6
Seq. ID
Method
                  BLASTX
                  g115783
NCBI GI
BLAST score
                  361
                  1.0e-34
E value
                  79
Match length
                  90
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  170623
Seq. No.
                  LIB35-030-Q1-E1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2429467
                  149
BLAST score
                  1.0e-09
E value
                   83
Match length
                   35
% identity
                  (AF025462) contains similarity to glutathione S
NCBI Description
                  transferases [Caenorhabditis elegans]
                  170624
Seq. No.
                  LIB35-030-Q1-E1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4544405
BLAST score
                   131
E value
                   2.0e-67
Match length
                   307
                   97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F2818 genomic
                   sequence, complete sequence
                   170625
Seq. No.
Seq. ID
                   LIB35-030-Q1-E1-A8
Method
                   BLASTX
NCBI GI
                   q1709794
BLAST score
                   492
                   9.0e-50
E value
Match length
                   128
% identity
                   90
                   26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN
NCBI Description
                   BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis
                   thaliana] >gi_446715\overline{0} emb_CAB37519_ (AL035540)
                   multiubiquitin chain binding protein (MBP1) [Arabidopsis
                   thaliana]
Seq. No.
                   170626
                   LIB35-030-Q1-E1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   505
E value
                   2.0e-51
                   95
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR



(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170627

Seq. ID LIB35-030-Q1-E1-D11

Method BLASTN
NCBI GI g531828
BLAST score 42
E value 1.0e-14
Match length 78
% identity 88

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 170628

Seq. ID LIB35-030-Q1-E1-D3

Method BLASTN
NCBI GI g2160155
BLAST score 202
E value 1.0e-110
Match length 368
% identity 98

NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 170629

Seq. ID LIB35-030-Q1-E1-E1

Method BLASTX
NCBI GI g2245079
BLAST score 156
E value 2.0e-10
Match length 64
% identity 56

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 170630

Seq. ID LIB35-030-Q1-E1-E7

Method BLASTX
NCBI GI g730526
BLAST score 411
E value 3.0e-40
Match length 113
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 170631

Seq. ID LIB35-030-Q1-E1-F1

Method BLASTX
NCBI GI g131398
BLAST score 386
E value 2.0e-37
Match length 98
% identity 80

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR



>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >qi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

170632 Seq. No. LIB35-030-Q1-E1-F12 Seq. ID Method BLASTX q131398 NCBI GI BLAST score 153 1.0e-10 E value Match length 48 67 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>qi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170633

LIB35-030-Q1-E1-G6 Seq. ID

BLASTX Method g131398 NCBI GI BLAST score 418 4.0e-41 E value Match length 100 84 % identity

NCBI Description

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis

Seq. No. 170634

Seq. ID LIB35-030-Q1-E1-H11

Method BLASTN NCBI GI g1710247

BLAST score 83

6.0e-39 E value Match length 159 % identity 87

Human protein disulfide isomerase-related protein P5 mRNA, NCBI Description

partial cds

Seq. No. 170635



```
LIB35-030-Q1-E1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q418854
BLAST score
                  473
E value
                  1.0e-47
Match length
                  120
                  13
% identity
NCBI Description
                  ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
                  (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                  [Petroselinum crispum]
Seq. No.
                  170636
                  LIB35-031-Q1-E1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586061
BLAST score
                  657
E value
                  5.0e-69
Match length
                  129
                  98
% identity
NCBI Description
                  (AC007020) putative BOP1 protein [Arabidopsis thaliana]
                  170637
Seq. No.
                  LIB35-031-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194139
BLAST score
                  171
E value
                  3.0e-12
                  100
Match length
                  41
% identity
NCBI Description
                  (AC002062) EST gb ATTS0887 comes from this gene.
                   [Arabidopsis thaliana]
                  170638
Seq. No.
                  LIB35-031-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4741184
BLAST score
                  146
E value
                  2.0e-76
Match length
                  319
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7
                   (ESSA project)
Seq. No.
                  170639
Seq. ID
                  LIB35-031-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g1168739
BLAST score
                  173
E value
                  1.0e-12
Match length
                  37
% identity
                  89
NCBI Description CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
                   (L18901) carbonic anhydrase [Arabidopsis thaliana]
```

Seq. No. 170640

Seq. ID LIB35-031-Q1-E1-D1

NCBI Description



```
Method
                  BLASTX
                  q1732572
NCBI GI
BLAST score
                  300
E value
                  3.0e-27
Match length
                  106
                  53
% identity
                  (U72154) beta-glucosidase [Brassica nigra]
NCBI Description
                  170641
Seq. No.
Seq. ID
                  LIB35-031-Q1-E1-D2
                  BLASTX
Method
NCBI GI
                  g115767
BLAST score
                  354
                  6.0e-35
E value
                  78
Match length
                  90
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  170642
Seq. No.
                  LIB35-031-Q1-E1-D6
Seq. ID
Method
                  BLASTN
                  g3510337
NCBI GI
BLAST score
                  97
                  3.0e-47
E value
Match length
                  355
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170643
Seq. ID
                  LIB35-031-Q1-E1-E6
Method
                  BLASTN
NCBI GI
                  q2618605
BLAST score
                  150
E value
                  8.0e-79
Match length
                  352
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUK11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170644
                  LIB35-031-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1175014
BLAST score
                  286
E value
                  1.0e-25
                  95
Match length
                  64
% identity
```

23258

PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi 629543 pir S44085

plasma membrane intrinsic protein 2b - Arabidopsis thaliana >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic



protein 2b [Arabidopsis thaliana]

```
Seq. No.
                  170645
Seq. ID
                  LIB35-031-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  g4741959
                  35
BLAST score
E value
                  2.0e-10
Match length
                  51
% identity
                  92
NCBI Description
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
                  170646
Seq. No.
Seq. ID
                  LIB35-031-Q1-E1-G4
Method
                  BLASTX
                  g3152558
NCBI GI
BLAST score
                  334
E value
                  2.0e-31
Match length
                  79
% identity
                  84
                  (AC002986) Similar to M. tuberculosis gene gb_Z96072 and M.
NCBI Description
                  leprae gene gb 400019. [Arabidopsis thaliana]
Seq. No.
                  170647
                  LIB35-031-Q1-E1-H6
Seq. ID
Method
                  BLASTN
                  g3176694
NCBI GI
                  307
BLAST score
E value
                  1.0e-172
Match length
                  307
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170648
Seq. ID
                  LIB35-031-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  q2809246
BLAST score
                  548
E value
                  2.0e-56
Match length
                  118
% identity
                  85
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                  170649
Seq. ID
                  LIB35-032-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  q585264
BLAST score
                  164
E value
                   6.0e-14
Match length
                  105
% identity
                   44
                  HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (HGPRT)
NCBI Description
                   (HGPRTASE) >gi_2127112_pir__S66098 hypoxanthine-guanine
```

phosphoribosyltransferase - Bacillus subtilis

>gi_467457_dbj_BAA05303_ (D26185) hypoxanthine-guanine



phosphoribosyltransferase [Bacillus subtilis]
>gi_2632335_emb_CAB11844_ (Z99104) hypoxanthine-guanine

phosphoribosyltransferase [Bacillus subtilis]

Seq. No. 170650

Seq. ID LIB35-032-Q1-E1-A7

Method BLASTN
NCBI GI g2760169
BLAST score 186
E value 1.0e-100
Match length 379
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFB13, complete sequence [Arabidopsis thaliana]

Seq. No. 170651

Seq. ID LIB35-032-Q1-E1-B4

Method BLASTX
NCBI GI g2499903
BLAST score 152
E value 6.0e-10
Match length 112
% identity 33

NCBI Description PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA) >gi 1184161

(U35646) aminopeptidase [Mus musculus]

>gi_1585925_prf__2202260A puromycin sensitive

aminopeptidase [Mus musculus]

Seq. No. 170652

Seq. ID LIB35-032-Q1-E1-C8

Method BLASTX
NCBI GI g4454029
BLAST score 417
E value 5.0e-41
Match length 80

% identity 100

NCBI Description (AL035394) tyrosine transaminase like protein [Arabidopsis

thaliana]

Seq. No. 170653

Seq. ID LIB35-032-Q1-E1-D9

Method BLASTN NCBI GI q3869067

BLAST score 96

E value 1.0e-46 Match length 371 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCK7, complete sequence [Arabidopsis thaliana]

Seq. No. 170654

Seq. ID LIB35-032-Q1-E1-E3

Method BLASTN
NCBI GI g1755171
BLAST score 43
E value 2.0e-15
Match length 55

23260



% identity 95 Arabidopsis thaliana germin-like protein (GLP3) mRNA, NCBI Description complete cds 170655 Seq. No. LIB35-032-Q1-E1-E6 Seq. ID BLASTX Method g4107103 NCBI GI 416 BLAST score 5.0e-41 E value Match length 84 96 % identity (AB015143) AHP3 [Arabidopsis thaliana] NCBI Description 170656 Seq. No. LIB35-032-Q1-E1-F3 Seq. ID BLASTX Method NCBI GI g115783 387 BLAST score 1.0e-37 E value 78 Match length 95 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana] 170657 Seq. No. LIB35-032-Q1-E1-H10 Seq. ID BLASTX Method NCBI GI q1592672 BLAST score 336 1.0e-31 E value 91 Match length 75 % identity NCBI Description (X91921) germin1 [Arabidopsis thaliana] 170658 Seq. No. Seq. ID LIB35-033-Q1-E1-A7 BLASTN Method NCBI GI q3821780 BLAST score 25 5.0e-05 E value Match length 37 61 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 170659

Seq. ID LIB35-033-Q1-E1-C1

Method BLASTX
NCBI GI g1709794
BLAST score 437
E value 2.0e-43
Match length 105
% identity 100

NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN BINDING PROTEIN) >gi 1165206 (U33269) MBP1 [Arabidopsis



thaliana] >gi_4467150_emb_CAB37519_ (AL035540) multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana]

Seq. No. 170660

Seq. ID LIB35-033-Q1-E1-D4

Method BLASTX
NCBI GI g115767
BLAST score 651
E value 2.0e-68
Match length 124
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170661

Seq. ID LIB35-033-Q1-E1-F9

Method BLASTX
NCBI GI g131397
BLAST score 225
E value 2.0e-18
Match length 109
% identity 55

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 170662

Seq. ID LIB35-033-Q1-E1-H1

Method BLASTN
NCBI GI g3033373
BLAST score 48
E value 4.0e-18
Match length 184
% identity 82

NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170663

Seq. ID LIB35-034-Q1-E1-B12

Method BLASTX
NCBI GI g2244827
BLAST score 211
E value 8.0e-30
Match length 128
% identity 29

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NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

23262

BLAST score

% identity

E value Match length 181 2.0e-97

287

97



170664 Seq. No. Seq. ID LIB35-034-Q1-E1-B2 BLASTN Method NCBI GI g2182287 162 BLAST score 6.0e-86 E value 339 Match length 99 % identity Genomic sequence for Arabidopsis thaliana BAC T7N9, NCBI Description complete sequence [Arabidopsis thaliana] 170665 Seq. No. LIB35-034-Q1-E1-C8 Seq. ID Method BLASTX g730463 NCBI GI BLAST score 306 7.0e-28 E value Match length 102 56 % identity NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae] 170666 Seq. No. Seq. ID LIB35-034-Q1-E1-E6 Method BLASTX NCBI GI q4039153 BLAST score 279 1.0e-24 E value Match length 54 100 % identity NCBI Description (AF104221) low temperature and salt responsive protein LTI6A [Arabidopsis thaliana] >gi 4325217_gb_AAD17302 (AF122005) hydrophobic protein [Arabidopsis thaliana] Seq. No. 170667 Seq. ID LIB35-034-Q1-E1-E7 Method BLASTX NCBI GI g4467116 BLAST score 310 E value 2.0e-28 Match length 88 % identity (AL035538) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 170668 Seq. ID LIB35-034-Q1-E1-F1 Method BLASTN NCBI GI g4325365

23263



```
NCBI Description Arabidopsis thaliana BAC T3H13
                   170669
Seq. No.
                   LIB35-034-Q1-E1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2651314
BLAST score
                   386
                   2.0e-37
E value
Match length
                   91
                   81
% identity
                   (AC002336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                   thaliana]
                   170670
Seq. No.
                   LIB35-034-Q1-E1-F4
Seq. ID
Method
                   BLASTX
                   g131398
NCBI GI
BLAST score
                   250
                   5.0e-22
E value
                   71
Match length
                   73
% identity
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                   gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                   come from this gene. [Arabidopsis
                   170671
Seq. No.
                   LIB35-034-Q1-E1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   632
E value
                   3.0e-66
Match length
                   122
% identity
                   98
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
                   170672
Seq. No.
Seq. ID
                   LIB35-034-Q1-E1-G12
```

Method BLASTX
NCBI GI g115783
BLAST score 445
E value 2.0e-44
Match length 85
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)



chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

170673 Seq. No. LIB35-034-Q1-E1-G3 Seq. ID BLASTN Method NCBI GI q4521999 259 BLAST score 1.0e-144 E value Match length 263

100

% identity Arabidopsis thaliana chromosome II BAC F2G1 genomic NCBI Description

sequence, complete sequence

170674 Seq. No.

LIB35-034-Q1-E1-G6 Seq. ID

BLASTX Method NCBI GI q4558568 BLAST score 645 1.0e-67 E value 132 Match length 96 % identity

(AC007138) hypothetical protein [Arabidopsis thaliana] NCBI Description

170675 Seq. No.

LIB35-034-Q1-E1-H4 Seq. ID

Method BLASTN g4559344 NCBI GI 67 BLAST score 9.0e-30 E value

90 Match length 96 % identity

Arabidopsis thaliana chromosome II BAC F27C12 genomic NCBI Description

sequence, complete sequence

170676 Seq. No.

Seq. ID LIB35-034-Q1-E1-H7

Method BLASTX NCBI GI g3766248 177 BLAST score 7.0e-13 E value Match length 49 65 % identity

(Y18227) blue copper binding-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 170677

Seq. ID LIB35-035-Q1-E1-A2

Method BLASTN NCBI GI g2494106 BLAST score 48 E value 6.0e-18 Match length 48 100 % identity

Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, NCBI Description

complete sequence [Arabidopsis thaliana]



Seq. No. 170678

Seq. ID LIB35-035-Q1-E1-A4

Method BLASTN
NCBI GI g2288979
BLAST score 82
E value 3.0e-38
Match length 248
% identity 78

NCBI Description Arabidopsis thaliana chromosome II BAC T01024 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170679

Seq. ID LIB35-035-Q1-E1-B6

Method BLASTX
NCBI GI g4741960
BLAST score 253
E value 6.0e-22
Match length 78
% identity 69

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 170680

Seq. ID LIB35-035-Q1-E1-B7

Method BLASTX
NCBI GI g2245066
BLAST score 208
E value 2.0e-16
Match length 93
% identity 52

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 170681

Seq. ID LIB35-035-Q1-E1-C2

Method BLASTN
NCBI GI g2494106
BLAST score 82

E value 2.0e-38 Match length 194 86

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 170682

Seq. ID LIB35-035-Q1-E1-C4

Method BLASTX
NCBI GI g461550
BLAST score 370
E value 1.0e-35
Match length 110
% identity 65

NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR

>gi 81635 pir B39732 H+-transporting ATP synthase (EC

3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase

gamma-subunit [Arabidopsis thaliana]

Seq. No. 170683



```
Seq. ID
                  LIB35-035-Q1-E1-D6
                  BLASTN
Method
                  g3335356
NCBI GI
                  88
BLAST score
E value
                  7.0e-42
                  104
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170684
                  LIB35-035-Q1-E1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3335356
                  80
BLAST score
E value
                  4.0e-37
                  209
Match length
                  88
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170685
Seq. ID
                  LIB35-035-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  261
E value
                  1.0e-22
                  77
Match length
                  71
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  170686
Seq. ID
                  LIB35-035-Q1-E1-E4
Method
                  BLASTX
NCBI GI
                  g3327222
BLAST score
                  236
E value
                  8.0e-20
Match length
                  114
% identity
NCBI Description (AB014604) KIAA0704 protein [Homo sapiens]
Seq. No.
                  170687
Seq. ID
                  LIB35-035-Q1-E1-E6
Method
                  BLASTN
NCBI GI
                  q2494106
BLAST score
                  64
E value
                  2.0e-27
Match length
                  276
% identity
                  85
NCBI Description
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
                  complete sequence [Arabidopsis thaliana]
```

Seq. No. 170688

Seq. ID LIB35-035-Q1-E1-E7

Method BLASTX NCBI GI g131398 BLAST score 180



3.0e-13 E value 69 Match length 59 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi_72714_pir___F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi 16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170689

LIB35-035-Q1-E1-E8 Seq. ID

Method BLASTX NCBI GI q115767 62 BLAST score 4.0e-10 E value 50 Match length 76 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein $ab16\overline{5}$ - Arabidopsis thaliana

>gi 16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

170690 Seq. No.

LIB35-035-Q1-E1-F7 Seq. ID

BLASTX Method g115767 NCBI GI 124 BLAST score 8.0e-50 E value 108 Match length 95 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein $ab16\overline{5}$ - Arabidopsis thaliana

>gi 16368 emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

170691 Seq. No.

Seq. ID LIB35-035-Q1-E1-G5

Method BLASTX NCBI GI q728880 184 BLAST score 1.0e-13 E value 52 Match length % identity 63

N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG NCBI Description

>gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl

transferase related protein [Homo sapiens]



```
170692
Seq. No.
                  LIB35-035-Q1-E1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1632775
BLAST score
                  179
E value
                  4.0e-96
Match length
                  339
                  88
% identity
NCBI Description A.thaliana t5r gene
Seq. No.
                  170693
                  LIB35-035-Q1-E1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131398
BLAST score
                  418
E value
                  4.0e-41
Match length
                  91
                  92
% identity
NCBI Description
                 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  170694
Seq. ID
                  LIB35-035-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  q3046851
BLAST score
                  96
E value
                  1.0e-46
Match length
                  332
% identity
                  93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170695
Seq. ID
                  LIB35-036-Q1-E2-A3
Method
                  BLASTN
NCBI GI
                  g4455168
BLAST score
                  339
E value
                  0.0e+00
Match length
                  343
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                  (ESSAII project)
```

Seq. No. 170696

Seq. ID LIB35-036-Q1-E2-A8

Method BLASTN
NCBI GI g4049332
BLAST score 80
E value 4.0e-37

E value

Match length % identity

3.0e-22 59

81



```
297
Match length
                   92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                   (ESSAII project)
Seq. No.
                  170697
                  LIB35-036-Q1-E2-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2832672
BLAST score
                   241
E value
                   9.0e-54
                  114
Match length
                   89
% identity
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170698
                  LIB35-036-Q1-E2-B9
Seq. ID
Method
                  BLASTX
                   g1172873
NCBI GI
BLAST score
                   578
                   7.0e-60
E value
Match length
                   120
                   95
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                   drought-inducible cysteine proteinase (\overline{EC} 3.4.\overline{22}.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                   170699
Seq. ID
                   LIB35-036-Q1-E2-E1
Method
                   BLASTX
                   g2501766
NCBI GI
BLAST score
                   156
E value
                   2.0e-10
Match length
                   43
                   77
% identity
NCBI Description
                  (U69174) calmodulin-like domain protein kinase isoenzyme
                   gamma [Glycine max]
                   170700
Seq. No.
Seq. ID
                   LIB35-036-Q1-E2-F11
Method
                   BLASTX
NCBI GI
                   g2104957
BLAST score
                   595
E value
                   8.0e-62
Match length
                   112
% identity
                   98
NCBI Description
                 (U96924) immunophilin [Arabidopsis thaliana]
                   170701
Seq. No.
Seq. ID
                   LIB35-036-Q1-E2-G11
Method
                   BLASTX
NCBI GI
                   g1827787
BLAST score
                   258
```

23270

% identity

NCBI Description

thaliana]



```
NCBI Description C-Terminal Domain Of Gelatinase A
                  170702
Seq. No.
                  LIB35-036-Q1-E2-H4
Seq. ID
                  BLASTN
Method
                  q3046856
NCBI GI
                  306
BLAST score
                   1.0e-172
E value
                   374
Match length
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI22, complete sequence [Arabidopsis thaliana]
                   170703
Seq. No.
                  LIB35-036-Q1-E2-H9
Seq. ID
Method
                   BLASTX
                   q3095186
NCBI GI
BLAST score
                   177
                   2.0e-13
E value
                   51
Match length
                   71
% identity
                  (AF057140) cargo selection protein TIP47 [Homo sapiens]
NCBI Description
Seq. No.
                   170704
                   LIB35-037-Q1-E1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115783
BLAST score
                   499
                   1.0e-50
E value
                   95
Match length
                   99
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                             (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   170705
Seq. No.
Seq. ID
                   LIB35-037-Q1-E1-D1
Method
                   BLASTX
                   g4582789
NCBI GI
                   97
BLAST score
                   6.0e - 35
E value
Match length
                   98
                   78
% identity
                   (AJ225088) Starch synthase isoform SS III [Vigna
NCBI Description
                   unguiculata]
                   170706
Seq. No.
                   LIB35-037-Q1-E1-D7
Seq. ID
Method
                   BLASTX
                   q3790567
NCBI GI
BLAST score
                   608
                   2.0e-63
E value
Match length
                   116
```

23271

(AF078821) RING-H2 finger protein RHA1b [Arabidopsis

NCBI Description



```
170707
Seq. No.
                  LIB35-037-Q1-E1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  616
E value
                  3.0e-64
                  132
Match length
                  94
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  170708
Seq. No.
                  LIB35-037-Q1-E1-H3
Seq. ID
Method
                  BLASTX
                  g4218123
NCBI GI
BLAST score
                  306
                  6.0e-28
E value
                  117
Match length
                  57
% identity
                  (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  170709
Seq. No.
                  LIB35-037-Q1-E1-H4
Seq. ID
                  {\tt BLASTN}
Method
NCBI GI
                  g2262135
                  57
BLAST score
                   3.0e-23
E value
                   340
Match length
                   83
% identity
NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                   cM, complete sequence
Seq. No.
                   170710
Seq. ID
                  LIB35-038-Q1-E1-B2
Method
                   BLASTN
NCBI GI
                   q4691223
                   209
BLAST score
                   1.0e-114
E value
                   353
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
                   (ESSA project)
                   170711
Seq. No.
Seq. ID
                   LIB35-038-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g1169201
BLAST score
                   48
E value
                   3.0e-17
Match length
                   109
% identity
                   54
```

DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]

>gi 421830 pir S33707 DRT112 protein - Arabidopsis



LIB35-038-Q1-E1-B6

Method BLASTX
NCBI GI g2244744
BLAST score 289
E value 6.0e-26
Match length 101
% identity 51

NCBI Description (Y13676) bZIP DNA-binding protein [Antirrhinum majus]

Seq. No. 170713

Seq. ID LIB35-038-Q1-E1-B8

Method BLASTX
NCBI GI g2342724
BLAST score 546
E value 5.0e-56
Match length 109
% identity 99

NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 170714

Seq. ID LIB35-038-Q1-E1-B9

Method BLASTN
NCBI GI g4159706
BLAST score 134
E value 4.0e-69
Match length 393
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 170715

Seq. ID LIB35-038-Q1-E1-C2

Method BLASTX
NCBI GI 94115918
BLAST score 227
E value 1.0e-18
Match length 54
% identity 81

NCBI Description (AF118222) similar to nascent polypeptide associated

complex alpha chain [Arabidopsis thaliana]

Seq. No. 170716

Seq. ID LIB35-038-Q1-E1-D2

Method BLASTX
NCBI GI g4505369
BLAST score 174
E value 2.0e-12
Match length 79
% identity 47

NCBI Description NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD)

(NADH-coenzyme Q reductase)

>gi_3287881_sp_043181_NUYM_HUMAN NADH-UBIQUINONE

OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD)

(CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_2655053

(AF020351) NADH: ubiquinone oxidoreductase 18 kDa IP subunit

[Homo sapiens]



Seq. No. 170717

Seq. ID LIB35-038-Q1-E1-D3

Method BLASTX
NCBI GI g131398
BLAST score 519
E value 7.0e-53
Match length 121
% identity 87

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
qb_T41858, qb_T88021, qb_R37531, qb_T04679, qb_N37520,

gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170718

Seq. ID LIB35-038-Q1-E1-D6

Method BLASTX

NCBI GI g131398

BLAST score 160

E value 6.0e-12

Match length 100

% identity 49

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

ge_noisos, ge_arrosz ana ge_noosoo, ge_norroo ana

come from this gene. [Arabidopsis

Seq. No. 170719

Seq. ID LIB35-038-Q1-E1-D8

Method BLASTX
NCBI GI 9479413
BLAST score 484
E value 8.0e-49
Match length 147
% identity 70

NCBI Description myosin-like protein - Arabidopsis thaliana

Seq. No. 170720

Seq. ID LIB35-038-Q1-E1-E3

Method BLASTX
NCBI GI g1175010
BLAST score 541
E value 2.0e-55
Match length 115
% identity 91

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi 629540 pir S44082



>gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No. 170721 Seq. ID LIB35-

Seq. ID LIB35-038-Q1-E1-E8

Method BLASTX
NCBI GI g131398
BLAST score 506
E value 2.0e-51
Match length 121
% identity 86

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170722

Seq. ID LIB35-038-Q1-E1-G5

Method BLASTX
NCBI GI g1168750
BLAST score 175
E value 2.0e-12
Match length 102
% identity 38

NCBI Description CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY

SUBUNIT) >gi 458230 (U04380) calcineurin B [Naegleria

gruberi]

Seq. No. 170723

Seq. ID LIB35-038-Q1-E1-G6

Method BLASTX
NCBI GI g3980389
BLAST score 507
E value 2.0e-51
Match length 117
% identity 86

NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis

thaliana]

Seq. No. 170724

Seq. ID LIB35-038-Q1-E1-G9

Method BLASTX
NCBI GI g2565275
BLAST score 506
E value 2.0e-51
Match length 106
% identity 85

NCBI Description (AF023611) Dim1p homolog [Homo sapiens]

Seq. No. 170725

Seq. ID LIB35-039-Q1-E1-A12

Method BLASTX



```
g3421087
NCBI GI
BLAST score
                  356
                  5.0e - 34
E value
Match length
                  73
                  99
% identity
                  (AF043524) 20S proteasome subunit PAE1 [Arabidopsis
NCBI Description
                  thaliana]
                  170726
Seq. No.
                  LIB35-039-Q1-E1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g626042
BLAST score
                  62
                  2.0e-22
E value
Match length
                  81
                  75
% identity
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase
                  [Zea mays]
                  170727
Seq. No.
                  LIB35-039-Q1-E1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115492
                  335
BLAST score
E value
                  2.0e-31
Match length
                  65
                  50
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
                  170728
Seq. No.
                  LIB35-039-Q1-E1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911085
BLAST score
                  239
E value
                  4.0e-20
                  99
Match length
% identity
NCBI Description
                  (AL021960) photosystem II oxygen-evolving complex protein
                  3-like [Arabidopsis thaliana] >gi 3402748 emb CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3
                   - like [Arabidopsis thaliana]
                  170729
Seq. No.
Seg. ID
                  LIB35-039-Q1-E1-B12
Method
                  BLASTN
NCBI GI
                  q3176694
BLAST score
                  43
                  5.0e-15
E value
```

Match length 67 91 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170730

Seq. ID LIB35-039-Q1-E1-B2



63

Method BLASTX g4587530 NCBI GI 89 BLAST score 1.0e-38 E value Match length 129

(AC007060) Strong similarity to F19I3.2 gi 3033375 putative NCBI Description

berberine bridge enzyme from Arabidopsis thaliana BAC

gb AC004238

Seq. No. 170731

% identity

LIB35-039-Q1-E1-B9 Seq. ID

BLASTX Method g1361155 NCBI GI BLAST score 187 5.0e-14 E value 89 Match length

% identity 46

hypothetical protein o215b - Escherichia coli >gi 537235 NCBI Description

(U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi 1790856 (AE000509) phosphoglyceromutase 2 [Escherichia

coli]

170732 Seq. No.

LIB35-039-Q1-E1-C11 Seq. ID

Method BLASTX NCBI GI g4335763 289 BLAST score 6.0e-26 E value 109 Match length 49 % identity

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

170733 Seq. No.

LIB35-039-Q1-E1-C2 Seq. ID

Method BLASTX NCBI GI q131398 BLAST score 488 E value 2.0e-49 Match length 105 92 % identity

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

> >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170734

LIB35-039-Q1-E1-C4 Seq. ID

Method BLASTX NCBI GI g3164134 BLAST score 420 E value 2.0e-41



Match length 105% identity 76

NCBI Description (D78602) cytochrome P450 monooxygenase [Arabidopsis

thaliana]

Seq. No. 170735

Seq. ID LIB35-039-Q1-E1-C8

Method BLASTN
NCBI GI g499161
BLAST score 32
E value 1.0e-08

Match length 92 % identity 84

NCBI Description A.thaliana mRNA Athb-6

Seq. No. 170736

Seq. ID LIB35-039-Q1-E1-C9

Method BLASTX
NCBI GI g2499810
BLAST score 238
E value 6.0e-20
Match length 46
% identity 98

NCBI Description PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From

Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana]

>gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No. 170737

Seq. ID LIB35-039-Q1-E1-D10

Method BLASTX
NCBI GI g131398
BLAST score 500
E value 1.0e-50
Match length 120
% identity 85

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170738

Seq. ID LIB35-039-Q1-E1-D11

Method BLASTX NCBI GI g3929651

BLAST score 93

E value 7.0e-38 Match length 118 % identity 71



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(AJ131206) microbody NAD-dependent malate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   170739
Seq. No.
                   LIB35-039-Q1-E1-D9
Seq. ID
                   BLASTX
Method
                   g4406816
NCBI GI
                   620
BLAST score
                   1.0e-64
E value
                   119
Match length
                   98
% identity
                   (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   170740
                   LIB35-039-Q1-E1-E10
Seq. ID
                   BLASTX
Method
                   g131398
NCBI GI
                   277
BLAST score
                   6.0e-25
E value
                   72
Match length
                   79
% identity
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                   come from this gene. [Arabidopsis
Seq. No.
                   170741
                   LIB35-039-Q1-E1-E2
Seq. ID
Method
                   BLASTN
                   q2341023
NCBI GI
BLAST score
                   347
E value
                   0.0e + 00
                   367
Match length
                   99
% identity
                   Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                    170742
Seq. No.
Seq. ID
                   LIB35-039-Q1-E1-E3
Method
                   BLASTX
NCBI GI
                   g3766248
BLAST score
                   425
                    7.0e-42
E value
Match length
                   101
% identity
```

NCBI Description

Seq. No. 170743

Seq. ID LIB35-039-Q1-E1-E4

thaliana]

Method BLASTX NCBI GI g117238

23279

(Y18227) blue copper binding-like protein [Arabidopsis



BLAST score 384 E value 4.0e-37 Match length 104 % identity 76

NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN

CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)

>gi_81656_pir__S12785 protein ch-42 precursor, chloroplast
- Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411)
protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana]
>gi_2832653_emb_CAA16728_ (AL021710) protein ch-42

precursor, chloroplast [Arabidopsis thaliana]

>gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene

[Euglena gracilis]

Seq. No. 170744

Seq. ID LIB35-039-Q1-E1-E9

Method BLASTX
NCBI GI g4206618
BLAST score 611
E value 1.0e-63
Match length 122

Match length 122 % identity 100

NCBI Description (AF066855) ATP synthase beta subunit [Nymania capensis]

Seq. No. 170745

Seq. ID LIB35-039-Q1-E1-F1

Method BLASTX
NCBI GI g1168750
BLAST score 169
F value 7 0e-12

E value 7.0e-12 Match length 97 % identity 38

NCBI Description CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY

SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria

gruberi]

Seq. No. 170746

Seq. ID LIB35-039-Q1-E1-F7

Method BLASTX
NCBI GI g1769905
BLAST score 437
E value 3.0e-43
Match length 114

% identity 74

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No. 170747

Seq. ID LIB35-039-Q1-E1-F8

Method BLASTX
NCBI GI g1169201
BLAST score 418
E value 5.0e-41
Match length 115
% identity 77

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR



>gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]

170748 Seq. No. Seq. ID LIB35-039-Q1-E1-G1 Method BLASTX NCBI GI g118104 BLAST score 445 2.0e-44 E value Match length 95 87 % identity NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) maize >gi 168461 (M55021) cyclophilin [Zea mays] >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays] 170749 Seq. No. LIB35-039-Q1-E1-G2 Seq. ID Method BLASTX g1709825 NCBI GI BLAST score 537 5.0e-55 E value Match length 112 98 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR NCBI Description (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana] Seq. No. 170750 LIB35-039-Q1-E1-G3 Seq. ID Method BLASTN NCBI GI g4490324 BLAST score 137 E value 2.0e-71 Match length 165 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project) 170751 Seq. No. Seq. ID LIB35-039-Q1-E1-H10 Method BLASTX NCBI GI g4587518 BLAST score 589

E value 3.0e-61Match length 113 % identity

NCBI Description (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF 01370 the NAD dependent

epimerase/dehydratase family. EST gb AA59

170752 Seq. No.

Seq. ID LIB35-039-Q1-E1-H12

Method BLASTX NCBI GI g3980400 BLAST score 48



E value 5.0e-27 Match length 91 % identity 80

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 170753

Seq. ID LIB35-039-Q1-E1-H2

Method BLASTX
NCBI GI g728867
BLAST score 182
E value 1.0e-13
Match length 98

% identity 42

NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR

>gi 99694 pir S21961 proline-rich protein APG -

Arabidopsis thaliana >gi 22599 emb CAA42925 (X60377) APG

[Arabidopsis thaliana]

Seq. No. 170754

Seq. ID LIB35-039-Q1-E1-H9

Method BLASTN
NCBI GI 94235150
BLAST score 212
E value 1.0e-116
Match length 216
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic

sequence, complete sequence

Seq. No. 170755

Seq. ID LIB35-040-Q1-E1-A3

Method BLASTX
NCBI GI g2088646
BLAST score 649
E value 3.0e-68
Match length 122
% identity 94

NCBI Description (AF002109) Sulp isolog [Arabidopsis thaliana]

Seq. No. 170756

Seq. ID LIB35-040-Q1-E1-A5

Method BLASTX
NCBI GI g131398
BLAST score 171
E value 1.0e-43
Match length 109
% identity 87

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis



Seq. No. 170757

LIB35-040-Q1-E1-B4 Seq. ID

BLASTX Method NCBI GI g1172872 404 BLAST score 2.0e-39 E value 113 Match length 73 % identity

CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 NCBI Description

drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_

(D13042) thiol protease [Arabidopsis thaliana]

>gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 170758

LIB35-040-Q1-E1-B7 Seq. ID

BLASTX Method NCBI GI g4049350 179 BLAST score 5.0e-13 E value 108 Match length

98 % identity

(AL034567) putative protein [Arabidopsis thaliana] NCBI Description

170759 Seq. No.

LIB35-040-Q1-E1-B8 Seq. ID

BLASTX Method q1172872 NCBI GI 473 BLAST score 2.0e-47E value 93 Match length 98 % identity

NCBI Description

CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_

(D13042) thiol protease [Arabidopsis thaliana]

>gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

170760 Seq. No.

LIB35-040-Q1-E1-C4 Seq. ID

Method BLASTN NCBI GI q2656030 187 BLAST score E value 1.0e-101 Match length 410 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

Seq. No. 170761

LIB35-040-Q1-E1-C6 Seq. ID

Method BLASTN NCBI GI g3128135 BLAST score 235



E value 1.0e-129 Match length 402 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E1, complete sequence [Arabidopsis thaliana]

Seq. No. 170762

Seq. ID LIB35-040-Q1-E1-C8

Method BLASTN
NCBI GI g3869069
BLAST score 321
E value 0.0e+00
Match length 404
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 170763

Seq. ID LIB35-040-Q1-E1-D10

Method BLASTX
NCBI GI g3859599
BLAST score 579
E value 6.0e-60
Match length 125
% identity 86

NCBI Description (AF104919) similar to class I chitinases (Pfam: PF00182,

E=1.2e-142, N=1) [Arabidopsis thaliana]

Seq. No. 170764

Seq. ID LIB35-040-Q1-E1-D7

Method BLASTX
NCBI GI g3378491
BLAST score 254
E value 8.0e-22
Match length 84
% identity 58

NCBI Description (AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No. 170765

Seq. ID LIB35-040-Q1-E1-D8

Method BLASTX
NCBI GI g4039153
BLAST score 279
E value 1.0e-24
Match length 54
% identity 100

NCBI Description (AF104221) low temperature and salt responsive protein

LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_(AF122005) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 170766

Seq. ID LIB35-040-Q1-E1-E10

Method BLASTX
NCBI GI g4567246
BLAST score 321
E value 1.0e-29
Match length 71



% identity

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.

170767

Seq. ID

LIB35-040-Q1-E1-E3

Method NCBI GI BLASTX g3548802

BLAST score E value

362 1.0e-34

Match length % identity

115 60

NCBI Description

(AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi 4335769 gb AAD17446 (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.

170768

Seq. ID

LIB35-040-Q1-E1-E4

Method

BLASTX

NCBI GI BLAST score q4584526 561

E value Match length 8.0e-58

% identity

112 99

NCBI Description

(AL049607) glutathione peroxidase-like protein [Arabidopsis

thaliana]

Seq. No.

170769

Seq. ID

LIB35-040-Q1-E1-E5

Method NCBI GI BLASTN q2088638

BLAST score

126

E value

2.0e-64

Match length

365

% identity

NCBI Description

Arabidopsis thaliana chromosome II BAC T28M21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

1-70770

Seq. ID Method

LIB35-040-Q1-E1-E6

NCBI GI

BLASTX

g2118220

BLAST score

284

E value

2.0e-25

Match length

92

% identity

66

NCBI Description

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >qi 926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi 3096941 emb CAA18851.1 (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi 4539311 emb CAB38812.1 (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi 4589976 gb AAD26493.1 AC007195 7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]



```
170771
Seq. No.
                   LIB35-040-Q1-E1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4741952
BLAST score
                   608
                   3.0e-63
E value
                   118
Match length
                   70
% identity
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                   170772
Seq. No.
                   LIB35-040-Q1-E1-E9
Seq. ID
Method
                   BLASTN
                   g2459406
NCBI GI
BLAST score
                   39
                   5.0e-13
E value
                   71
Match length
                   92
% identity
                   Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170773
Seq. No.
                   LIB35-040-Q1-E1-F1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4220468
                   402
BLAST score
                   0.0e + 00
E value
                   410
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   170774
Seq. No.
                   LIB35-040-Q1-E1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g131398
BLAST score
                   511
E value
                    6.0e-52
Match length
                   120
% identity
                    87
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                    photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                    >qi 3152571 (AC002986) Match to photosystem II 10kDa
                    polypeptide gb X55970. ESTs gb Z17693, gb_N37616,
                    gb T41858, gb T88021, gb R37531, gb T04679, gb N37520,
                    gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                    come from this gene. [Arabidopsis
                    170775
Seq. No.
                    LIB35-040-Q1-E1-F11
Seq. ID
                   BLASTX
Method
```

NCBI GI g2335108 BLAST score 237 E value 7.0e-20 Match length 129

23286



% identity 93 (AC002339) putative isulinase [Arabidopsis thaliana] NCBI Description 170776 Seq. No. LIB35-040-Q1-E1-G2 Seq. ID BLASTX Method NCBI GI g131398 405 BLAST score 1.0e-39 E value 99 Match length 85 % identity PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis Seq. No. 170777 LIB35-040-Q1-E1-H2 Seq. ID Method BLASTX NCBI GI g2244952 370 BLAST score E value 7.0e-3681 Match length 85 % identity (Z97340) strong similarity to ZK688.3 protein -NCBI Description Caenorhabditis elegans [Arabidopsis thaliana] 170778 Seq. No. LIB35-040-Q1-E1-H4 Seq. ID Method BLASTX NCBI GI q3924598 BLAST score 349 E value 3.0e-33 79 Match length % identity NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana] 170779 Seq. No. Seq. ID LIB35-040-Q1-E1-H5 Method BLASTX NCBI GI q3415115 BLAST score 326 E value 2.0e-30 Match length 103

% identity 62

NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]

170780 Seq. No.

Seq. ID LIB35-040-Q1-E1-H7

Method BLASTN NCBI GI g4406752 BLAST score 189



E value 1.0e-102 Match length 376 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170781

Seq. ID LIB35-041-Q1-E1-A9

Method BLASTX
NCBI GI g2842494
BLAST score 305
E value 8.0e-28
Match length 80
% identity 81

NCBI Description (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]

>gi_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No. 170782

Seq. ID LIB35-041-Q1-E1-B10

Method BLASTX
NCBI GI g131398
BLAST score 479
E value 3.0e-48
Match length 113
% identity 86

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170783

Seq. ID LIB35-041-Q1-E1-B11

Method BLASTN
NCBI GI g1694973
BLAST score 57
E value 2.0e-23
Match length 137
% identity 85

NCBI Description A.thaliana mRNA for plastid ribosomal protein

Seq. No. 170784

Seq. ID LIB35-041-Q1-E1-B12

Method BLASTX
NCBI GI g1408473
BLAST score 439
E value 2.0e-43
Match length 85
% identity 99

NCBI Description (U48939) actin depolymerizing factor 2 [Arabidopsis

thaliana]



```
170785
Seq. No.
                  LIB35-041-Q1-E1-C12
Seq. ID
                  BLASTX
Method
                  g4150963
NCBI GI
                  308
BLAST score
                  4.0e-28
E value
                  89
Match length
                  63
% identity
                  (Y18620) DsPTP1 protein [Arabidopsis thaliana]
NCBI Description
                  170786
Seq. No.
                  LIB35-041-Q1-E1-C9
Seq. ID
                  BLASTX
Method
                  g4006934
NCBI GI
                  551
BLAST score
                  1.0e-56
E value
                  108
Match length
                  96
% identity
                  (AJ012571) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                  170787
Seq. No.
                  LIB35-041-Q1-E1-D9
Seq. ID
                  BLASTN
Method
                  g4199934
NCBI GI
BLAST score
                  267
                   1.0e-148
E value
Match length
                   389
                   97
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
                  170788
Seq. No.
                  LIB35-041-Q1-E1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4335744
BLAST score
                   401
E value
                   0.0e + 00
                   409
Match length
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   170789
Seq. No.
Seq. ID
                   LIB35-041-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g131398
BLAST score
                   504
E value
                   4.0e-51
Match length
                   120
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
```

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,



gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

 Seq. No.
 170790

 Seq. ID
 LIB35-041-Q1-E1-E12

 Method
 BLASTX

 NCBI GI
 g115767

 BLAST score
 683

BLAST score 683 E value 4.0e-72 Match length 134 % identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170791

Seq. ID LIB35-041-Q1-E1-E9

Method BLASTX
NCBI GI g115767
BLAST score 241
E value 1.0e-20
Match length 67
% identity 73

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170792

Seq. ID LIB35-041-Q1-E1-F10

Method BLASTX
NCBI GI g1345516
BLAST score 385
E value 4.0e-37
Match length 130
% identity 62

NCBI Description (X57600) lti140 [Arabidopsis thaliana]

Seq. No. 170793

Seq. ID LIB35-041-Q1-E1-F9

Method BLASTN
NCBI GI g2182287
BLAST score 354
E value 0.0e+00
Match length 403
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,

complete sequence [Arabidopsis thaliana]

Seq. No. 170794

23290



LIB35-042-Q1-E1-A10

Method BLASTX
NCBI GI g131398
BLAST score 510
E value 8.0e-52
Match length 118
% identity 87

Seq. ID

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170795

Seq. ID LIB35-042-Q1-E1-A2

Method BLASTX
NCBI GI 94033469
BLAST score 404
E value 2.0e-39
Match length 96
% identity 51

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41

>gi_1707370_emb_CAA67799_ (X99436) splicing factor

[Arabidopsis thaliana]

Seq. No. 170796

Seq. ID LIB35-042-Q1-E1-A4

Method BLASTX
NCBI GI g4559372
BLAST score 677
E value 2.0e-71
Match length 128
% identity 98

NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]

>gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative

CONSTANS protein [Arabidopsis thaliana]

Seq. No. 170797

Seq. ID LIB35-042-Q1-E1-A8

Method BLASTX
NCBI GI g1172969
BLAST score 520
E value 1.0e-52
Match length 115
% identity 97

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033

ribosomal protein L11.e - Arabidopsis thaliana

>gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16

[Arabidopsis thaliana]

Seq. No. 170798

Seq. ID LIB35-042-Q1-E1-A9

Method BLASTX



```
g2194127
NCBI GI
BLAST score
                   688
                   1.0e-72
E value
                  129
Match length
                  100
% identity
                   (AC002062) Strong similarity to Arabidopsis receptor-like
NCBI Description
                  protein kinase (gb ATLECGENE) and F20P5.16. [Arabidopsis
                  thaliana]
                  170799
Seq. No.
                  LIB35-042-Q1-E1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245115
BLAST score
                  185
E value
                  1.0e-13
                  52
Match length
% identity
                  73
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170800
                  LIB35-042-Q1-E1-B2
Seq. ID
Method
                  BLASTN
                   g4309719
NCBI GI
BLAST score
                   343
E value
                   0.0e + 0.0
Match length
                   383
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC T30D6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   170801
Seq. No.
                   LIB35-042-Q1-E1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   329
E value
                   7.0e-31
Match length
                   68
% identity
                   96
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                             (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   170802
Seq. No.
Seq. ID
                   LIB35-042-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g4769004
BLAST score
                   440
E value
                   1.0e-43
                   78
Match length
% identity
                   95
NCBI Description
                   (AF140598) ring-box protein 1 [Homo sapiens]
                   >gi_4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box
                  protein 1 [Mus musculus]
```

Seq. ID LIB35-042-Q1-E1-B7



```
Method
                  BLASTX
NCBI GI
                  g1747310
                  390
BLAST score
                  8.0e-38
E value
                  77
Match length
                  97
% identity
                  (D58424) Myb-like DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  170804
Seq. No.
                  LIB35-042-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160158
BLAST score
                  715
                  7.0e-76
E value
Match length
                  133
                  98
% identity
                  (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  170805
                  LIB35-042-Q1-E1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262180
BLAST score
                  630
E value
                  7.0e-66
Match length
                  121
                  97
% identity
NCBI Description (AC005508) 29621 [Arabidopsis thaliana]
                  170806
Seq. No.
                  LIB35-042-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160296
BLAST score
                  623
E value
                  4.0e-65
Match length
                  130
% identity
                  90
NCBI Description (D61395) gamma-VPE [Arabidopsis thaliana]
Seq. No.
                  170807
                  LIB35-042-Q1-E1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2832667
BLAST score
                  133
E value
                   1.0e-68
Match length
                  320
% identity
                   95
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14
                   (ESSAII project)
```

LIB35-042-Q1-E1-C8 Seq. ID

Method BLASTX NCBI GI g267077 BLAST score 685



```
E value
                  2.0e-72
Match length
                  134
% identity
                  98
                  TUBULIN BETA-5 CHAIN >gi 320186 pir JQ1589 tubulin beta-5
NCBI Description
                  chain - Arabidopsis thaliana >gi 166902 (M84702) beta-5
                  tubulin [Arabidopsis thaliana]
                  170809
Seq. No.
                  LIB35-042-Q1-E1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953481
BLAST score
                  688
                  1.0e-72
E value
Match length
                  133
% identity
                  52
                  (AC002328) F2202.26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170810
                  LIB35-042-Q1-E1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264314
BLAST score
                  103
E value
                  1.0e-50
Match length
                  350
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170811
                  LIB35-042-Q1-E1-D3
Seq. ID
                  BLASTX
Method
                  g4490705
NCBI GI
BLAST score
                   381
                  7.0e-37
E value
                  80
Match length
                   96
% identity
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   170812
Seq. No.
                  LIB35-042-Q1-E1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3021277
BLAST score
                   225
                   2.0e-18
E value
Match length
                   102
                   24
% identity
NCBI Description
                   (AL022347) protein kinase - like protein [Arabidopsis
                  thaliana]
                   170813
```

LIB35-042-Q1-E1-D6 Seq. ID Method BLASTN

NCBI GI g3869075 BLAST score 373 E value 0.0e+00Match length 388



% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 170814

Seq. ID LIB35-042-Q1-E1-D9

Method BLASTX
NCBI GI 94741952
BLAST score 566
E value 2.0e-58
Match length 106
% identity 76

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 170815

Seq. ID LIB35-042-Q1-E1-E1

Method BLASTX
NCBI GI g131398
BLAST score 533
E value 2.0e-54
Match length 125
% identity 87

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170816

Seq. ID LIB35-042-Q1-E1-E10

Method BLASTN
NCBI GI g1946354
BLAST score 397
E value 0.0e+00
Match length 397
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No. 170817

Seq. ID LIB35-042-Q1-E1-E12

Method BLASTX
NCBI GI g2497702
BLAST score 154
E value 4.0e-10
Match length 103
% identity 41

NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR

>gi_2121019_pir__I40710 outer membrane lipoprotein Citrobacter freundii >gi 717136 (U21727) lipocalin

precursor [Citrobacter freundii]

Seq. No. 170818

23295



```
LIB35-042-Q1-E1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757405
BLAST score
                  105
                  7.0e-52
E value
Match length
                  371
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
Seq. No.
                  170819
                  LIB35-042-Q1-E1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  a4038029
```

Method BLASTN
NCBI GI g4038029
BLAST score 232
E value 1.0e-128
Match length 304
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F504 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 170820

 Seq. ID
 LIB35-042-Q1-E1-E8

 Method
 BLASTX

 NCBI GI
 g4150963

 BLAST score
 353

 E value
 2.0e-33

 Match length
 99

Match length 99 % identity 67

NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No. 170821

Seq. ID LIB35-042-Q1-E1-F1

Method BLASTX
NCBI GI g131398
BLAST score 431
E value 1.0e-42
Match length 104
% identity 85

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170822

Seq. ID LIB35-042-Q1-E1-F3

Method BLASTN
NCBI GI g4558521
BLAST score 243
E value 1.0e-134
Match length 391
% identity 63



Genomic sequence for Arabidopsis thaliana BAC T10024, NCBI Description complete sequence 170823 Seq. No. LIB35-042-Q1-E1-F8 Seq. ID Method BLASTX NCBI GI g3879119 BLAST score 260 2.0e-22 E value 135 Match length 47 % identity (Z70310) similar to Glutathione S-transferases. NCBI Description [Caenorhabditis elegans] 170824 Seq. No. LIB35-042-Q1-E1-G11 Seq. ID Method BLASTX NCBI GI g127041 273 BLAST score 5.0e-24E value 50 Match length 98 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana] 170825 Seq. No. LIB35-042-Q1-E1-G12 Seq. ID Method BLASTN NCBI GI g4662609 BLAST score 108 E value 3.0e-54 108 Match length 100 % identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence 170826 Seq. No. Seq. ID LIB35-042-01-E1-G4 Method BLASTX NCBI GI g3914557 BLAST score 689 E value 8.0e-73 Match length 134 % identity 96 NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi_1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

Seq. No. 170827

Seq. ID LIB35-042-Q1-E1-G8

Method BLASTX NCBI GI g2244827 BLAST score 489 E value 2.0e-49



```
Match length
                  91
                  49
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  170828
Seq. No.
                  LIB35-042-Q1-E1-H1
Seq. ID
Method
                  BLASTX
                  g131398
NCBI GI
                  368
BLAST score
                  2.0e-35
E value
                  77
Match length
                  95
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb Z17693, gb N37616,
                  gb T41858, gb T88021, gb R37531, gb T04679, gb N37520,
                  gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  170829
                  LIB35-042-Q1-E1-H10
Seq. ID
                  BLASTX
Method
                  g4567273
NCBI GI
                  353
BLAST score
E value
                  2.0e-33
                  68
Match length
                  100
% identity
                  (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                   [Arabidopsis thaliana]
                  170830
Seq. No.
                  LIB35-042-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281869
                   379
BLAST score
                   1.0e-36
E value
                   71
Match length
                   100
% identity
                   (AL031004) RSZp22 splicing factor [Arabidopsis thaliana]
NCBI Description
                   >gi 3435094_gb_AAD12769.1_ (AF033586) 9G8-like SR protein
                   [Arabidopsis thaliana]
                   170831
Seq. No.
                   LIB35-042-Q1-E1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832672
BLAST score
                   628
                   1.0e-65
E value
Match length
                   123
% identity
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB35-043-Q1-E1-B9



Method BLASTX
NCBI GI g2129733
BLAST score 311
E value 1.0e-28
Match length 103
% identity 83

NCBI Description serine O-acetyltransferase (EC 2.3.1.30) SAT1 precursor -

Arabidopsis thaliana >gi_1184048 (U22964) serine

acetyltransferase [Arabidopsis thaliana]

Seq. No. 170833

Seq. ID LIB35-043-Q1-E1-C4

Method BLASTN
NCBI GI g3413422
BLAST score 84
E value 2.0e-39
Match length 162
% identity 100

NCBI Description Arabidopsis thaliana gene encoding protein tyrosine

phosphatase, ORF1 and ORF2 genes

Seq. No. 170834

Seq. ID LIB35-043-Q1-E1-D12

Method BLASTX
NCBI GI g115783
BLAST score 527
E value 7.0e-54
Match length 101
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170835

Seq. ID LIB35-043-Q1-E1-E2

Method BLASTX
NCBI GI g131398
BLAST score 221
E value 4.0e-18
Match length 94
% identity 53

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170836

Seq. ID LIB35-043-Q1-E1-G5

Method BLASTX NCBI GI g115767 BLAST score 419



```
E value
                  3.0e-41
Match length
                  117
                  72
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  170837
Seq. ID
                  LIB35-043-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q3355468
BLAST score
                  189
E value
                  2.0e-14
Match length
                  38
                  97
% identity
NCBI Description
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
                  thaliana]
                  170838
Seq. No.
Seq. ID
                  LIB35-043-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                  g2244879
BLAST score
                  244
E value
                  1.0e-20
Match length
                  47
                  100
% identity
NCBI Description
                  (Z97338) Nucleotide sequence of a cDNA clone encoding a
                  beta-amylase from Arabidopsis thaliana
                  170839
Seq. No.
                  LIB35-043-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911085
BLAST score
                  253
E value
                  9.0e-22
Match length
                  120
% identity
NCBI Description
                   (AL021960) photosystem II oxygen-evolving complex protein
                  3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3
                  - like [Arabidopsis thaliana]
Seq. No.
                  170840
Seq. ID
                  LIB35-043-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                  220
E value
                  3.0e-18
Match length
                  80
% identity
```

NCBI Description

23300

(AF034946) ubiquitin conjugating enzyme [Zea mays]

Method

NCBI GI



```
LIB35-044-Q1-E1-B4
  Seq. ID
  Method
                     BLASTX
                     g567893
  NCBI GI
  BLAST score
                     147
. E value
                     2.0e-09
                     93
  Match length
                     35
  % identity
                     (L37382) beta-galactosidase-complementation protein
  NCBI Description
                     [Cloning vector]
                     170842
  Seq. No.
                     LIB35-044-Q1-E1-B6
  Seq. ID
  Method
                     BLASTN
                     g3327922
  NCBI GI
  BLAST score
                     71
  E value
                     1.0e-31
                     273
  Match length
                     86
  % identity
                     Arabidopsis thaliana chromosome II BAC T31E10 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
                     170843
  Seq. No.
                     LIB35-044-Q1-E1-D2
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q4335755
                     174
  BLAST score
  E value
                     2.0e-12
                     81
  Match length
                     44
  % identity
  NCBI Description
                     (AC006284) putative hydroxyproline-rich glycoprotein
                     [Arabidopsis thaliana]
                     170844
  Seq. No.
                     LIB35-044-Q1-E1-D5
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q3688175
  BLAST score
                     260
  E value
                     1.0e-33
  Match length
                     125
  % identity
  NCBI Description
                     (AL031804) gamma-VPE (vacuolar processing enzyme)
                     [Arabidopsis thaliana]
  Seq. No.
                     170845
                     LIB35-044-Q1-E1-E8
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g4006934
  BLAST score
                     180
                     7.0e-26
  E value
                     97
  Match length
                     64
  % identity
  NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]
                     170846
  Seq. No.
  Seq. ID
                     LIB35-044-Q1-E1-F11
                     BLASTN
```

23301

g4220641



```
BLAST score
                   34
                   1.0e-09
E value
Match length
                   54
                   93
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: NCBI Description

MUL3, complete sequence [Arabidopsis thaliana]

170847 Seq. No. LIB35-044-Q1-E1-F2 Seq. ID BLASTN Method g2828182 NCBI GI

BLAST score 47 2.0e-17 E value Match length 348 68 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MOJ9, complete sequence [Arabidopsis thaliana]

170848 Seq. No.

LIB35-044-Q1-E1-G12 Seq. ID

Method BLASTX NCBI GI g2565275 BLAST score 219 1.0e-17 E value Match length 135 35 % identity

(AF023611) Dim1p homolog [Homo sapiens] NCBI Description

Seq. No. 170849

LIB35-044-Q1-E1-H2 Seq. ID

BLASTX Method g131398 NCBI GI 571 BLAST score 4.0e-59 E value 113 Match length 96 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

170850 Seq. No.

Seq. ID LIB35-045-Q1-E1-A10

Method BLASTN q2760829 NCBI GI 37 BLAST score 1.0e-11 E value Match length 99 % identity

Arabidopsis thaliana chromosome II BAC F18A8 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   170851
                   LIB35-045-Q1-E1-A12
Seq. ID
Method
                   BLASTX
                   g131398
NCBI GI
BLAST score
                   261
                   6.0e-23
E value
                   80
Match length
```

69

% identity PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb T41858, gb T88021, gb R37531, gb T04679, gb N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

```
Seq. No.
                   170852
                  LIB35-045-Q1-E1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1922964
                   154
BLAST score
                   3.0e-10
E value
```

45 Match length 67 % identity

NCBI Description (AC000106) Similar to Schizosaccharomyces CCAAT-binding

factor (gb U88525). EST gb T04310 comes from this gene.

[Arabidopsis thaliana]

170853 Seq. No. Seq. ID LIB35-045-Q1-E1-C2 Method BLASTX g131398 NCBI GI BLAST score 289 3.0e-26 E value

Match length 74 % identity 84

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170854

Seq. ID LIB35-045-Q1-E1-E7

Method BLASTN NCBI GI q3510337 BLAST score 429 E value 0.0e+00Match length 429 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



K19E20, complete sequence [Arabidopsis thaliana]

170855 Seq. No. _ LIB35-045-Q1-E1-G12 Seq. ID Method BLASTX NCBI GI g3219267 BLAST score 345 1.0e-32 E value 114 Match length 65 % identity (AB015313) MAP kinase kinase 2 [Arabidopsis thaliana] NCBI Description Seq. No. 170856 LIB35-045-Q1-E1-H1 Seq. ID Method BLASTX NCBI GI g2662469 BLAST score 427 2.0e-42 E value 83 Match length 95 % identity NCBI Description (AF034217) ribosomal protein S6 [Arabidopsis thaliana] 170857 Seq. No. LIB35-046-Q1-E1-B11 Seq. ID Method BLASTN NCBI GI g3399678 BLAST score 366 0.0e + 00E value 374 Match length 99 % identity Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, NCBI Description complete sequence [Arabidopsis thaliana] 170858 Seq. No. LIB35-046-Q1-E1-B3 Seq. ID Method BLASTN NCBI GI g4519188 BLAST score 115 E value 2.0e-58 Match length 123 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence Seq. No. 170859 Seq. ID LIB35-046-Q1-E1-B9 Method BLASTN NCBI GI g2191157 99 BLAST score 3.0e-48E value 283 Match length % identity 84 NCBI Description Arabidopsis thaliana BAC IG002P16

Seq. No. 170860

Seq. ID LIB35-046-Q1-E1-C12

Method BLASTX

23304



```
g131398
NCBI GI
                   300
BLAST score
                   8.0e-29
E value
                   110
Match length
                   65
% identity
```

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

```
170861
Seq. No.
                   LIB35-046-Q1-E1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131398
BLAST score
                   246
                   6.0e-21
E value
                   109
Match length
                   54
```

% identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

```
Seq. No.
                   170862
Seq. ID
                   LIB35-046-Q1-E1-E3
Method
                   BLASTX
NCBI GI
                   g2129687
BLAST score
                   267
E value
                   2.0e-23
```

Match length 54 98 % identity

NCBI Description protein kinase AK19 - Arabidopsis thaliana (fragment)

>gi_2146756_pir__S66332 protein kinase AK19 - Arabidopsis
thaliana (fragment) >gi_928904_emb_CAA60527_ (X86964) protein kinase catalytic domain (fragment) [Arabidopsis

thaliana]

Seq. No. 170863

Seq. ID LIB35-046-Q1-E1-F12

Method BLASTX NCBI GI g4006934 BLAST score 486 E value 5.0e-49 Match length 114 82 % identity

NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]



```
170864
Seq. No.
Seq. ID
                  LIB35-046-Q1-E1-G2
                  BLASTN
Method
NCBI GI
                  q4662609
                  48
BLAST score
                  3.0e-18
E value
                  88
Match length
                  89
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
NCBI Description
                  complete sequence
                  170865
Seq. No.
                  LIB35-046-Q1-E1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2160155
                   44
BLAST score
                  2.0e-15
E value
                   60
Match length
                   93
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                  170866
Seq. No.
                  LIB35-047-Q1-E1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213584
BLAST score
                   408
                  2.0e-40
E value
Match length
                   81
                   93
% identity
NCBI Description (AC000348) T7N9.4 [Arabidopsis thaliana]
                   170867
Seq. No.
                  LIB35-047-Q1-E1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2190544
BLAST score
                   258
                   1.0e-22
E value
Match length
                   70
% identity
                   (AC001229) Similar to Saccharomyces hypothetical protein
NCBI Description
                   P9642.2 (gb U40828). [Arabidopsis thaliana]
                   170868
Seq. No.
Seq. ID
                   LIB35-047-Q1-E1-B4
Method
                   BLASTN
NCBI GI
                   g2828278
BLAST score
                   94
                   2.0e-45
E value
                   278
Match length
% identity
                   90
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
                   (ESSAII project)
```

Seq. ID LIB35-047-Q1-E1-C12

Method BLASTX

or steps with

NCBI GI g131398 BLAST score 259 E value 5.0e-28 Match length 119 % identity 57

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170870

Seq. ID LIB35-047-Q1-E1-D10

Method BLASTX
NCBI GI g131398
BLAST score 172
E value 2.0e-12
Match length 79
% identity 53

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64065_cb_717503_ard_b_N673665_cb_717503_br_b_N673665_cb_717503_br_b_N673665_cb_7

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170871

Seq. ID LIB35-047-Q1-E1-E8

Method BLASTN
NCBI GI g2494110
BLAST score 159
E value 2.0e-84
Match length 175
% identity 98

NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 170872

Seq. ID LIB35-047-Q1-E1-F1

Method BLASTX
NCBI GI g3914722
BLAST score 173
E value 2.0e-12
Match length 47
% identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L29

Seq. No. 170873

Seq. ID LIB35-047-Q1-E1-F12

Method BLASTN



```
g4335744
NCBI GI
                  51
BLAST score
E value
                  1.0e-19
                  190
Match length
                  83
% identity
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170874
                  LIB35-047-Q1-E1-H8
Seq. ID
Method
                  BLASTN
                  g3985958
```

Method BLASIN
NCBI GI g3985958
BLAST score 84
E value 2.0e-39
Match length 283
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZN1, complete sequence [Arabidopsis thaliana]

 Seq. No.
 170875

 Seq. ID
 LIB35-048-Q1-E1-A4

 Method
 BLASTX

NCBI GI g131398
BLAST score 345
E value 1.0e-32
Match length 95
% identity 75

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabi \overline{d} opsis

Seq. No. 170876

Seq. ID LIB35-048-Q1-E1-A9

Method BLASTN
NCBI GI g3128137
BLAST score 154
E value 2.0e-81
Match length 170
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 170877

Seq. ID LIB35-048-Q1-E1-B4

Method BLASTN
NCBI GI g531828
BLAST score 48
E value 3.0e-18
Match length 76
% identity 91

NCBI Description Cloning vector pSport1, complete cds



```
Seq. No. 170878
Seq. ID LIB35-048-Q1-E1-D10
```

Method BLASTX
NCBI GI g595768
BLAST score 151
E value 8.0e-10
Match length 47

% identity 62 NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]

Seq. No. 170879

Seq. ID LIB35-048-Q1-E1-D2

Method BLASTN
NCBI GI g2351065
BLAST score 165
E value 5.0e-88
Match length 169
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 170880

Seq. ID LIB35-048-Q1-E1-E11

Method BLASTX-NCBI GI g131398
BLAST score 191
E value 1.0e-14
Match length 101
% identity 48

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 170881

Seq. ID LIB35-048-Q1-E1-E5

Method BLASTX
NCBI GI 94678346
BLAST score 200
E value 7.0e-16
Match length 68
% identity 65

NCBI Description (AL049659) putative protein [Arabidopsis thaliana]

Seq. No. 170882

Seq. ID LIB35-048-Q1-E1-E7

Method BLASTX
NCBI GI g1169278
BLAST score 244
E value 1.0e-20
Match length 67

23309



% identity 78

NCBI Description DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 170883

Seq. ID LIB35-048-Q1-E1-G2

Method BLASTN
NCBI GI g3540210
BLAST score 98
E value 1.0e-47
Match length 98
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170884

Seq. ID LIB35-048-Q1-E1-G3

Method BLASTN
NCBI GI 94519188
BLAST score 122
E value 5.0e-62
Match length 334
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L19, complete sequence

Seq. No. 170885

Seq. ID LIB35-048-Q1-E1-G6

Method BLASTX
NCBI GI g131398
BLAST score 134
E value 8.0e-23
Match length 92
% identity 66

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170886

Seq. ID LIB35-048-Q1-E1-H6

Method BLASTX
NCBI GI g2244835
BLAST score 599
E value 2.0e-62
Match length 137
% identity 78

NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 170887

Seq. ID LIB35-049-Q1-E1-C3

Method BLASTN

```
NCBI GI
                  g4757390
BLAST score
                  231
E value
                  1.0e-127
                  361
Match length
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F24B18, complete sequence
                  170888
Seq. No.
                  LIB35-049-Q1-E1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  144
                   4.0e-09
E value
                  63
Match length
                  49
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  170889
Seq. No.
                  LIB35-050-Q1-E1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519195
BLAST score
                  47
E value
                   3.0e-17
                  103
Match length
% identity
                  86
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
                   170890
Seq. No.
                  LIB35-050-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2129622
BLAST score
                   292
E value
                   6.0e-27
Match length
                   67
% identity
                   immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
NCBI Description
                   (U52046) immunophilin [Arabidopsis thaliana]
Seq. No.
                   170891
                   LIB35-050-Q1-E1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3869072
BLAST score
                   121
E value
                   2.0e-61
Match length
                   365
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MJB24, complete sequence [Arabidopsis thaliana]

170892 Seq. No.

Seq. ID LIB35-050-Q1-E1-D11

Method BLASTN NCBI GI g16446 BLAST score 95



E value 4.0e-46 Match length 167 % identity 90 NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide 170893 Seq. No. LIB35-050-Q1-E1-D3 Seq. ID Method BLASTX NCBI GI g1064883 BLAST score 448 1.0e-44 E value Match length 87 99 % identity NCBI Description (X92976) ZAP1 [Arabidopsis thaliana] Seq. No. 170894 LIB35-050-Q1-E1-E1 Seq. ID Method BLASTX q4583542 NCBI GI BLAST score 293 2.0e-26 E value Match length 121 % identity 58 (Y16847) 16 kDa polypeptide of oxygen-evolving complex NCBI Description [Arabidopsis thaliana] 170895 Seq. No. Seq. ID LIB35-050-Q1-E1-E9 Method BLASTX g3738322 NCBI GI BLAST score 141 3.0e-09 E value Match length 32 88 % identity (AC005170) putative small nuclear ribonucleoprotein NCBI Description [Arabidopsis thaliana] Seq. No. 170896 LIB35-050-Q1-E1-G10 Seq. ID Method BLASTN g3046847 NCBI GI BLAST score 47 E value 2.0e-17 Match length 47 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana] 170897 Seq. No.

Seq. ID LIB35-050-Q1-E1-H9 Method BLASTX

q464987 NCBI GI BLAST score 517 E value 9.0e-53 Match length 96 98 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN



LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
>gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana
>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

 Seq. No.
 170898

 Seq. ID
 LIB35-051-Q1-E1-A3

 Method
 BLASTN

 NCBI GI
 g4199934

 BLAST score
 61

BLAST score 61 E value 7.0e-26 Match length 189 % identity 88

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 170899

Seq. ID LIB35-051-Q1-E1-A4

Method BLASTN
NCBI GI g2827644
BLAST score 191
E value 1.0e-103
Match length 263

Match length 263 % identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4

(ESSAII project)

Seq. No. 170900

Seq. ID LIB35-051-Q1-E1-A5

Method BLASTX
NCBI GI g115783
BLAST score 310
E value 1.0e-28
Match length 60
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170901

Seq. ID LIB35-051-Q1-E1-A6

Method BLASTX
NCBI GI g3599968
BLAST score 331
E value 4.0e-31
Match length 100
% identity 62

NCBI Description (AF032123) clp protease [Arabidopsis thaliana]

Seq. No. 170902

Seq. ID LIB35-051-Q1-E1-B8

Method BLASTX NCBI GI g115783 BLAST score 257



E value 2.0e-22 Match length 74

% identity 72

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170903

Seq. ID LIB35-051-Q1-E1-D5

Method BLASTN
NCBI GI 94662609
BLAST score 68
E value 5.0e-30
Match length 76
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 170904

Seq. ID LIB35-051-Q1-E1-G10

Method BLASTX
NCBI GI g2979565
BLAST score 319
E value 1.0e-29

Match length 91 % identity 71

NCBI Description (AC003680) putative sin3 associated polypeptide (SAP18)

[Arabidopsis thaliana]

Seq. No. 170905

Seq. ID LIB35-051-Q1-E1-G9

Method BLASTN
NCBI GI g3128137
BLAST score 91
E value 7.0e-44
Match length 147
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 170906

Seq. ID LIB35-051-Q1-E1-H6

Method BLASTN
NCBI GI g3047074
BLAST score 117
E value 3.0e-59
Match length 198
% identity 93

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 170907

Seq. ID LIB35-052-Q1-E1-A9

Method BLASTX
NCBI GI g485518
BLAST score 317
E value 6.0e-48



Match length 98 % identity 97

NCBI Description ubiquitin / ribosomal protein CEP52 - rice

>gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal

polyprotein [Oryza sativa]

Seq. No. 170908

Seq. ID LIB35-052-Q1-E1-B1

Method BLASTX
NCBI GI g3355476
BLAST score 568
E value 1.0e-58
Match length 121
% identity 90

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 170909

Seq. ID LIB35-052-Q1-E1-C11

Method BLASTN
NCBI GI g4539402
BLAST score 245
E value 1.0e-135
Match length 301
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13

(ESSA project)

Seq. No. 170910

Seq. ID LIB35-052-Q1-E1-D4

Method BLASTN
NCBI GI g4757407
BLAST score 50
E value 3.0e-19
Match length 225
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQD19, complete sequence

Seq. No. 170911

Seq. ID LIB35-052-Q1-E1-F11

Method BLASTX
NCBI GI g131398
BLAST score 528
E value 4.0e-54
Match length 122
% identity 88

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965_gb_Z17592_and_gb_N65338_gb_N37466_and_gb_T45400

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170912

Method

NCBI GI

BLAST score

BLASTX

661

g4586256



```
Seq. ID
                  LIB35-052-Q1-E1-G11
                  BLASTX
Method
                  g4741960
NCBI GI
BLAST score
                  271
                  6.0e-24
E value
Match length
                  89
                  64
% identity
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
                  170913
Seq. No.
                  LIB35-052-Q1-E1-G2
Seq. ID
Method
                  BLASTN
                  g4557061
NCBI GI
BLAST score
                  110
                   6.0e - 55
E value
Match length
                  372
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC F23M2 genomic
NCBI Description
                  sequence, complete sequence
                  170914
Seq. No.
                  LIB35-052-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335729
                   125
BLAST score
                   9.0e-07
E value
                  129
Match length
% identity
                   3
                  (AC006248) putative salt-inducible protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   170915
                  LIB35-052-Q1-E1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4757662
BLAST score
                   190
E value
                   1.0e-102
                   337
Match length
                   99
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from
                   chromosome I, complete sequence
                   170916
Seq. No.
                   LIB35-053-Q1-E1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q595768
BLAST score
                   140
E value
                   1.0e-08
Match length
                   49
% identity
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
                   170917
                   LIB35-053-Q1-E1-B1
Seq. ID
```



```
1.0e-69
E value
                  134
Match length
                  99
% identity
                  (AL049640) probable photosystem I chain XI precursor
NCBI Description
                  [Arabidopsis thaliana]
                  170918
Seq. No.
                  LIB35-053-Q1-E1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738320
BLAST score
                  513
                  3.0e-52
E value
                  108
Match length
                  89
% identity
                  (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  170919
Seq. No.
                  LIB35-053-Q1-E1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585875
BLAST score
                  479
                  3.0e-48
E value
Match length
                  113
                  79
% identity
NCBI Description (AC005850) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  170920
                  LIB35-053-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746125
BLAST score
                  650
E value
                  2.0e-68
Match length
                  126
% identity
                  100
NCBI Description (U73786) ACC synthase [Arabidopsis thaliana]
                  170921
Seq. No.
Seq. ID
                  LIB35-053-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  440
E value
                  1.0e-43
Match length
                  105
                  86
% identity
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
```

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170922

Seq. ID LIB35-053-Q1-E1-F7



Method BLASTX
NCBI GI g115783
BLAST score 498
E value 2.0e-50
Match length 95
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 170923

Seq. ID LIB35-053-Q1-E1-G12

Method BLASTX
NCBI GI g4455325
BLAST score 350
E value 4.0e-33

Match length 79 % identity 85

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 170924

Seq. ID LIB35-053-Q1-E1-H3

Method BLASTX
NCBI GI g115767
BLAST score 594
E value 8.0e-62
Match length 114
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 170925

Seq. ID LIB35-053-Q1-E1-H4

Method BLASTX
NCBI GI g131398
BLAST score 507
E value 2.0e-51
Match length 120
% identity 86

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 170926

Seq. ID LIB35-054-Q1-E1-A12



```
Method
                  BLASTX
                  g3080414
NCBI GI
BLAST score
                  247
                  3.0e-21
E value
Match length
                  72
                  76
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                  170927
Seq. No.
Seq. ID
                  LIB35-054-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  g2262176
BLAST score
                  443
                  4.0e-44
E value
Match length
                  104
                  85
% identity
                  (AC002329) putative RING zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana] >gi 3790573 (AF078824) RING-H2 finger protein
                  RHA3a [Arabidopsis thaliana]
                   170928
Seq. No.
                  LIB35-054-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159704
BLAST score
                   244
                   1.0e-135
E value
Match length
                   283
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
                   170929
Seq. No.
                  LIB35-054-Q1-E1-D2
Seq. ID
Method
                   BLASTN
                   g3985934
NCBI GI
BLAST score
                   312
                   1.0e-175
E value
Match length
                   312
% identity
                   68
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJE7, complete sequence [Arabidopsis thaliana]
                   170930
Seq. No.
                   LIB35-054-Q1-E1-E12
Seq. ID
                   BLASTX
Method
                   g3309620
NCBI GI
                   118
BLAST score
                   1.0e-10
E value
                   68
Match length
                   53
% identity
                  (AF074916) resistance to Pseudomonas syringae protein 5
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID LIB35-054-Q1-E1-E3

Method BLASTX NCBI GI g2501448



BLAST score 147 E value 1.0e-09 Match length 60 % identity 53

NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923_ (X99609) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 170932

Seq. ID LIB35-054-Q1-E1-F2

Method BLASTN
NCBI GI g3046847
BLAST score 136
E value 2.0e-70
Match length 302
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 170933

Seq. ID LIB35-054-Q1-E1-G2

Method BLASTX
NCBI GI g3047123
BLAST score 251
E value 2.0e-25
Match length 80
% identity 78

NCBI Description (AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

Seq. No. 170934

Seq. ID LIB35-054-Q1-E1-G6

Method BLASTN
NCBI GI g3759176
BLAST score 132
E value 4.0e-68
Match length 264
% identity 88

NCBI Description Arabidopsis thaliana mRNA for 3-phosphoserine phosphatase,

complete cds

Seq. No. 170935

Seq. ID LIB35-054-Q1-E1-H5

Method BLASTN
NCBI GI g2244950
BLAST score 42
E value 2.0e-14
Match length 46
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 170936

Seq. ID LIB35-054-Q1-E1-H8

Method BLASTX NCBI GI g131398 BLAST score 182 E value 7.0e-14



```
Match length
                  52
% identity
                  79
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >qi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >qi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide qb X55970. ESTs qb Z17693, qb N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  170937
                  LIB35-055-Q1-E2-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q531829
BLAST score
                  144
E value
                  5.0e-09
Match length
                  77
% identity
                  44
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                  170938
                  LIB35-055-Q1-E2-E3
Seq. ID
                  BLASTX
Method
                  q1346871
NCBI GI
BLAST score
                  180
E value
                  1.0e-13
Match length
                  63
                  57
% identity
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >qi 967968
                  (L31936) photosystem II 10kDa polypeptide [Brassica
                  campestris]
                  170939
Seq. No.
                  LIB35-055-Q1-E2-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  155
E value
                  9.0e-82
                  299
Match length
                  88
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUF9, complete sequence [Arabidopsis thaliana]
                  170940
Seq. No.
                  LIB35-055-Q1-E2-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567281
                  235
BLAST score
E value
                  8.0e-20
```

105 Match length 47 % identity

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

170941 Seq. No.

BLAST score

Match length

E value

372

372

0.0e+00



```
Seq. ID
                  LIB35-056-Q1-E1-C8
Method
                  BLASTN
                  g4469002
NCBI GI
                  323
BLAST score
                  0.0e + 00
E value
Match length
                  327
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                  (ESSA project)
                  170942
Seq. No.
Seq. ID
                  LIB35-056-Q1-E2-A9
Method
                  BLASTX
NCBI GI
                  g4585925
BLAST score
                  352
                  2.0e-33
E value
Match length
                  112
% identity
                  58
NCBI Description (AC007211) unknown protein [Arabidopsis thaliana]
                  170943
Seq. No.
                  LIB35-056-Q1-E2-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587567
BLAST score
                  244
                  1.0e-20
E value
Match length
                  85
% identity
                  54
NCBI Description (AC006550) F1003.7 [Arabidopsis thaliana]
                  170944
Seq. No.
                  LIB35-056-Q1-E2-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1279640
BLAST score
                  331
                  8.0e-31
E value
Match length
                  124
% identity
                  53
NCBI Description (X92204) NAM [Petunia x hybrida]
Seq. No.
                  170945
Seq. ID
                  LIB35-056-Q1-E2-C9
Method
                  BLASTX
                  g3063444
NCBI GI
                  96
BLAST score
                  7.0e-29
E value
Match length
                  75
% identity
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
                  170946
Seq. No.
Seq. ID
                  LIB35-056-Q1-E2-D2
Method
                  BLASTN
NCBI GI
                  g4469002
```

23322

Seq. ID

170952

jC-alX22036Q1E1A07a1



```
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
NCBI Description
                  (ESSA project)
                  170947
Seq. No.
                  LIB35-056-Q1-E2-E3
Seq. ID
Method
                  BLASTN
                  g531828
NCBI GI
                  49
BLAST score
                  6.0e-19
E value
Match length
                  81
% identity
                  90
NCBI Description Cloning vector pSport1, complete cds
                  170948
Seq. No.
Seq. ID
                  LIB35-056-Q1-E2-F9
Method
                  BLASTN
NCBI GI
                  q551209
BLAST score
                  88
                  1.0e-41
E value
Match length
                  165
                  86
% identity
NCBI Description T.aestivumn (subclone pAWJL175) AWJL175 gene
                  170949
Seq. No.
                  LIB35-056-Q1-E2-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4741954
BLAST score
                  586
                  8.0e-61
E value
                  124
Match length
                  90
% identity
NCBI Description (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
                  170950
Seq. No.
                  LIB35-056-Q1-E2-H9
Seq. ID
Method
                  BLASTX
                  g4574406
NCBI GI
BLAST score
                  344
                  2.0e-32
E value
Match length
                  110
                  59
% identity
NCBI Description (AF121139) RIM2 protein [Oryza sativa]
                  170951
Seq. No.
                  jC-alX22035Q1E1H05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2833627
BLAST score
                  267
                  1.0e-148
E value
Match length
                  321
                  95
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F1707 complete
                  sequence [Arabidopsis thaliana]
```

23323



Method BLASTN
NCBI GI 94455168
BLAST score 294
E value 1.0e-165
Match length 314
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10

(ESSAII project)

Seq. No. 170953

Seq. ID jC-alX22043Q1E1F06a1

Method BLASTN
NCBI GI g4454447
BLAST score 133
E value 5.0e-69
Match length 153
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170954

Seq. ID jC-alX22044Q1E1C11a1

Method BLASTN
NCBI GI g2656029
BLAST score 73

E value 4.0e-33 Match length 173 % identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQB2

Seq. No. 170955

Seq. ID jC-alX22045Q1E1B02a1

Method BLASTN
NCBI GI 94455229
BLAST score 148
E value 9.0e-78
Match length 209
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23

(ESSAII project)

Seq. No. 170956

Seq. ID jC-alX22045Q1E1C02b1

Method BLASTX
NCBI GI g549975
BLAST score 301
E value 2.0e-27
Match length 98
% identity 68

NCBI Description (U12858) nucleosome assembly protein I-like protein;

similar to mouse nap I, PIR Accession Number JS0707

[Arabidopsis thaliana]

Seq. No. 170957

Seq. ID jC-alX22046Q1E1A10a1

Method BLASTX



q2832623 NCBI GI BLAST score 156 1.0e-10 E value Match length 25 100 % identity (AL021711) protein kinase - like protein [Arabidopsis NCBI Description thaliana] 170958 Seq. No. Seq. ID jC-a1X22080Q1E2F05a1 Method BLASTX g3021344 NCBI GI BLAST score 285 2.0e-25 E value Match length 64 83 % identity (AJ004959) hypothetical protein [Cicer arietinum] NCBI Description Seq. No. 170959 Seq. ID jC-alX22082Q1E2F07a1 Method BLASTN NCBI GI q2104523 273 BLAST score 1.0e-152 E value Match length 301 % identity Arabidopsis thaliana BAC T10M13 from chromosome IV, from NCBI Description 10.8 cM to 11.6 cM, complete sequence Seq. No. 170960 jC-alX22082Q1E2H11a1 Seq. ID BLASTX Method NCBI GI q3806098 BLAST score 155 E value 2.0e-10 Match length 53 % identity 64

(AF079100) arginine-tRNA-protein transferase 1; Atelp NCBI Description

[Arabidopsis thaliana]

Seq. No. 170961

jC-a1X22082Q1E2H12a1 Seq. ID

Method BLASTX q1709358 NCBI GI BLAST score 175 1.0e-12 E value 49 Match length 63 % identity

NCBI Description NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE

PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859

nucleoside triphosphatase - garden pea

>gi 2129890 pir S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea

>qi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase

[Pisum satīvum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]



```
Seq. No.
                  170962
                  jC-alX22083Q1E2F01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2702271
BLAST score
                  256
                  4.0e-22
E value
Match length
                  49
% identity
                  100
                  (AC003033) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  170963
Seq. ID
                  jC-alX22085Q1E2C09a1
Method
                  BLASTN
NCBI GI
                  g2795802
BLAST score
                  209
E value
                  1.0e-114
Match length
                  422
% identity
                  95
                  Arabidopsis thaliana chromosome II BAC F17A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170964
Seq. ID
                  jC-a1X24001Q1E1A02a1
Method
                  BLASTN
NCBI GI
                  g4417264
BLAST score
                  178
                  1.0e-95
E value
Match length
                  256
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC F7D8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  170965
                  jC-alX24003Q1E1A11a1
Seq. ID
                  BLASTX
Method
                  g2281088
NCBI GI
BLAST score
                  264
E value
                  2.0e-23
Match length
                  61
                  85
% identity
                  (AC002333) indole-3-acetate beta-glucosyltransferase isolog
NCBI Description
                   [Arabidopsis thaliana]
                  170966
Seq. No.
                   jC-alX24003Q1E1E12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2443751
BLAST score
                  311
E value
                  1.0e-28
Match length
                  67
                  91
% identity
```

NCBI Description

Seq. ID jC-alX24003Q1E1F06a1

Method BLASTN

(AF020303) fumarase [Arabidopsis thaliana] >gi 2529676

(AC002535) putative fumarase [Arabidopsis thaliana]

BLAST score

E value Match length 246 1.0e-136

440



```
NCBI GI
                  g4468801
                  421
BLAST score
                  0.0e + 00
E value
                  429
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                  (ESSA project)
                  170968
Seq. No.
                  jC-a1X24004Q1E1E03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459575
BLAST score
                  115
                  1.0e-05
E value
Match length
                  85
% identity
                  13
                  (U75346) envelope protein [Chlamydomonas reinhardtii]
NCBI Description
                  170969
Seq. No.
                  jC-alX24004Q1E1F09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3236234
BLAST score
                  130
                  7.0e-67
E value
                  270
Match length
% identity
                  94
NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  170970
Seq. No.
                  jC-a1X24006Q1E1D07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2245031
                  170
BLAST score
                   6.0e-91
E value
                  234
Match length
                  93
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  170971
Seq. No.
                   jC-alX24006Q1E1G04a1
Seq. ID
Method
                  BLASTX
                  g3522961
NCBI GI
BLAST score
                   288
                   8.0e-26
E value
Match length
                  75
% identity
                   77
NCBI Description (AC004411) putative pto kinase [Arabidopsis thaliana]
                  170972
Seq. No.
                   jC-alX24006Q1E1G10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4415905
```

23327



% identity 98 Arabidopsis thaliana chromosome II BAC F13K3 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 170973 Seq. No. jC-alX24049Q1E2B01a1 Seq. ID Method BLASTN g3548797 NCBI GI 87 BLAST score 1.0e-41 E value 138 Match length % identity 91 Arabidopsis thaliana chromosome II BAC T18E12 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 170974 Seq. No. jC-alX24049Q1E2E07a1 Seq. ID BLASTX Method g2129622 NCBI GI 311 BLAST score 1.0e-28 E value Match length 66 89 % identity immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 NCBI Description (U52046) immunophilin [Arabidopsis thaliana] 170975 Seq. No. jC-alX24051Q1E1C08a1 Seq. ID BLASTN Method g2264302 NCBI GI 76 BLAST score 4.0e-35 E value 132 Match length 89 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MAC12, complete sequence [Arabidopsis thaliana] 170976 Seq. No. Seq. ID jC-alX24071Q1E1H03a1 BLASTN Method NCBI GI q3128166 BLAST score 104 2.0e-51 E value 246 Match length 93 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170977

jC-alX24076Q1E1E10a1 Seq. ID

Method BLASTX NCBI GI q1703153 BLAST score 188 E value 2.0e-14 Match length 37 % identity

NCBI Description ACTIN >gi 2147076 pir__S65079 actin - Cyanidioschyzon



merolae >gi_1167501_dbj_BAA06866_ (D32140) actin
[Cyanidioschyzon merolae]

Seq. No. 170978

Seq. ID jC-alX24076Q1E1E12a1

Method BLASTX
NCBI GI g2425066
BLAST score 161
E value 3.0e-11
Match length 52

NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No. 170979

% identity

Seq. ID jC-alX24077Q1E1B10a1

50

Method BLASTN
NCBI GI g2738247
BLAST score 110
E value 5.0e-55
Match length 278
% identity 84

NCBI Description Arabidopsis thaliana cobalamin-independent methionine

synthase (ATCIMS) mRNA, complete cds

Seq. No. 170980

Seq. ID jC-alX24077Q1E1F09a1

Method BLASTN
NCBI GI 94589439
BLAST score 265
E value 1.0e-147
Match length 353
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 170981

Seq. ID jC-alX24077Q1E1G12a1

Method BLASTX
NCBI GI g3128172
BLAST score 294
E value 1.0e-26
Match length 66
% identity 83

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 170982

Seq. ID jC-alX24078Q1E1A08b1

Method BLASTX
NCBI GI g4337175
BLAST score 167
E value 3.0e-12
Match length 44
% identity 77

NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906,

gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]



170983

Seq. No.

```
jC-alX24078Q1E1B12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618601
                  92
BLAST score
                  2.0e-44
E value
Match length
                  199
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHJ24, complete sequence [Arabidopsis thaliana]
                  170984
Seq. No.
                  jC-alX24081Q1E1B11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570223
BLAST score
                  154
                  2.0e-81
E value
Match length
                  262
% identity
                  90
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  170985
Seq. No.
Seq. ID
                  jC-alX24081Q1E1D04a1
                  BLASTN
Method
                  g2244991
NCBI GI
                  189
BLAST score
E value
                  1.0e-102
Match length
                  237
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  170986
Seq. No.
                  jC-alX24081Q1E1D04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245004
BLAST score
                   317
                   9.0e-30
E value
Match length
                  74
                  86
% identity
                   (Z97341) similarity to membrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   170987
Seq. No.
                   jC-alX24081Q1E1E09a1
Seq. ID
                  BLASTN
Method
                   g3785992
NCBI GI
BLAST score
                   65
                   2.0e-28
E value
                   97
Match length
                   92
% identity
                  Arabidopsis thaliana chromosome II BAC T6A23 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

23330

170988

Seq. No.



Seq. ID jC-alX24082Q1E1B01a1 BLASTX Method NCBI GI g2809251 BLAST score 141 1.0e-08 E value Match length 52 48 % identity (AC002560) F21B7.20 [Arabidopsis thaliana] NCBI Description 170989 Seq. No. Seq. ID jC-alX24082Q1E1C08a1 BLASTN Method NCBI GI g3927822 BLAST score 147 3.0e-77 E value Match length 245 % identity 88 Arabidopsis thaliana chromosome II BAC F8N16 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 170990 Seq. No. jC-alX24082Q1E1G10a1 Seq. ID Method BLASTX NCBI GI g3395440 BLAST score 180 4.0e-13 E value Match length 66 52 % identity (AC004683) hypothetical protein [Arabidopsis thaliana] NCBI Description 170991 Seq. No. jC-alX24083Q1E1A02a1 Seq. ID BLASTN Method g2244788 NCBI GI 55 BLAST score 3.0e-22 E value 127 Match length 86 % identity Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No 170992 Seq. No. jC-a1X24085Q1E1A02a1 Seq. ID Method BLASTN NCBI GI g3242700 BLAST score 203 1.0e-110 E value Match length 203 100 % identity Arabidopsis thaliana chromosome II BAC F26B6 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 170993

Seq. ID jC-alX24085Q1E1B04b1

Method BLASTN NCBI GI g431263 BLAST score 69

% identity



```
E value
                  5.0e-31
Match length
                  101
                  92
% identity
                  Arabidopsis thaliana 16kDa ubiquitin conjugating enzyme
NCBI Description
                  (UBC2) gene, complete cds
                  170994
Seq. No.
Seq. ID
                  jC-alX24085Q1E1E09a1
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  121
                  9.0e-62
E value
Match length
                  181
% identity
                  92
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
                  170995
Seq. No.
Seq. ID
                  jC-alX24085Q1E1F08a1
                  BLASTX
Method
NCBI GI
                  q2829910
BLAST score
                  157
                   2.0e-10
E value
Match length
                   51
                   51
% identity
                  (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                   170996
                   jC-alX24086Q1E1D04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3894183
                   197
BLAST score
                   3.0e-15
E value
                   52
Match length
                   71
% identity
                  (AC005662) calmodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   170997
Seq. No.
                   jC-alX24086Q1E1D12a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3869062
BLAST score
                   273
                   1.0e-152
E value
Match length
                   325
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K11I1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   170998
                   jC-a1X24086Q1E1F10a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3046850
BLAST score
                   44
                   1.0e-15
E value
Match length
                   222
```



```
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K24G6, complete sequence [Arabidopsis thaliana]
                  170999
Seq. No.
                  jC-alX24087Q1E1F06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519187
BLAST score
                  218
E value
                  1.0e-119
Match length
                  316
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K1G2, complete sequence
Seq. No.
                  171000
Seq. ID
                  jC-alX24088Q1E1C02a1
Method
                  BLASTN
NCBI GI
                  g3335356
BLAST score
                  206
                  1.0e-112
E value
Match length
                  351
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171001
Seq. No.
                   jC-alX24089Q1E1G11a1
Seq. ID
Method
                   BLASTN
                  g2827513
NCBI GI
BLAST score
                   304
                   1.0e-170
E value
                   397
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
NCBI Description
                   (ESSAII project)
Seq. No.
                   171002
Seq. ID
                   jC-alX24090Q1E1A03a1
Method
                   BLASTN
NCBI GI
                   g3128134
                   393
BLAST score
                   0.0e+00
E value
                   396
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18G13, complete sequence [Arabidopsis thaliana]
```

Seq. No. 171003

jC-alX24090Q1E1E03a1 Seq. ID

Method BLASTN q3540210 NCBI GI BLAST score 54 E value 1.0e-21

Match length 78 92 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

```
171004
Seq. No.
Seq. ID
                  jC-alX24091Q1E1A06a1
Method
                  BLASTN
NCBI GI
                  g3449321
BLAST score
                  392
                  0.0e+00
E value
Match length
                  420
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171005
                  jC-alX24091Q1E1D03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924653
BLAST score
                  208
                  1.0e-113
E value
Match length
                  405
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDA7, complete sequence [Arabidopsis thaliana]
                  171006
Seq. No.
                  jC-alX24091Q1E1D07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3510347
BLAST score
                  185
                   1.0e-100
E value
Match length
                   248
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                   171007
Seq. No.
                   jC-alX24092Q1E1A05a1
Seq. ID
                   BLASTX
Method
                   g3132696
NCBI GI
                   186
BLAST score
                   5.0e-14
E value
                   44
Match length
                   77
% identity
                  (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
NCBI Description
                   171008
Seq. No.
                   jC-alX24092Q1E1C10a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2760171
                   202
BLAST score
                   1.0e-110
E value
                   274
Match length
                   93
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPA24, complete sequence [Arabidopsis thaliana]
                   171009
Seq. No.
                   jC-alX24092Q1E1E02a1
Seq. ID
```

NCBI GI BLAST score

E value

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The about to de
```

```
Method
                  BLASTN
                  g2252848
NCBI GI
BLAST score
                  50
                  3.0e-19
E value
                  125
Match length
                  90
% identity
                  Arabidopsis thaliana BAC TM018A10
NCBI Description
                  171010
Seq. No.
                  jC-alX24092Q1E1F02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4521999
                  79
BLAST score
                  1.0e-36
E value
Match length
                  151
% identity
                  89
                  Arabidopsis thaliana chromosome II BAC F2G1 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  171011
                  jC-alX24093Q1E1C01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3319365
BLAST score
                  74
                  1.0e-33
E value
Match length
                  179
                  87
% identity
NCBI Description Arabidopsis thaliana BAC T24M8
                  171012
Seq. No.
                   jC-alX24093Q1E1H07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2351066
BLAST score
                   164
                   3.0e-87
E value
                   260
Match length
% identity
                   91
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP9, complete sequence [Arabidopsis thaliana]
                   171013
Seq. No.
                   jC-alX24094Q1E1F10a1
Seq. ID
                   BLASTN
Method
                   g2244950
NCBI GI
                   208
BLAST score
                   1.0e-113
E value
Match length
                   366
                   94
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   171014
Seq. No.
                   jC-alX24094Q1E1G03a1
Seq. ID
Method
                   BLASTN
```

23335

g2618599

5.0e-29



Match length 130 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 171015

Seq. ID jC-alX24095Q1E1A12a1

Method BLASTX
NCBI GI g3702332
BLAST score 340
E value 6.0e-32
Match length 66
% identity 100

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 171016

Seq. ID jC-alX24096Q1E1F02a1

Method BLASTN
NCBI GI g666976
BLAST score 71
E value 5.0e-32
Match length 143
% identity 87

NCBI Description A.thaliana TYKY mRNA for NADH:ubiquinone oxidoreductase

Seq. No. 171017

Seq. ID jC-alX24097Q1E1D04a1

Method BLASTN
NCBI GI g3046851
BLAST score 64
E value 6.0e-28
Match length 132
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 171018

Seq. ID jC-alX24097Q1E1E11a1

Method BLASTN
NCBI GI g2213606
BLAST score 370
E value 0.0e+00
Match length 377
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,

complete sequence [Arabidopsis thaliana]

Seq. No. 171019

Seq. ID jC-alX24097Q1E1F09a1

Method BLASTN
NCBI GI 94063737
BLAST score 105
E value 2.0e-52
Match length 113
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
171020
Seq. No.
                  jC-alX24097Q1E1G09a1
Seq. ID
Method
                  BLASTN
                  q1086462
NCBI GI
                  125
BLAST score
E value
                  4.0e-64
                  130
Match length
                  78
% identity
                  Arabidopsis thaliana Columbia ecotype metallothionein
NCBI Description
                   (MT2b) gene, complete cds
                  171021
Seq. No.
                  jC-alX24099Q1E1A11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2098816
                  227
BLAST score
E value
                  1.0e-125
Match length
                  251
                  98
% identity
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
Seq. No.
                   171022
                  jC-alX24099Q1E1A11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2098816
BLAST score
                  232
E value
                  1.0e-128
Match length
                  296
                   97
% identity
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
                   171023
Seq. No.
                   jC-alX24099Q1E1E09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3747111
BLAST score
                   149
E value
                   4.0e-10
                   43
Match length
% identity
                   70
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   171024
Seq. No.
                   jC-alX24099Q1E1F06a1
Seq. ID
Method
                   BLASTN
                   g2392762
NCBI GI
BLAST score
                   251
E value
                   1.0e-139
Match length
                   381
% identity
                   99
```

Seq. No. 171025

Seq. ID jC-alX24100Q1E1A04a1

Method BLASTN NCBI GI g4159712

23337

NCBI Description Arabidopsis thaliana BAC T32N15 from chromsome III near 54

cM, complete sequence



```
BLAST score
                  175
                   6.0e-94
E value
Match length
                  183
                   73
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
                   171026
Seq. No.
                   jC-alX24100Q1E1F09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16151
BLAST score
                   79
                   2.0e-36
E value
Match length
                   245
                   88
% identity
                  Arabidopsis thaliana gene for acyl carrier protein
NCBI Description
                   171027
Seq. No.
                   jC-alX24100Q1E1G07a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4490291
BLAST score
                   153
                   8.0e-81
E value
Match length
                   185
                   96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
NCBI Description
                   (ESSA project)
Seq. No.
                   171028
                   jC-alX24114Q1E1G02a1
Seq. ID
Method
                   BLASTN
                   q3617740
NCBI GI
                   115
BLAST score
                   4.0e-58
E value
Match length
                   179
                   91
% identity
                   Arabidopsis thaliana BAC F1I21 from chromosome 1, near 59
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
                   171029
Seq. No.
                   jC-alX24119Q1E1A11b1
Seq. ID
                   BLASTX
Method
                   g1346724
NCBI GI
                   185
BLAST score
                   2.0e-14
E value
                   42
Match length
                   90
% identity
NCBI Description
                   FLORAL HOMEOTIC PROTEIN PISTILLATA >gi 625970 pir A53839 B
                   function floral homeotic protein PI - Arabidopsis thaliana
                   >gi_493620_dbj_BAA06465_ (D30807) PI protein [Arabidopsis
                   thaliana]
```

171030 Seq. No.

jC-alX24124Q1E1H01b1 Seq. ID

Method BLASTN g2264315 NCBI GI 180 BLAST score



```
E value
                   7.0e-97
Match length
                   232
                   94
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MRN17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171031
Seq. ID
                   jC-alX24127Q1E1F05b1
                   BLASTN
Method
NCBI GI
                   g3046851
BLAST score
                   272
                   1.0e-151
E value
Match length
                   272
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIJ24, complete sequence [Arabidopsis thaliana]
                   171032
Seq. No.
                   jC-alX24134Q1E1E05a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4589436
BLAST score
                   215
                   1.0e-117
E value
Match length
                   325
                   93
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPA22, complete sequence
Seq. No.
                   171033
Seq. ID
                   jC-alX25021Q1E1D01a1
Method
                   BLASTN
NCBI GI
                   g2529657
BLAST score
                   344
E value
                   0.0e + 00
                   372
Match length
                   98
% identity
                   Arabidopsis thaliana chromosome II BAC T30B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171034
Seq. No.
                   jC-alX25027Q1E1B10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2865175
BLAST score
                   358
                   4.0e-34
E value
                   93
·Match length
                   75
% identity
                  (AB010945) AtRer1A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   171035
                   jC-alX25027Q1E1E07a1
Seq. ID
```

Mothod DIACTY

Method BLASTX
NCBI GI g3522942
BLAST score 408
E value 7.0e-40
Match length 137
% identity 53

% identity



```
(AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171036
                  jC-alX25027Q1E1G08a1
Seq. ID
Method
                  BLASTX
                  q1351221
NCBI GI
BLAST score
                  232
                  2.0e-19
E value
                  46
Match length
                  96
% identity
                  TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945085
NCBI Description
                   (U31096) transcription factor TFIIB [Arabidopsis thaliana]
                  >gi 2618697 (AC002510) transcription factor TFIIB
                   [Arabidopsis thaliana]
Seq. No.
                  171037
                  jC-alX25028Q1E1G11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2529657
BLAST score
                  283
E value
                  1.0e-158
Match length
                  283
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T30B22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171038
Seq. No.
Seq. ID
                   jC-a1X25028Q1E1G11b1
Method
                   BLASTN
                  g2529657
NCBI GI
BLAST score
                   215
                   1.0e-117
E value
Match length
                   313
                   93
% identity
                  Arabidopsis thaliana chromosome II BAC T30B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171039
                   jC-a1X25034Q1E1H07a1
Seq. ID
Method
                   BLASTN
                   g4220627
NCBI GI
BLAST score
                   329
E value
                   0.0e + 00
                   341
Match length
                   99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K20J1, complete sequence [Arabidopsis thaliana]
                   171040
Seq. No.
Seq. ID
                   jC-alX25037Q1E1A06a1
Method
                  BLASTN
                   q4678705
NCBI GI
BLAST score
                   305
                   1.0e-171
E value
Match length
                   325
```

23340

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7



(ESSA project)

```
171041
Seq. No.
Seq. ID
                  jC-alX25037Q1E1B04a1
Method
                  BLASTN
                  g1931636
NCBI GI
                  255
BLAST score
E value
                  1.0e-141
                  271
Match length
                  99
% identity
                  Arabidopsis thaliana BAC T19D16 genomic sequence
NCBI Description
                  171042
Seq. No.
                  jC-alX25037Q1E1B11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2564050
BLAST score
                  328
                  0.0e + 00
E value
                  332
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUA22, complete sequence [Arabidopsis thaliana]
                  171043
Seq. No.
                   jC-alX25037Q1E1C07a1
Seq. ID
Method
                  BLASTN
                   g2358139
NCBI GI
                   208
BLAST score
                   1.0e-113
E value
                   316
Match length
                   91
% identity
                  Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
NCBI Description
                   sequence [Arabidopsis thaliana]
Seq. No.
                   171044
Seq. ID
                   jC-a1X25042Q1E1C04a1
Method
                   BLASTN
                   g4519192
NCBI GI
BLAST score
                   126
                   1.0e-64
E value
Match length
                   231
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MBK21, complete sequence
                   171045
Seq. No.
Seq. ID
                   jC-alX25042Q1E1H07a1
Method
                   BLASTN
NCBI GI
                   g2244829
BLAST score
                   93
E value
                   6.0e-45
Match length
                   208
% identity
                   45
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
```

Seq. No. 171046

fragment No



Seq. ID jC-alX25043Q1E1C03a1

Method BLASTN
NCBI GI g4519192
BLAST score 60
E value 2.0e-25
Match length 125
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MBK21, complete sequence

Seq. No. 171047

Seq. ID jC-alX25043Q1E1E04a1

Method BLASTX
NCBI GI g1350930
BLAST score 322
E value 7.0e-30
Match length 63
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S13

Seq. No. 171048

Seq. ID jC-alX25045Q1E1D09a1

Method BLASTN
NCBI GI g3641835
BLAST score 71
E value 8.0e-32
Match length 242

Match length 242 % identity 80

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20

(ESSAII project)

Seq. No. 171049

Seq. ID jC-alX25046Q1E1B08a1

Method BLASTN
NCBI GI g3046853
BLAST score 97
E value 2.0e-47
Match length 177
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRA19, complete sequence [Arabidopsis thaliana]

Seq. No. 171050

Seq. ID jC-alX25046Q1E1D03a1

Method BLASTN
NCBI GI g3702729
BLAST score 49
E value 1.0e-18
Match length 237
% identity 79

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A11, complete sequence [Arabidopsis thaliana]

Seq. No. 171051

Seq. ID jC-alX25046Q1E1G09a1

Method BLASTX NCBI GI g2160176

BLAST score

% identity

E value Match length 94 7.0e-46

126

94

```
193
BLAST score
                  9.0e-15
E value
                  67
Match length
                  58
% identity
                  (AC000132) F21M12.25 gene product [Arabidopsis thaliana]
NCBI Description
                  171052
Seq. No.
                  jC-alX25047Q1E1B06a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3128138
BLAST score
                  188
                  1.0e-101
E value
                  303
Match length
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFO20, complete sequence [Arabidopsis thaliana]
                  171053
Seq. No.
                  jC-a1X25048Q1E1A07a1
Seq. ID
                  BLASTN
Method
                  g3702738
NCBI GI
                  172
BLAST score
                  4.0e-92
E value
                  250
Match length
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWJ3, complete sequence [Arabidopsis thaliana]
                  171054
Seq. No.
                  jC-a1X25049Q1E1A06b1
Seq. ID
                  BLASTN
Method
                  g2924505
NCBI GI
                  56
BLAST score
                   4.0e-23
E value
                  141
Match length
                   92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
NCBI Description
                   (ESSAII project)
                   171055
Seq. No.
                   jC-a1X25049Q1E1C12a1
Seq. ID
                   BLASTX
Method
                   g3063396
NCBI GI
BLAST score
                   184
                   8.0e-14
E value
Match length
                   48
                   75
% identity
NCBI Description
                  (AB012947) vcCyP [Vicia faba]
Seq. No.
                   171056
                   jC-alX25073Q1E1C07a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3550981
```

Seq. ID



```
NCBI Description Arabidopsis thaliana mutM homologue gene, complete cds
Seq. No.
                  171057
                  jC-alX25074Q1E2C06b1
Seq. ID
                  BLASTN
Method
                  q3047100
NCBI GI
                  99
BLAST score
                  1.0e-48
E value
                  159
Match length
% identity
                  91
                  Arabidopsis thaliana BAC F6N23
NCBI Description
                  171058
Seq. No.
                  jC-alX25079Q1E1H05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3641835
BLAST score
                   46
E value
                   4.0e-17
Match length
                   143
                   90
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
NCBI Description
                   (ESSAII project)
                 - 171059
Seq. No.
                   jC-alX25080Q1E1H10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4589412
BLAST score
                   54
E value
                   6.0e-22
                   118
Match length
                   86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                   F6N7, complete sequence
                   171060
Seq. No.
                   jC-alX25081Q1E1H04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3426041
BLAST score
                   167
                   7.0e-12
E value
                   32
Match length
                   91
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   171061
Seq. No.
                   jC-alX25083Q1E1B07b1
Seq. ID
                   BLASTN
Method
                   g2245073
NCBI GI
BLAST score
                   62
E value
                   1.0e-26
                   144
Match length
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   171062
Seq. No.
```

23344

jC-alX25086Q1E1D03a1



```
BLASTX
Method
NCBI GI
                  g4262240
                  376
BLAST score
                  2.0e-36
E value
                  72
Match length
                  100
% identity
                  (AC006200) putative stress protein [Arabidopsis thaliana]
NCBI Description
                  171063
Seq. No.
Seq. ID
                  jC-alX25088Q1E1C04b1
Method
                  BLASTN
NCBI GI
                  g3241920
BLAST score
                  45
                  5.0e-16
E value
                  103
Match length
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171064
                  jC-alX25088Q1E1G03b1
Seq. ID
                  BLASTN
Method
                  q3600029
NCBI GI
BLAST score
                  168
E value
                  2.0e-89
                  418
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana BAC T12H20
Seq. No.
                  171065
                  jC-alX25089Q1E1F01a1
Seq. ID
                  BLASTN
Method
                  q4678258
NCBI GI
                  265
BLAST score
E value
                   1.0e-147
                   331
Match length
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F617
NCBI Description
                   (ESSA project)
Seq. No.
                   171066
Seq. ID
                   jC-alX25089Q1E1F01b1
                   BLASTN
Method
NCBI GI
                   g4678258
BLAST score
                   214
E value
                   1.0e-117
Match length
                   372
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F617
NCBI Description
                   (ESSA project)
                   171067
Seq. No.
Seq. ID
                   jC-alX25092Q1E1A12a1
                   BLASTN
Method
                   g1497986
NCBI GI
```

23345

77

2.0e-35

BLAST score

E value



```
Match length
                  101
                  94
% identity
                  Arabidopsis thaliana SCARECROW (SCARECROW1) gene, complete
NCBI Description
                  171068
Seq. No.
                  jC-alX25092Q1E1B03a1
Seq. ID
                  BLASTN
Method
                  q3063690
NCBI GI
                  72
BLAST score
                  1.0e-32
E value
Match length
                  140
                   88
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
NCBI Description
                   (ESSAII project)
                   171069
Seq. No.
Seq. ID
                   jC-alX25102Q1E1D08a1
Method
                   BLASTN
NCBI GI
                   g3046855
BLAST score
                   359
                   0.0e+00
E value
Match length
                   387
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171070
                   jC-alX25106Q1E1D02a1
Seq. ID
                   BLASTX
Method
                   q21579
NCBI GI
                   288
BLAST score
                   5.0e-26
E value
                   58
Match length
                   90
% identity
                  (X52385) starch phosphorylase (AA 1-966) [Solanum
NCBI Description
                   tuberosum]
                   171071
Seq. No.
                   jC-alX25109Q1E1A07a1
Seq. ID
                   BLASTX
Method
                   g2462737
NCBI GI
                   349
BLAST score
                   3.0e - 33
E value
                   69
Match length
                   100
% identity
                  (AC002292) similar to "Mx" GTP-binding proteins
NCBI Description
                   [Arabidopsis thaliana]
                   171072
Seq. No.
                   jC-alX25109Q1E1A09a1
Seq. ID
                   BLASTN
Method
                   g2341023
NCBI GI
BLAST score
                   43
                   4.0e-15
E value
```

23346

135

81

Match length

% identity



```
Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171073
                  jC-a1X25109Q1E1E01a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3056579
BLAST score
                  263
                  1.0e-146
E value
                  263
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana BAC T1F9 chromosome 1, complete
                  sequence [Arabidopsis thaliana]
                  171074
Seq. No.
Seq. ID
                  jC-alX25112Q1E1H02a1
Method
                  BLASTN
NCBI GI
                  g3366536
BLAST score
                  147
                  4.0e-77
E value
Match length
                  223
                  91
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T25N2O,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  171075
Seq. No.
                  jC-alX25113Q1E1D07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3600040
                  221
BLAST score
                  2.0e-18
E value
                  88
Match length
                   50
% identity
                  (AF080119) similar to Arabidopsis thaliana disease
NCBI Description
                  resistance protein RPS2 (GB:U14158) [Arabidopsis thaliana]
                   171076
Seq. No.
Seq. ID
                   jC-a1X25113Q1E1G09a1
                  BLASTN
Method
                   g4760411
NCBI GI
                   50
BLAST score
                   4.0e-19
E value
Match length
                   106
                   87
% identity
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
                   complete sequence
                   171077
Seq. No.
                   jC-alX25114Q1E1G02a1
Seq. ID
Method
                   BLASTN
                   q2760164
NCBI GI
                   238
BLAST score
E value
                   1.0e-131
Match length
                   292
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
```

K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.

171083



Seq. No.

171078

```
jC-alX25114Q1E1G09a1
Seq. ID
Method
                  BLASTX
                  g3164132
NCBI GI
                  299
BLAST score
                  4.0e-27
E value
                  67
Match length
                  81
% identity
                  (D78601) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                  thaliana]
                  171079
Seq. No.
                  jC-alX25116Q1E1A06a1
Seq. ID
Method
                  BLASTN
                  g3335356
NCBI GI
                  362
BLAST score
                  0.0e + 00
E value
                  362
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171080
Seq. No.
                  jC-alX25116Q1E1B11a1
Seq. ID
Method
                  BLASTN
                  g4589435
NCBI GI
BLAST score
                  244
E value
                  1.0e-135
Match length
                  340
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOE17, complete sequence
                   171081
Seq. No.
                   jC-alX25116Q1E1E02a1
Seq. ID
Method
                   BLASTN
                   g2696018
NCBI GI
                   200
BLAST score
                   1.0e-108
E value
                   256
Match length
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC9, complete sequence [Arabidopsis thaliana]
                   171082
Seq. No.
                   jC-alX25116Q1E1G03a1
Seq. ID
Method
                   BLASTN
                   g3738275
NCBI GI
                   67
BLAST score
                   1.0e-29
E value
Match length
                   142
% identity
                   88
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```



jC-alX25116Q1E1H02a1 Seq. ID Method BLASTX NCBI GI g1705463 BLAST score 463 3.0e-46E value 100 Match length 92 % identity BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi 2129547 pir S71201 NCBI Description biotin sythase - Arabidopsis thaliana $>gi_1045316$ ($\overline{U2}4147$) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi 2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi 1589016 prf 2209438A biotin synthase [Arabidopsis thaliana] Seq. No. 171084 Seq. ID jC-alX25117Q1E1B07a1 Method BLASTN q2098816 NCBI GI BLAST score 272 1.0e-151 E value 296 Match length % identity 97 Arabidopsis thaliana BAC F19G10, complete sequence NCBI. Description 171085 Seq. No. jC-alX25117Q1E1D06a1 Seq. ID Method BLASTN NCBI GI g2494106 BLAST score 61 5.0e-26 E value Match length 180 82 % identity Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, NCBI Description complete sequence [Arabidopsis thaliana] 171086 Seq. No. Seq. ID jC-alX25117Q1E1G11a1 Method BLASTN NCBI GI g3885325 BLAST score 212 1.0e-116 E value Match length 384 94 % identity Arabidopsis thaliana chromosome II BAC T20P8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171087 Seq. No. jC-alX35029Q1E1B11a1 Seq. ID Method BLASTN g4199934 NCBI GI 109 BLAST score

E value 3.0e-54167 Match length 53 % identity

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

Seq. ID



complete sequence [Arabidopsis thaliana]

Seq. No. 171088 jC-alX35043Q1E1D09a1 Seq. ID Method BLASTX g3386603 NCBI GI BLAST score 207 1.0e-16 E value 72 Match length 51 % identity (AC004665) unknown protein [Arabidopsis thaliana] NCBI Description 171089 Seq. No. jC-alX35044Q1E1G11a1 Seq. ID Method BLASTN NCBI GI g166891 BLAST score 128 5.0e-66 E value 180 Match length 93 % identity A.thaliana tryptophan synthase beta subunit (trpB) gene, NCBI Description complete cds 171090 Seq. No. jC-alX35044Q1E1H12a1 Seq. ID Method BLASTN q4539290 NCBI GI BLAST score 235 1.0e-129 E value 300 Match length 94 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 NCBI Description (ESSA project) 171091 Seq. No. jC-alX35047Q1E1F11a1 Seq. ID BLASTN Method g3548797 NCBI GI 227 BLAST score 1.0e-125 E value 320 Match length 99 % identity Arabidopsis thaliana chromosome II BAC T18E12 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171092 Seq. No. jC-alX35047Q1E1G06b1 Seq. ID Method BLASTN NCBI GI q4106527 25 BLAST score 1.0e-04 E value 139 Match length % identity 57 NCBI Description Mus musculus Pontin52 mRNA, complete cds 171093 Seq. No.

23350

jC-alX35048Q1E1F09a1



Method BLASTN NCBI GI q4185128 BLAST score 237 E value 1.0e-131 Match length 336 96 % identity

NCBI Description Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171094

jC-alX35049Q1E1B12a1 Seq. ID

Method BLASTN NCBI GI q2337888 BLAST score 322 E value 0.0e + 00

Match length 350 % identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 171095

jC-alX35055Q1E2B03a1 Seq. ID

Method BLASTX NCBI GI g2129640 BLAST score 391 5.0e-38 E value Match length 75 % identity 99

NCBI Description magnesium chelatase chain - Arabidopsis thaliana

>gi 1154627 emb CAA92802 (Z68495) magnesium chelatase

subunit [Arabidopsis thaliana]

171096 Seq. No.

Seq. ID jC-alXLIB327434P1a06a1

Method BLASTN NCBI GI g540252 BLAST score 35 E value 5.0e-10 35 Match length 100 % identity

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No. 171097

jC-alXLIB327434P1a07b1 Seq. ID

Method BLASTX NCBI GI g3183570 BLAST score 254 E value 1.0e-21 Match length 116 % identity 43

NCBI Description HYPOTHETICAL 36.8 KD PROTEIN IN DINF-QOR INTERGENIC REGION

Seq. No. 171098

Seq. ID jC-alXLIB327434P1a08a1

Method BLASTN NCBI GI g2462264

BLAST score 49



E value 2.0e-18 Match length 49 100 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 171099 Seq. No. jC-alXLIB327434P1a09b1 Seq. ID Method BLASTN q2582640 NCBI GI 60 BLAST score 6.0e-25 E value 76 Match length % identity 96 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 Seq. No. 171100 jC-alXLIB327434P1a12b1 Seq. ID Method BLASTX q140400 NCBI GI BLAST score 538 5.0e-55 E value Match length 134 % identity 75 NCBI Description YCL059c, len:316 [Saccharomyces cerevisiae]

HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1 INTERGENIC REGION >gi_83176_pir__S19389 hypothetical protein YCL059c - yeast

(Saccharomyces cerevisiae) >gi 5300 emb CAA42386 (X59720)

Seq. No. 171101

jC-alXLIB327434P1b01b1 Seq. ID

BLASTX Method NCBI GI q4406764 BLAST score 424 E value 1.0e-41Match length 149 % identity 60

(AC006836) putative uridylyl transferase [Arabidopsis NCBI Description

thaliana]

Seq. No. 171102

jC-alXLIB327434P1b07a1 Seq. ID

Method BLASTX g2739389 NCBI GI BLAST score 356 1.0e-33 E value 86 Match length 54 % identity

(AC002505) Cf-2.2 like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 171103

jC-alXLIB327434P1b09b1 Seq. ID

BLASTN Method NCBI GI g3366536 BLAST score 273 1.0e-152 E value 468 Match length



% identity 100 Genomic sequence for Arabidopsis thaliana BAC T25N20, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 171104 jC-alXLIB327434P1b10b1 Seq. ID BLASTN Method NCBI GI q2582640 BLAST score 64 3.0e-27 E value Match length 76 97 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 171105 Seq. No. Seq. ID jC-alXLIB327434P1b11a1 BLASTN Method NCBI GI g531828 BLAST score 58 1.0e-23 E value Match length 62 98 % identity NCBI Description Cloning vector pSport1, complete cds 171106 Seq. No. jC-alXLIB327434P1b11b1 Seq. ID Method BLASTX g2979559 NCBI GI 274 BLAST score 5.0e-24E value 90 Match length 61 % identity (AC003680) putative DNA binding protein [Arabidopsis NCBI Description thaliana] 171107 Seq. No. Seq. ID jC-alXLIB327434P1c01b1 Method BLASTN g4589410 NCBI GI 332 BLAST score 0.0e + 00E value 414 Match length 100 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2015, complete sequence 171108 Seq. No. jC-alXLIB327434P1c02b1 Seq. ID Method BLASTN g2443328 NCBI GI BLAST score 466 E value 0.0e + 00466 Match length

Arabidopsis thaliana mRNA for Mei2-like protein, complete cds

100

% identity

NCBI Description

```
Seq. No.
                  171109
Seq. ID
                  jC-alXLIB327434P1c03b1
Method
                  BLASTX
NCBI GI
                  q2497733
BLAST score
                  615
                  5.0e-64
E value
Match length
                  118
                  100
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1177796 (M80567) non-specific lipid transfer protein
                   [Arabidopsis thaliana] >gi 3786018 (AC005499) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  171110
Seq. ID
                  jC-alXLIB327434P1c09a1
Method
                  BLASTN
NCBI GI
                   q2462264
BLAST score
                   51
                  1.0e-19
E value
Match length
                   51
                  100
% identity
NCBI Description
                  Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   171111
                   jC-alXLIB327434P1c10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4587641
BLAST score
                   472
                   0.0e + 00
E value
Match length
                   472
                   100
% identity
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                   sequence, complete sequence
                   171112
Seq. No.
                   jC-alXLIB327434P1d02b1
Seq. ID
                   BLASTX
Method
                   g282964
NCBI GI
                   350
BLAST score
                   6.0e-33
E value
                   93
Match length
                   70
% identity
                  transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                   petunia >gi 20563 emb CAA78386 (Z13996) protein 1 [Petunia
                   x hybrida]
                   171113
Seq. No.
                   jC-alXLIB327434P1d08b1
Seq. ID
Method
                   BLASTN
```

NCBI GI g2582640
BLAST score 66
E value 2.0e-28
Match length 74
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

```
Seq. No.
                  171114
Seq. ID
                  jC-alXLIB327434P1d10b1
Method
                  BLASTX
                  g3386622
NCBI GI
                  739
BLAST score
                  2.0e-78
E value
Match length
                  150
                  97
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                  171115
Seq. No.
                  jC-alXLIB327434P1d12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2342727
BLAST score
                  535
                  1.0e-54
E value
Match length
                  129
% identity
                  79
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  171116
Seq. No.
Seq. ID
                  jC-alXLIB327434P1e01b1
Method
                  BLASTX
NCBI GI
                   g3746067
BLAST score
                   704
                   2.0e-74
E value
Match length
                   155
% identity
                   92
                  (AC005311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   171117
Seq. No.
                   jC-alXLIB327434P1e02b1
Seq. ID
Method
                   BLASTX
                   g3668175
NCBI GI
                   755
BLAST score
                   2.0e-80
E value
Match length
                   152
% identity
                   94
                   (AB006778) vegetative storage protein [Arabidopsis
NCBI Description
                   thaliana]
                   171118
Seq. No.
                   jC-alXLIB327434P1e06b1
Seq. ID
                   BLASTX
Method
                   g1174623
NCBI GI
                   575
BLAST score
                   3.0e-59
E value
                   161
Match length
                   72
% identity
                   T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                   >gi 529705 (U13070) C. elegans cct-6 (similar to T complex
                   proteins, Tcp-1-related, Cctz) [Caenorhabditis elegans]
                   171119
Seq. No.
                   jC-alXLIB327434P1e09b1
Seq. ID
Method
                   BLASTX
```

E value

Match length



```
NCBI GI
                  q3461845
BLAST score
                  396
                  2.0e-38
E value
Match length
                  111
                  72
% identity
                  (AC005315) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  171120
Seq. No.
                  jC-alXLIB327434P1f02a1
Seq. ID
                  BLASTN
Method
                  q4538990
NCBI GI
                   108
BLAST score
                   1.0e-53
E value
                   216
Match length
                   88
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                   (ESSA project)
Seq. No.
                   171121
                   jC-alXLIB327434P1f02b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4538990
BLAST score
                   86
                   2.0e-40
E value
                   122
Match length
                   93
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                   (ESSA project)
                   171122
Seq. No.
                   jC-alXLIB327434P1f05b1
Seq. ID
                   BLASTX
Method
                   g4741940
NCBI GI
BLAST score
                   677
                   3.0e-71
E value
Match length
                   126
                   98
% identity
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                   171123
Seq. No.
                   jC-alXLIB327434P1f08b1
Seq. ID
                   BLASTX
Method
                   g3341679
NCBI GI
                   513
BLAST score
                   5.0e-52
E value
                   149
Match length
                   69
% identity
                   (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
                   171124
Seq. No.
                   jC-alXLIB327434P1f09b1
Seq. ID
                   BLASTN
Method
                   q3985934
NCBI GI
                   232
BLAST score
```

1.0e-127



% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 171125

Seq. ID jC-alXLIB327434P1g02b1

Method BLASTN
NCBI GI g2582640
BLAST score 64
E value 3.0e-27
Match length 76
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171126

Seq. ID jC-alXLIB327434P1g05b1

Method BLASTN
NCBI GI g2335089
BLAST score 121
E value 2.0e-61
Match length 170
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171127

Seq. ID jC-alXLIB327434Plg06b1

Method BLASTX
NCBI GI g3377800
BLAST score 636
E value 2.0e-66
Match length 135
% identity 90

NCBI Description (AF075597) similar to glycosyl hydrolases family 9

(PFam:glycosyl hydro5.hmm, score: 100.70) [Arabidopsis

thaliana]

Seq. No. 171128

Seq. ID jC-alXLIB327434P1g10b1

Method BLASTX
NCBI GI g3334123
BLAST score 572
E value 6.0e-59
Match length 137
% identity 88

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi 1655480 dbj BAA13599 (D88374) gamma subunit of

mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787

(AC002334) mitochondrial F1-ATPase, gamma subunit

[Arabidopsis thaliana]

Seq. No. 171129

Seq. ID jC-alXLIB327434P1g11b1

Method BLASTX
NCBI GI g4539301
BLAST score 378

E value Match length

% identity



```
E value
                  3.0e - 36
Match length
                  156
                  54
% identity
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  171130
                  jC-alXLIB327434P1g12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021336
BLAST score
                  818
E value
                  8.0e-88
Match length
                  158
                  100
% identity
NCBI Description
                  (AJ224957) RGA-like [Arabidopsis thaliana]
Seq. No.
                  171131
Seq. ID
                  jC-alXLIB327434P1h05a1
Method
                  BLASTN
NCBI GI
                  q4490701
BLAST score
                  83
                  1.0e-38
E value
Match length
                  87
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
NCBI Description
                  (ESSA project)
Seq. No.
                  171132
Seq. ID
                  jC-alXLIB327434P1h07b1
Method
                  BLASTX
                  q2760072
NCBI GI
                  453
BLAST score
                  5.0e-45
E value
                  91
Match length
                   99
% identity
                  (X98080) dihydrodipicolinate synthase [Arabidopsis
NCBI Description
                  thaliana]
                  171133
Seq. No.
                  jC-alXLIB327434P1h08b1
Seq. ID
                  BLASTX
Method
                  g2760072
NCBI GI
                   433
BLAST score
                  1.0e-42
E value
                  87
Match length
                   99
% identity
                  (X98080) dihydrodipicolinate synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  171134
                   jC-alXLIB327434P1h10a1
Seq. ID
Method
                  BLASTN
                  g531828
NCBI GI
BLAST score
                   56
```

23358

2.0e-22

60



```
NCBI Description Cloning vector pSport1, complete cds
                  171135
Seq. No.
                  jC-alXLIB327434P1h10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  59
                  3.0e-24
E value
Match length
                  75
                  96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  171136
Seq. ID
                  jC-alXLIB327434P2a06a1
                  BLASTN
Method
NCBI GI
                  q540252
BLAST score
                  33
E value
                  8.0e-09
                  33
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  171137
Seq. ID
                  jC-alXLIB327434P2a06b1
                  BLASTX
Method
NCBI GI
                  q2062170
BLAST score
                  395
E value
                  3.0e-38
Match length
                  102
                  75
% identity
                  (AC001645) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171138
                  jC-alXLIB327434P2a09b1
Seq. ID
                  BLASTX
Method
                  g1169599
NCBI GI
BLAST score
                  671
                  1.0e-70
E value
                  150
Match length
                  82
% identity
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_541883_pir__JQ2336 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CFD - Arabidopsis thaliana >gi_408481 (L22961)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid
                   desaturase [Arabidopsis thaliana] >gi_541653_dbj_BAA03106_
```

(D14007) omega-3-desaturase [Arabidopsis thaliana]

Seq. No. 171139

iC-alXLIB327434P2b05b1

Method BLASTX
NCBI GI g1542941
BLAST score 507
E value 2.0e-51
Match length 136
% identity 74

Seq. ID



```
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                  171140
Seq. No.
                  jC-alXLIB327434P2c06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4468103
BLAST score
                  205
E value
                  1.0e-111
                  456
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
NCBI Description
                  (ESSA project)
                  171141
Seq. No.
                  jC-alXLIB327434P2c10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2511715
BLAST score
                  730
E value
                  2.0e-77
                  153
Match length
                  93
% identity
                  (AF019380) putative phosphatidylinositol-4-phosphate
NCBI Description
                  5-kinase [Arabidopsis thaliana]
                  171142
Seq. No.
                  jC-alXLIB327434P2d05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2529679
BLAST score
                  155
E value
                  5.0e-10
Match length
                  56
                  48
% identity
                  (AC002535) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  171143
Seq. No.
                  jC-alXLIB327434P2d06b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                  67
                  4.0e-29
E value
                  75
Match length
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171144
Seq. No.
                  jC-alXLIB327434P2d07a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  51
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
```

23360

171145

jC-alXLIB327434P2d07b1

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q135391
BLAST score
                  698
                  9.0e-74
E value
Match length
                  131
                  99
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 71583 pir UBMUAM tubulin alpha-1
NCBI Description
                  chain - Arabidopsis thaliana >gi 166896 (M21414)
                  alpha-1-tubulin [Arabidopsis thaliana]
                  171146
Seq. No.
                  jC-alXLIB327434P2e02a1
Seq. ID
Method
                  BLASTN
                  g2462264
NCBI GI
                  51
BLAST score
                  2.0e-19
E value
Match length
                  51
                  100
% identity
NCBI Description
                  Cucumis sativus mRNA for patatin-like protein, partial
                  171147
Seq. No.
Seq. ID
                  jC-alXLIB327434P2e03a1
Method
                  BLASTN
NCBI GI
                  q531832
BLAST score
                  45
                  5.0e-16
E value
Match length
                  60
                  93
% identity
NCBI Description Cloning vector pSport2, complete sequence
Seq. No.
                  171148
                  jC-alXLIB327434P2e03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618602
BLAST score
                  214
                  1.0e-117
E value
Match length
                  430
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  171149
Seq. No.
                  jC-alXLIB327434P2e07b1
Seq. ID
Method
                  BLASTN
                  g2264320
NCBI GI
BLAST score
                  118
E value
                  6.0e-60
Match length
                  129
                  98
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXI10, complete sequence [Arabidopsis thaliana]
```

Seq. No. 171150

Seq. ID jC-alXLIB327434P2e09a1

Method BLASTN NCBI GI g3461834 BLAST score 53



E value 1.0e-20 Match length 133 86 % identity Arabidopsis thaliana chromosome II BAC T9I4 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171151 Seq. No. Seq. ID jC-alXLIB327434P2e12b1 BLASTN Method g2582640 NCBI GI 52 BLAST score 4.0e-20 E value Match length 68 94 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 171152 Seq. No. Seq. ID jC-alXLIB327434P2f06a1 BLASTN Method g2290120 NCBI GI 44 BLAST score 2.0e-15 E value Match length 62 95 % identity NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env) gene, partial cds Seq. No. 171153 Seq. ID jC-alXLIB327434P2f07b1 BLASTX Method NCBI GI g2854070 BLAST score 531 E value 4.0e-54 Match length 104 100 % identity (AF044914) putative histone deacetylase [Arabidopsis NCBI Description thaliana] 171154 Seq. No. jC-alXLIB327434P2f09b1 Seq. ID BLASTX Method NCBI GI g4835240 785 BLAST score 6.0e-84 E value 143 Match length 100 % identity (AL049862) putative protein [Arabidopsis thaliana] NCBI Description 171155 Seq. No. jC-alXLIB327434P2f10b1 Seq. ID Method BLASTX g2209332 NCBI GI 815 BLAST score E value 2.0e-87

23362

156

100

Match length

% identity



NCBI Description (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] >gi 3927828 (AC005727) chloroplast membrane

protein ALBINO3 [Arabidopsis thaliana]

Seq. No. 171156

Seq. ID jC-alXLIB327434P2g03b1

Method BLASTN
NCBI GI g2582640
BLAST score 41
E value 1.0e-13
Match length 49
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171157

Seq. ID jC-alXLIB327434P2h06a1

Method BLASTN
NCBI GI g531828
BLAST score 55
E value 6.0e-22
Match length 62
% identity 97

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 171158

Seq. ID jC-alXLIB327434P2h06b1

Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 6.0e-27
Match length 71
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171159

Seq. ID jC-alXLIB327434P3a02a1

Method BLASTN
NCBI GI g540252
BLAST score 41
E value 5.0e-14
Match length 41
% identity 100

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No. 171160

Seq. ID jC-alXLIB327434P3a04b1

Method BLASTX
NCBI GI g1046373
BLAST score 891
E value 3.0e-96
Match length 175
% identity 98

NCBI Description (U37336) SAG12 protein [Arabidopsis thaliana]

Seq. No. 171161

E value

Match length

% identity

6.0e-38

393

85



Seq. ID jC-alXLIB327434P3a10a1 Method BLASTN NCBI GI g2462264 BLAST score 50 7.0e-19 E value Match length 57 % identity 96 Cucumis sativus mRNA for patatin-like protein, partial NCBI Description Seq. No. 171162 jC-alXLIB327434P3a12a1 Seq. ID Method BLASTN NCBI GI g2462264 BLAST score 47 E value 4.0e-17 Match length 47 % identity 100 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 171163 Seq. ID jC-alXLIB327434P3b05a1 Method BLASTN NCBI GI g531828 BLAST score 46 E value 2.0e-16 Match length 65 92 % identity NCBI Description Cloning vector pSport1, complete cds Seq. No. 171164 jC-alXLIB327434P3c02a1 Seq. ID BLASTN Method NCBI GI g2462264 BLAST score 54 2.0e-21 E value 54 Match length 100 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 171165 jC-alXLIB327434P3c05a1 Seq. ID Method BLASTN g531828 NCBI GI BLAST score 51 E value 2.0e-19 Match length 66 97 % identity NCBI Description Cloning vector pSport1, complete cds 171166 Seq. No. Seq. ID jC-alXLIB327434P3d01b1 Method BLASTN NCBI GI q2618602 BLAST score 82



```
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171167
                  jC-alXLIB327434P3e06a1
Seq. ID
                  BLASTN
Method
                  q531828
NCBI GI
BLAST score
                  47
                  4.0e-17
E value
                  66
Match length
                  92
% identity
                  Cloning vector pSport1, complete cds
NCBI Description
                  171168
Seq. No.
                  jC-alXLIB327434P3f07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4756963
BLAST score
                  531
E value
                  0.0e + 00
                  531
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                  171169
                  jC-alXLIB327434P3f08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g531828
BLAST score
                   48
                  1.0e-17
E value
Match length
                   66
                   96
% identity
NCBI Description Cloning vector pSport1, complete cds
                   171170
Seq. No.
                   jC-alXLIB327434P3g02a1
Seq. ID
                   BLASTX
Method
                   g2979548
NCBI GI
BLAST score
                   316
                   7.0e-29
E value
                   81
Match length
                   75
% identity
                  (AC003680) putative 7-ethoxycoumarin O-deethylase
NCBI Description
                   [Arabidopsis thaliana]
                   171171
Seq. No.
                   jC-alXLIB327434P3h01a1
Seq. ID
Method
                   BLASTN
                   g2760167
NCBI GI
BLAST score
                   118
E value
                   2.0e-59
                   158
Match length
% identity
                   95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MCO15, complete sequence [Arabidopsis thaliana]

23365

171172

Seq. No.

NCBI GI

BLAST score



```
jC-alXLIB327434P3h01b1
Seq. ID
Method
                  BLASTN
                  g2760167
NCBI GI
BLAST score
                  83
                  1.0e-38
E value
                  223
Match length
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCO15, complete sequence [Arabidopsis thaliana]
                  171173
Seq. No.
                  jC-alXLIB327434P3h04a1
Seq. ID
Method
                  BLASTN
                  q2462264
NCBI GI
                  50
BLAST score
                  7.0e-19
E value
Match length
                  54
% identity
                  98
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  171174
Seq. No.
                  jC-alXLIB327434P3h07b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2582640
                   65
BLAST score
                   8.0e-28
E value
                   81
Match length
                   95
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                   171175
Seq. ID
                   jC-alXLIB327434P4b01b1
Method
                   BLASTN
                   g3869064
NCBI GI
BLAST score
                   332
                   0.0e+00
E value
                   545
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K1013, complete sequence [Arabidopsis thaliana]
                   171176
Seq. No.
                   jC-alXLIB327434P4b05a1
Seq. ID
Method
                   BLASTN
                   g2462264
NCBI GI
                   46
BLAST score
                   1.0e-16
E value
                   58
Match length
                   95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   171177
Seq. No.
                   jC-alXLIB327434P4c07b1
Seq. ID
                   BLASTN
Method
```

q3869074



```
E value
                  0.0e + 00
Match length
                  542
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMI9, complete sequence [Arabidopsis thaliana]
                  171178
Seq. No.
Seq. ID
                  jC-alXLIB327434P4c12a1
                  BLASTN
Method
NCBI GI
                  q2462264
                  45
BLAST score
                  6.0e-16
E value
Match length
                  57
% identity
                  95
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                  171179
                  jC-alXLIB327434P4d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q419760
BLAST score
                  588
                  9.0e-75
E value
Match length
                  166
% identity
                  57
                  P-glycoprotein atpgp1 - Arabidopsis thaliana
NCBI Description
                  >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
Seq. No.
                  171180
Seq. ID
                  jC-alXLIB327434P4e02a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  54
E value
                  3.0e-21
Match length
                  54
                  100
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                  171181
                  jC-alXLIB327434P4e04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  62
E value
                  3.0e-26
                  77
Match length
                  96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  171182
                  jC-alXLIB327434P4e09a1
Seq. ID
Method
                  BLASTN
```

NCBI GI g2462264
BLAST score 44
E value 2.0e-15
Match length 48
% identity 98



NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 171183 Seq. No. jC-alXLIB327434P4f01b1 Sea. ID BLASTN Method g2582640 NCBI GI BLAST score 53 1.0e-20 E value Match length 65 97 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 171184 Seq. No. Seq. ID jC-alXLIB327434P4f04b1 Method BLASTN q2582640 NCBI GI BLAST score 53 1.0e-20 E value Match length 80 94 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 171185 Seq. No. jC-alXLIB327434P4f07a1 Seq. ID Method BLASTN NCBI GI g2462264 54 BLAST score 3.0e-21E value 54 Match length 100 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 171186 Seq. No. jC-alXLIB327434P4f07b1 Seq. ID BLASTN Method g2582640 NCBI GI BLAST score 61 2.0e-25 E value 80 Match length 95 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 171187 Seq. No.

jC-alXLIB327434P4f08b1 Seq. ID

Method BLASTX g2493133 NCBI GI BLAST score 221 E value 8.0e-20 Match length 111 % identity 48

VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) NCBI Description

>gi 2183244 (AF002134) Vma8p [Candida albicans]

Seq. No. 171188

BLAST score

E value

1.0e-38



```
Seq. ID
                  iC-alXLIB327434P4f10a1
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  38
                  9.0e-12
E value
                  57
Match length
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171189
Seq. No.
Seq. ID
                  jC-alXLIB327434P4g02b1
                  BLASTX
Method
NCBI GI
                  g4163997
                  945
BLAST score
                  1.0e-102
E value
                  181
Match length
                  99
% identity
                  (AF087483) alpha-xylosidase precursor [Arabidopsis
NCBI Description
                  thaliana]
                  171190
Seq. No.
                  jC-alXLIB327434P4h01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g404690
                  245
BLAST score
                  1.0e-20
E value
                  120
Match length
                   41
% identity
                  (L19075) cytochrome P450 [Catharanthus roseus]
NCBI Description
                  171191
Seq. No.
                   jC-alXLIB327434P4h02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2462264
BLAST score
                   56
                   2.0e-22
E value
Match length
                   56
                   100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   171192
                   jC-alXLIB327434P4h05a1
Seq. ID
                   BLASTN
Method
                   q2618602
NCBI GI
BLAST score
                   48
                   1.0e-17
E value
                   258
Match length
                   88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   171193
Seq. No.
                   jC-alXLIB327434P4h05b1
Seq. ID
                   BLASTN
Method
                   g2618602
NCBI GI
                   83
```



```
Match length
                  269
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171194
Seq. ID
                  jC-alXLIB327434P4h07b1
Method
                  BLASTN
NCBI GI
                  q3212846
BLAST score
                  234
                  1.0e-128
E value
Match length
                  255
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171195
Seq. ID
                   jC-alXLIB327434P4h10a1
Method
                  BLASTX
NCBI GI
                  q4588012
BLAST score
                   436
E value
                  5.0e-43
Match length
                  100
% identity
                  79
                  (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
                   171196
Seq. No.
Seq. ID
                   jC-alXLIB327434P4h11a1
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   46
                   2.0e-16
E value
                   46
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   171197
Seq. No.
Seq. ID
                   jC-alXLIB327434P4h11b1
                  BLASTN
Method
                   g2582640
NCBI GI
                   51
BLAST score
E value
                   2.0e-19
                   71
Match length
                   93
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
Seq. No.
                   171198
                   jC-alXLIB327434P4h12a1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g4651204
BLAST score 179
E value 7.0e-13
Match length 39
% identity 67

NCBI Description (AB026262) ring finger protein [Cicer arietinum]

Method

NCBI GI

E value

BLAST score

BLASTN

51

g2462264

1.0e-19



```
171199
Seq. No.
Seq. ID
                  jC-alXLIB327435P1a02b1
Method
                  BLASTN
                  q2462264
NCBI GI
                  35
BLAST score
E value
                  5.0e-10
Match length
                  43
                  95
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                  171200
                  jC-alXLIB327435P1b01b1
Seq. ID
Method
                  BLASTN
                  g2462264
NCBI GI
                  40
BLAST score
                  4.0e-13
E value
                  55
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171201
Seq. No.
Seq. ID
                  jC-alXLIB327435P1b05b1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  55
                  6.0e-22
E value
Match length
                  66
                  95
% identity
NCBI Description Cloning vector pSport1, complete cds
                  171202
Seq. No.
Seq. ID
                  jC-alXLIB327435P1b09b1
                  BLASTN
Method
                  g540252
NCBI GI
                  33
BLAST score
E value
                  8.0e-09
Match length
                  33
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  171203
Seq. No.
                   jC-alXLIB327435P1c03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
                  54
BLAST score
E value
                  2.0e-21
Match length
                  54
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   171204
Seq. No.
Seq. ID
                   jC-alXLIB327435P1c08a1
```



```
Match length
                  51
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171205
                  iC-alXLIB327435P1c08b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  35
                  5.0e-10
E value
                  54
Match length
                  95
% identity
                 Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  171206
Seq. No.
                  jC-alXLIB327435P1c11a1
Seq. ID
Method
                  BLASTN
                  q2462264
NCBI GI
BLAST score
                  42
                  3.0e-14
E value
                  42
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171207
Seq. No.
                  jC-alXLIB327435P1d02a1
Seq. ID
                  BLASTN
Method
                  q2462264
NCBI GI
BLAST score
                  41
E value
                  9.0e-14
Match length
                  41
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171208
Seq. No.
                 jC-alXLIB327435P1d05b1
Seq. ID
Method
                  BLASTX
                  q4512675
NCBI GI
BLAST score
                  241
                  3.0e-20
E value
                  57
Match length
                  75
% identity
                  (AC006931) putative citrate synthase [Arabidopsis thaliana]
NCBI Description
                  171209
Seq. No.
                   jC-alXLIB327435P1e02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4454447
                  97
BLAST score
                   5.0e-47
E value
                  297
Match length
                   86
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
```

171210

jC-alXLIB327435P1e06b1

Seq. No.

Seq. ID

Match length

51



```
Method
                  BLASTX
NCBI GI
                  g3927836
BLAST score
                  283
                  4.0e-25
E value
Match length
                  74
                  70
% identity
NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]
Seq. No.
                  171211
                  jC-alXLIB327435P1e07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  54
                  2.0e-21
E value
Match length
                  54
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171212
                  jC-alXLIB327435P1e09b1
Seq. ID
                  BLASTN
Method
                  g2290120
NCBI GI
BLAST score
                  55
E value
                  6.0e-22
Match length
                  59
% identity
                  98
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  171213
Seq. ID
                  jC-alXLIB327435P1f01b1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  57
                  4.0e-23
E value
Match length
                  65
                  97
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  171214
                  jC-alXLIB327435P1f02b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
                  37
BLAST score
                  3.0e-11
E value
                  41
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171215
                  jC-alXLIB327435P1f06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  48
                  9.0e-18
E value
```



```
% identity
                   98
                   Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                   171216
                   jC-alXLIB327435P1f06b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q531828
BLAST score
                   45
E value
                   5.0e-16
Match length
                   64
                   92
% identity
NCBI Description Cloning vector pSport1, complete cds
                   171217
Seq. No.
Seq. ID
                   jC-alXLIB327435P1f11b1
Method
                   BLASTN
NCBI GI
                   g836895
BLAST score
                   44
                   2.0e-15
E value
Match length
                   56
                   95
% identity
NCBI Description Saccharomyces cerevisiae CSP2 gene, complete cds
Seq. No.
                   171218
                   jC-alXLIB327435P1g04b1
Seq. ID
Method
                   BLASTN
                   g2290120
NCBI GI
BLAST score
                   42
E value
                   3.0e-14
Match length
                   64
                   94
% identity
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                   gene, partial cds
Seq. No.
                   171219
                   jC-alXLIB327435P1g06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1706547
                   90
BLAST score
E value
                   1.0e-17
                   76
Match length
                   62
% identity
                   GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
NCBI Description
                   PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                   ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_2129912_pir__S65077 beta-1,3-glucanase class I
                   precursor - Para rubber tree >gi 1184668 (U22147)
                   beta-1,3-glucanase [Hevea brasiliensis]
Seq. No.
                   171220
                   jC-alXLIB327435P1g06b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2462264
BLAST score
                   41
                   9.0e-14
E value
Match length
                   61
```

23374

92

% identity



```
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171221
Seq. ID
                  jC-alXLIB327435P1g12b1
Method
                  BLASTN
NCBI GI
                  q3395421
BLAST score
                  407
E value
                  0.0e + 00
                  411
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T19C21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171222
Seq. No.
                  jC-alXLIB327435P1h04b1
Seq. ID
                  BLASTN
Method
                  g4079614
NCBI GI
                  79
BLAST score
E value
                  3.0e-36
                  254
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171223
Seq. No.
Seq. ID
                  jC-alXLIB327435P1h11b1
                  BLASTN
Method
NCBI GI
                  g2290120
BLAST score
                  54
E value
                  2.0e-21
Match length
                   66
                   95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  171224
Seq. No.
                  jC-alXLIB327435P1h12a1
Seq. ID
                  BLASTN
Method
                  g2290120
NCBI GI
                  45
BLAST score
                  5.0e-16
E value
                  69
Match length
                  93
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
                   171225
Seq. No.
```

jC-alXLIB327435P2a02b1 Seq. ID

Method BLASTX NCBI GI q4097569 157 BLAST score E value 2.0e-10 59 Match length 56 % identity

(U64915) GMFP4 [Glycine max] NCBI Description

171226 Seq. No.



```
jC-alXLIB327435P2a03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  35
                  5.0e-10
E value
                  70
Match length
                  92
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171227
Seq. No.
                  jC-alXLIB327435P2a07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2443878
BLAST score
                  518
                  1.0e-52
E value
                  115
Match length
% identity
                  86
NCBI Description
                  (AC002294) Unknown protein [Arabidopsis thaliana]
                  171228
Seq. No.
Seq. ID
                  jC-alXLIB327435P2b12b1
Method
                  BLASTN
NCBI GI
                  g2582640
                  52
BLAST score
                  3.0e-20
E value
Match length
                  76
                  95
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  171229
Seq. No.
Seq. ID
                  jC-alXLIB327435P2e05a1
                  BLASTN
Method
NCBI GI
                  g2213606
BLAST score
                  208
                  1.0e-113
E value
Match length
                  442
% identity
                  100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
                  171230
Seq. No.
                  jC-alXLIB327435P2e06a1
Seq. ID
Method
                  BLASTN
                  g2582640
NCBI GI
                  62
BLAST score
                  4.0e-26
E value
Match length
                  77
% identity
                  96
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
```

Seq. No. 171231

Seq. ID jC-alXLIB327435P2f02b1

Method BLASTN NCBI GI g2582640



BLAST score 46
E value 9.0e-17
Match length 73
% identity 90

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171232

Seq. ID jC-alXLIB327435P2g09a1

Method BLASTX
NCBI GI g3080433
BLAST score 615
E value 5.0e-64
Match length 131
% identity 90

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]

Seq. No. 171233

Seq. ID jC-alXLIB327435P2q12b1

Method BLASTN
NCBI GI g2582640
BLAST score 52
E value 3.0e-20
Match length 66
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171234

Seq. ID jC-alXLIB327435P2h04a1

Method BLASTN
NCBI GI g2582640
BLAST score 58
E value 1.0e-23
Match length 77
% identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171235

Seq. ID jC-alXLIB327435P2h05a1

Method BLASTX
NCBI GI g1170895
BLAST score 663
E value 1.0e-69
Match length 146
% identity 86

NCBI Description MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR

(NADP-MDH) >gi 725262 (L40958) NADP-malate dehydrogenase

[Flaveria bidentis]

Seq. No. 171236

Seq. ID jC-alXLIB327435P2h08b1

Method BLASTX NCBI GI g3122388 BLAST score 125



E value 2.0e-67 Match length 129 % identity 92

NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40

repeat protein [Arabidopsis thaliana]

>gi 4581121 gb AAD24611.1_AC005825_18 (AC005825) putative

WD-40 protein MSI2 [Arabidopsis thaliana]

Seq. No. 171237

Seq. ID jC-alXLIB327435P3a08a1

Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 2.0e-15
Match length 55
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 171238

Seq. ID jC-alXLIB327435P3a08b1

Method BLASTX
NCBI GI g4102839
BLAST score 355
E value 2.0e-33
Match length 143
% identity 50

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 171239

Seq. ID jC-alXLIB327435P3b02a1

Method BLASTN
NCBI GI g2462264
BLAST score 47
E value 4.0e-17
Match length 51
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 171240

Seq. ID jC-alXLIB327435P3b06b1

Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 5.0e-27
Match length 71
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171241

Seq. ID jC-alXLIB327435P3c01a1

Method BLASTX
NCBI GI g4455273
BLAST score 52

E value 7.0e-34 Match length 155 % identity 57

Seq. No.



```
(AL035527) subtilisin proteinase-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  171242
                  jC-alXLIB327435P3c01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  44
                  3.0e-15
E value
                  76
Match length
                  95
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171243
Seq. No.
                  jC-alXLIB327435P3c05a1
Seq. ID
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  45
                  6.0e-16
E value
                  77
Match length
                  90
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                   171244
Seq. No.
                  jC-alXLIB327435P3c12a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   38
                   4.0e-12
E value
                   46
Match length
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   171245
Seq. No.
                   jC-alXLIB327435P3d01a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129769
BLAST score
                   255
                   1.0e-21
E value
                   117
Match length
                   40
% identity
                  xyloglucan endo-transglycosylase precursor - Arabidopsis
NCBI Description
                   thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan
                   transferase [Arabidopsis thaliana]
                   171246
Seq. No.
                   jC-alXLIB327435P3d04a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q531828
                   41
BLAST score
                   9.0e-14
E value
                   60
Match length
                   95
% identity
NCBI Description Cloning vector pSport1, complete cds
```

NCBI GI



```
jC-alXLIB327435P3d05a1
Seq. ID
                  BLASTN
Method
                  g2290120
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
Match length
                  61
                  89
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  171248
                  jC-alXLIB327435P3e01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  43
                  9.0e-15
E value
Match length
                  65
                  94
% identity
NCBI Description Cloning vector pSport1, complete cds
                  171249
Seq. No.
Seq. ID
                  jC-alXLIB327435P3e03b1
                  BLASTN
Method
NCBI GI
                  g4519185
                  556
BLAST score
E value
                  0.0e + 00
Match length
                  572
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15015, complete sequence
Seq. No.
                  171250
                  jC-alXLIB327435P3e06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4191771
BLAST score
                  266
E value
                  1.0e-148
Match length
                  344
                  96
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F3P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171251
Seq. No.
                  jC-alXLIB327435P3e07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3643609
BLAST score
                  413
E value
                  4.0e-83
Match length
                  190
% identity
                  (AC005395) putative Cys3His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  171252
                  jC-alXLIB327435P3e08a1
Seq. ID
Method
                  BLASTN
```

23380

g3860243

E value : Match length

% identity



```
BLAST score
                  106
                  3.0e-52
E value
Match length
                  254.
% identity
                  86
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171253
                  jC-alXLIB327435P3e09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  36
                  1.0e-10
E value
                  51
Match length
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171254
Seq. ID
                  jC-alXLIB327435P3q04b1
Method
                  BLASTX
NCBI GI
                  g2239236
BLAST score
                  83
E value
                  4.0e-22
Match length
                  179
% identity
                  39
NCBI Description
                  (Z97211) probable involvement in ergosterol synthesis
                  [Schizosaccharomyces pombe]
Seq. No.
                  171255
                  jC-alXLIB327435P3g07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2342673
BLAST score
                  112
                  7.0e-56
E value
                  254
Match length
                  89
% identity
                  Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  171256
Seq. No.
                  jC-alXLIB327435P3h02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  41
E value
                  1.0e-13
                  49
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171257
Seq. No.
                  jC-alXLIB327435P3h02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2582640
                  33
BLAST score
```

23381

8.0e-09



```
NCBI Description
                 Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  171258
Seq. No.
                  jC-alXLIB327435P3h09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757410
                  105
BLAST score
                  8.0e-52
E value
Match length
                  304
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MVE11, complete sequence

Seq. No. 171259

Seq. ID jC-alXLIB327435P4a01a1
Method BLASTN
NCBI GI g2182287
BLAST score 182
E value 8.0e-98
Match length 210
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,

complete sequence [Arabidopsis thaliana]

Seq. No. 171260

Seq. ID jC-alXLIB327435P4b01a1

Method BLASTN
NCBI GI g4006885
BLAST score 186
E value 1.0e-100
Match length 238
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 171261

Seq. ID jC-alXLIB327435P4b06a1

Method BLASTN
NCBI GI g2351070
BLAST score 179
E value 5.0e-96
Match length 246
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH12, complete sequence [Arabidopsis thaliana]

Seq. No. 171262

Seq. ID jC-alXLIB327435P4b10a1

Method BLASTN
NCBI GI g2245126
BLAST score 247
E value 1.0e-136
Match length 283
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No



Seq. No. 171263 Seq. ID jC-alXLIB327435P4c01a1 BLASTN Method NCBI GI g2290120 BLAST score 42 3.0e-14 E value Match length 64 94 % identity HIV-1 strain MO2 from USA, envelope glycoprotein (env) NCBI Description gene, partial cds Seq. No. 171264 jC-alXLIB327435P4c07a1 Seq. ID Method BLASTN NCBI GI q2708736 BLAST score 59 E value 3.0e-24Match length 184 89 % identity Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 NCBI Description cM, complete sequence [Arabidopsis thaliana] Seq. No. 171265 jC-alXLIB327435P4c10a1 Seq. ID Method BLASTN NCBI GI g2462264 BLAST score 36 E value 2.0e-10 Match length 44 95 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 171266 jC-alXLIB327435P4d07a1 Seq. ID BLASTN Method g2290120 NCBI GI BLAST score 52 E value 3.0e-20 60 Match length 97 % identity NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds 171267 Seq. No. jC-alXLIB327435P4d09a1 Seq. ID BLASTN Method NCBI GI g2462264 44

Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 2.0e-15
Match length 52
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 171268

Seq. ID jC-alXLIB327435P4e07a1

Method BLASTN



NCBI GI g3128137 BLAST score 302 E value 1.0e-169 Match length 325 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 171269

Seq. ID jC-alXLIB327435P4e08b1

Method BLASTN
NCBI GI g2582640
BLAST score 56
E value 2.0e-22
Match length 64
% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171270

Seq. ID jC-alXLIB327435P4f04a1

Method BLASTN
NCBI GI g531828
BLAST score 51
E value 2.0e-19
Match length 66
% identity 94

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 171271

Seq. ID jC-alXLIB327435P4f05a1

Method BLASTX
NCBI GI 93402749
BLAST score 541
E value 2.0e-64
Match length 161
% identity 21

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 171272

Seq. ID jC-alXLIB327435P4f06a1

Method BLASTN
NCBI GI g2245031
BLAST score 157
E value 5.0e-83
Match length 200
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 171273

Seq. ID jC-alXLIB327435P4f07a1

Method BLASTN
NCBI GI g166802
BLAST score 165
E value 1.0e-87
Match length 249



% identity 92

NCBI Description Arabidopsis thaliana phosphoprotein phosphatase-type 1

catalytic site mRNA, complete cds

Seq. No. 171274

Seq. ID jC-alXLIB327435P4f07b1

Method BLASTX
NCBI GI g1346759
BLAST score 766
E value 1.0e-81
Match length 144
% identity 100

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 5

>gi_421854_pir__S31089 phosphoprotein phosphatase (EC
3.1.3.16) 1 catalytic chain (clone TOPP5) - Arabidopsis
thaliana >gi_166803 (M93412) phosphoprotein phosphatase 1

[Arabidopsis thaliana]

Seq. No. 171275

Seq. ID jC-alXLIB327435P4f09a1

Method BLASTN
NCBI GI g4519191
BLAST score 77
E value 4.0e-35
Match length 157

Match length 157 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9P8, complete sequence

Seq. No. 171276

Seq. ID jC-alXLIB327435P4f10a1

Method BLASTN
NCBI GI g3449330
BLAST score 336
E value 0.0e+00
Match length 424
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No. 171277

Seq. ID jC-alXLIB327435P4g06a1

Method BLASTN
NCBI GI g4490701
BLAST score 46
E value 2.0e-16
Match length 66
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18

(ESSA project)

Seq. No. 171278

Seq. ID jC-alXLIB327435P4g08a1

Method BLASTN
NCBI GI g2264306
BLAST score 369
E value 0.0e+00



```
Match length
                  405
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171279
Seq. ID
                  jC-alXLIB327435P4h01a1
Method
                  BLASTN
NCBI GI
                  q540252
BLAST score
                  37
E value
                  4.0e-11
Match length
                  45
% identity
                  96
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  171280
Seq. No.
Seq. ID
                  †C-alXLIB327435P4h06a1
                  BLASTN
Method
NCBI GI
                  q540252
BLAST score
                  55
                  7.0e-22
E value
Match length
                  59
                  98
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  171281
Seq. No.
Seq. ID
                  jC-alXLIB327435P4h08b1
Method
                  BLASTX
NCBI GI
                  q2149640
BLAST score
                  44
                  2.0e-88
E value
Match length
                  196
                  90
% identity
                 (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                  171282
Seq. No.
                  jC-alXLIB327435P4h10b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g469109
BLAST score
                   402
                  0.0e+00
E value
Match length
                  424
                  99
% identity
NCBI Description A.thaliana (Columbia) Di19 mRNA
                  171283
Seq. No.
                   jC-alXLIB327436P1a03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  40
                  5.0e-13
E value
Match length
                  40
% identity
                  100
```

Seq. No. 171284

Seq. ID jC-alXLIB327436Pla03b1

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  41
E value
                  1.0e-13
Match length
                  45
                  98
% identity
                 Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171285
Seq. No.
Seq. ID
                  jC-alXLIB327436P1a09b1
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                  39
                  2.0e-12
E value
                  62
Match length
% identity
                  90
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  171286
Seq. No.
Seq. ID
                  jC-alXLIB327436P1b05a1
                  BLASTN
Method
                  g531828
NCBI GI
BLAST score
                  43
                  8.0e-15
E value
Match length
                  65
                  94
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  171287
                  jC-alXLIB327436P1b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461845
BLAST score
                  425
                  8.0e-42
E value
Match length
                  111
                  76
% identity
NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]
                  171288
Seq. No.
                  jC-alXLIB327436P1c02a1
Seq. ID
Method
                  BLASTN
                  g3293583
NCBI GI
BLAST score
                  131
E value
                  3.0e-67
Match length
                  206
% identity
                  94
NCBI Description Arabidopsis thaliana BAC T27D20
                  171289
Seq. No.
```

Seq. ID jC-alXLIB327436P1c07a1

Method BLASTN
NCBI GI g2290120
BLAST score 50
E value 5.0e-19
Match length 66

Seq. No.

Seq. ID

171295

jC-alXLIB327436P1d08a1



```
% identity
                  95
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  171290
Seq. No.
                  jC-alXLIB327436P1c10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  35
                  5.0e-10
E value
Match length
                  43
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171291
Seq. ID
                  jC-alXLIB327436P1c10b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  47
                  2.0e-17
E value
Match length
                  63
                  94
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  171292
Seq. ID
                  jC-alXLIB327436P1c12a1
Method
                  BLASTN
NCBI GI
                  q540252
                  44
BLAST score
                  2.0e-15
E value
                  59
Match length
                  93
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  171293
                  jC-alXLIB327436P1d02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531828
                  43
BLAST score
                  6.0e-15
E value
                  43
Match length
% identity
                  100
NCBI Description Cloning vector pSport1, complete cds
                  171294
Seq. No.
                  jC-alXLIB327436P1d06b1
Seq. ID
Method
                  BLASTX
                  g336392
NCBI GI
BLAST score
                  500
E value
                  1.0e-50
Match length
                  119
% identity
                  87
NCBI Description (J05215) ribosomal protein S17 [Arabidopsis thaliana]
```



```
Method
                  BLASTN
                  q2462264
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
                  34
Match length
                  100
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  171296
Seq. No.
                  jC-alXLIB327436P1e12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244901
                  282
BLAST score
                  1.0e-157
E value
Match length
                  350
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  171297
Seq. No.
                  jC-alXLIB327436P1f09a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
                  34
BLAST score
                  2.0e-09
E value
                  50
Match length
                  94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171298
Seq. No.
                  jC-alXLIB327436P1q08a1
Seq. ID
                  BLASTN
Method
                  g259446
NCBI GI
                  71
BLAST score
                   2.0e-31
E value
                  114
Match length
% identity
                   95
                  glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,
NCBI Description
                  C24, mRNA, 680 nt]
                   171299
Seq. No.
                   jC-alXLIB327436P1g08b1
Seq. ID
Method
                   BLASTN
                   g3800746
NCBI GI
                   42
BLAST score
                   2.0e-14
E value
Match length
                   50
% identity
                   96
```

NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,

complete cds

Seq. No. 171300

Seq. ID jC-alXLIB327436P1g09a1

Method BLASTX
NCBI GI g3790567
BLAST score 412
E value 3.0e-40



```
Match length
                  73
% identity
                  96
NCBI Description
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
                  thaliana]
Seq. No.
                  171301
Seq. ID
                  jC-alXLIB327436P1q09b1
Method
                  BLASTX
NCBI GI
                  q3790567
BLAST score
                  624
E value
                  4.0e-65
Match length
                  116
% identity
                  99
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  171302
Seq. ID
                  jC-alXLIB327436P2a06b1
Method
                  BLASTN
NCBI GI
                  q3128141
BLAST score
                  242
                  1.0e-133
E value
Match length
                  364
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171303
Seq. ID
                  jC-alXLIB327436P2a07b1
Method
                  BLASTN
NCBI GI
                  q2351068
BLAST score
                  365
E value
                  0.0e+00
                  380
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRH10, complete sequence [Arabidopsis thaliana]
                  171304
Seq. No.
Seq. ID
                  jC-alXLIB327436P2a08a1
Method
                  BLASTN
NCBI GI
                  g540252
BLAST score
                  33
                  7.0e-09
E value
                  33
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  171305
Seq. No.
```

jC-alXLIB327436P2b07a1 Seq. ID

Method BLASTX NCBI GI q2911042 BLAST score 311 2.0e-28 E value Match length 62 % identity 100

(AL021961) Phosphoglycerate dehydrogenase - like protein NCBI Description



[Arabidopsis thaliana]

Seq. No. 171306 Seq. ID jC-alXLIB327436P2d01a1 Method BLASTX NCBI GI g131187 BLAST score 186 E value 8.0e-14 Match length 60 55 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_72681_pir__F1SP3 photosystem I chain III precursor spinach >gi 21303 emb CAA31523 (X13133) PSI subunit IV

preprotein (AA -77 to 154) [Spinacia oleracea]

>gi_226166_prf__1413236A photosystem I reaction center IV

[Spinacia oleracea]

Seq. No. 171307

Seq. ID jC-alXLIB327436P2d07a1

Method BLASTX NCBI GI q4309698 BLAST score 61 E value 3.0e-46 Match length-93 88 % identity

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

171308 Seq. No.

jC-alXLIB327436P2d09b1 Seq. ID

BLASTN Method NCBI GI g2582640 BLAST score 57 4.0e-23 E value

Match length 77 94 % identity

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171309

Seq. ID jC-alXLIB327436P2e07b1

Method BLASTN NCBI GI g2582640 BLAST score 63 E value 1.0e-26 78 Match length 96 % identity

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

171310 Seq. No.

Seq. ID jC-alXLIB327436P2q04b1

Method BLASTN NCBI GI g2582640 BLAST score 50 6.0e-19 E value



Match length 77 % identity 92

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171311

Seq. ID jC-alXLIB327436P2g12a1

Method BLASTN
NCBI GI 9836895
BLAST score 36
E value 1.0e-10
Match length 40
% identity 97

NCBI Description Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No. 171312

Seq. ID jC-alXLIB327436P2h01a1

Method BLASTN
NCBI GI 94468801
BLAST score 137
E value 7.0e-71
Match length 300
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17

(ESSA project)

Seq. No. 171313

Seq. ID jC-alXLIB327436P2h03a1

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 2.0e-21
Match length 54
% identity 100

% identity 100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 171314

Seq. ID jC-alXLIB327436P3a04b1

Method BLASTX
NCBI GI g3170525
BLAST score 668
E value 3.0e-70
Match length 144
% identity 81

NCBI Description (AF054615) cellulase [Fragaria x ananassa]

Seq. No. 171315

Seq. ID jC-alXLIB327436P3c01a1

Method BLASTN
NCBI GI g2462264
BLAST score 45
E value 5.0e-16
Match length 60
% identity 97

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 171316



Seq. ID jC-alXLIB327436P3c03a1 Method BLASTN NCBI GI q2462264 BLAST score 42 E value 3.0e-14 Match length 54 94 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 171317 Seq. No. Seq. ID jC-alXLIB327436P3c07b1 BLASTN Method NCBI GI q2582640 BLAST score 47 3.0e-17 E value Match length 74 % identity 92 NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40 Seq. No. 171318 Seq. ID jC-alXLIB327436P3d05b1 Method BLASTN NCBI GI g4159706 BLAST score 431 0.0e+00E value Match length 431 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence 171319 Seq. No. jC-alXLIB327436P3e04b1 Seq. ID Method BLASTN g2582640 NCBI GI 64 BLAST score 2.0e-27 E value Match length 76 97 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 171320 Seq. No. jC-alXLIB327436P3e11a1 Seq. ID Method BLASTN NCBI GI g2462264 BLAST score 44 E value 2.0e-15 52 Match length % identity 96 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 171321

Seq. ID jC-alXLIB327436P3f04b1

Method BLASTN
NCBI GI g3702735
BLAST score 333



E value 0.0e+00 Match length 435 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQL5, complete sequence [Arabidopsis thaliana]

Seq. No. 171322

Seq. ID jC-alXLIB327436P3g10b1

Method BLASTX
NCBI GI g4455301
BLAST score 655
E value 9.0e-69
Match length 138
% identity 96

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 171323

Seq. ID jC-alXLIB327436P3h04b1

Method BLASTN
NCBI GI g2351375
BLAST score 449
E value 0.0e+00
Match length 453
% identity 100

NCBI Description Arabidopsis thaliana translation initiation factor eIF2 p47

subunit homolog mRNA, complete cds

Seq. No. 171324

Seq. ID jC-alXLIB327436P3h06b1

Method BLASTN
NCBI GI g2582640
BLAST score 64
E value 3.0e-27
Match length 76
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171325

Seq. ID jC-alXLIB327436P3h10a1

Method BLASTN
NCBI GI g2290120
BLAST score 56
E value 1.0e-22
Match length 64
% identity 97

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 171326

Seq. ID jC-alXLIB327436P4a05b1

Method BLASTX
NCBI GI g2262167
BLAST score 653
E value 2.0e-68
Match length 153
% identity 84



```
(ACO02329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
                  171327
Seq. No.
                  jC-alXLIB327436P4a09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3869074
                  79
BLAST score
                  3.0e - 36
E value
                  271
Match length
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171328
                  jC-alXLIB327436P4a10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2290120
BLAST score
                  46
                  1.0e-16
E value
Match length
                  66
% identity
                  92
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  171329
Seq. No.
                  jC-alXLIB327436P4c07a1
Seq. ID
Method
                  BLASTN
                  g4115912
NCBI GI
                  92
BLAST score
                  5.0e-44
E value
                  590
Match length
                   67
% identity
                  Arabidopsis thaliana BAC F3H7
NCBI Description
                  171330
Seq. No.
                   jC-alXLIB327436P4d02b1
Seq. ID
Method
                  BLASTN
                   g2264314
NCBI GI
                   60
BLAST score
                   6.0e-25
E value
                   247
Match length
                   90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
                   171331
Seq. No.
                   jC-alXLIB327436P4d03a1
```

Seq. ID

Method BLASTN g2462264 NCBI GI 53 BLAST score 9.0e-21E value Match length 57 % identity

Cucumis sativus mRNA for patatin-like protein, partial NCBI Description

171332 Seq. No.



```
Seq. ID
                  jC-alXLIB327436P4d08a1
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  49
                  2.0e-18
E value
                  57
Match length
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  171333
                  jC-alXLIB327436P4d11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  54
E value
                  2.0e-21
Match length
                  66
% identity
                  97
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  171334
                  jC-alXLIB327436P4e06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135751
BLAST score
                  317
                  4.0e-29
E value
Match length
                  62
                  97
% identity
NCBI Description
                  (AJ006095) 26S protease regulatory subunit 6 [Cicer
                  arietinum]
                  171335
Seq. No.
                  jC-alXLIB327436P4e11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g531828
                  53
BLAST score
                  9.0e-21
E value
Match length
                  65
% identity
                  95
NCBI Description Cloning vector pSport1, complete cds
                  171336
Seq. No.
Seq. ID
                  jC-alXLIB327436P4e12a1
Method
                  BLASTX
                  g2129629
NCBI GI
BLAST score
                  172
                  1.0e-20
E value
Match length
                  86
% identity
                  71
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis
                  thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate
                  peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_
                   (X98276) L-ascorbate peroxidase [Arabidopsis thaliana]
                  >gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis
                  thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023)
```

Seq. No. 171337

L-ascorbate peroxidase [Arabidopsis thaliana]

% identity



jC-alXLIB327436P4e12b1 Seq. ID BLASTX Method g2129629 NCBI GI 71 BLAST score 2.0e-22 E value Match length 127 50 % identity L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis NCBI Description thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_ (X98276) L-ascorbate peroxidase [Arabidopsis thaliana] >gi 2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis thaliana] >gi 2924511 emb CAA17765.1_ (AL022023) L-ascorbate peroxidase [Arabidopsis thaliana] Seq. No. 171338 jC-alXLIB327436P4f01a1 Seq. ID Method BLASTN q4757403 NCBI GI 218 BLAST score 1.0e-119 E value Match length 254 97 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MJL12, complete sequence 171339 Seq. No. Seq. ID jC-alXLIB327436P4f04a1 Method BLASTN q4757412 NCBI GI 160 BLAST score 1.0e-84 E value Match length 311 93 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MXK23, complete sequence Seq. No. 171340 jC-alXLIB327436P4f05a1 Seq. ID BLASTN Method q3779020 NCBI GI BLAST score 82 E value 5.0e-38 Match length 222 84 % identity Arabidopsis thaliana chromosome II BAC T4E14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171341 Seq. No. jC-alXLIB327436P4g02a1 Seq. ID BLASTN Method q3241922 NCBI GI BLAST score 89 3.0e-42E value Match length 308

23397

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:



MLM24, complete sequence [Arabidopsis thaliana]

Seq. No. 171342 Seq. ID jC-alXLIB327436P4q03a1 Method BLASTN NCBI GI q4455229 BLAST score 98 E value 1.0e-47 Match length 178 89 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project) Seq. No. 171343 Seq. ID jC-alXLIB327436P4g10a1 Method BLASTX NCBI GI q4689479 BLAST score 412 E value 3.0e-40Match length 87 90 % identity NCBI Description (AC007213) hypothetical protein [Arabidopsis thaliana] Seq. No. 171344 Seq. ID jC-alXLIB327436P4g11a1 Method BLASTN NCBI GI q4220632 BLAST score 326 E value 0.0e + 00Match length 403 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana] Seq. No. 171345 jC-alXLIB327436P4h02a1 Seq. ID Method BLASTN NCBI GI g2462264 48 BLAST score 9.0e-18 E value 56 Match length % identity 96 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 171346 Seq. No. jC-alXLIB327436P4h08b1 Seq. ID Method BLASTX NCBI GI g1703091 BLAST score 597 E value 6.0e-62 Match length 122 98 % identity

NCBI Description ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP)

(NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1)

>gi_903689 (L23574) acyl carrier protein precursor
[Arabidopsis thaliana] >gi 3341682 (AC003672) acyl carrier

protein [Arabidopsis thaliana]



```
Seq. No.
                  171347
Seq. ID
                  jC-alXLIB327436P4h09a1
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  44
                  2.0e-15
E value
Match length
                  64
                  92
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  171348
Seq. ID
                  jC-atX22003Q1E1E02a1
Method
                  BLASTX
NCBI GI
                  q285286
BLAST score
                  145
E value
                  5.0e-09
Match length
                  67
% identity
                  48
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
                  171349
Seq. No.
Seq. ID
                  jC-atX22004Q1E1A10a1
Method
                  BLASTN
NCBI GI
                  g4115930
BLAST score
                  215
                  1.0e-117
E value
Match length
                  337
% identity
                  99
NCBI Description Arabidopsis thaliana BAC T4B21
Seq. No.
                  171350
                  jC-atX22004Q1E1E06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263711
BLAST score
                  266
                  1.0e-23
E value
                  80
Match length
% identity
                  65
                  (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  171351
Seq. ID
                  jC-atX22005Q1E1G04a1
Method
                  BLASTN
NCBI GI
                  g2853071
BLAST score
                  341
                  0.0e+00
E value
Match length
                  416
                  96
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7
                   (ESSA project)
Seq. No.
                  171352
```

Seq. ID jC-atX22006Q1E1E05a1

Method BLASTN NCBI GI g2618683

Match length

% identity

114 97



```
BLAST score
                  202
E value
                  1.0e-110
Match length
                  202
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171353
Seq. No.
                  jC-atX22006Q1E1F07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3228516
BLAST score
                  38
E value
                  2.0e-12
Match length
                  82
                  87
% identity
NCBI Description Arabidopsis thaliana ETTIN gene, complete cds
Seq. No.
                  171354
                  jC-atX22006Q1E1G09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1083762
BLAST score
                  275
E value
                  2.0e-24
Match length
                  68
                  76
% identity
NCBI Description prolactin-induced T cell protein c15 - rat
                  >gi 619907 emb CAA57825 (X82445) RnudC [Rattus norvegicus]
Seq. No.
                  171355
                  jC-atX22006Q1E1H04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244752
BLAST score
                  230
                  6.0e-19
E value
Match length
                  86
                  53
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  171356
Seq. ID
                  jC-atX22007Q1E1A05a1
Method
                  BLASTX
NCBI GI
                  q2911082
BLAST score
                  207
E value
                  1.0e-16
Match length
                  43
% identity
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  171357
Seq. ID
                  jC-atX22007Q1E1H03a1
Method
                  BLASTN
NCBI GI
                  g3138971
BLAST score
                  102
E value
                  2.0e-50
```

23400

NCBI Description Arabidopsis thaliana dihydrolipoylacyltransferase subunit



of the branched-chain alpha-keto acid dehydrogenase complex (LTA1) mRNA, complete cds

Seq. No. 171358

Seq. ID jC-atX22008Q1E1B10a1

Method BLASTN
NCBI GI g3766106
BLAST score 33
E value 3.0e-09
Match length 101
% identity 83

NCBI Description Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171359

Seq. ID jC-atX22008Q1E1E10a1

Method BLASTN
NCBI GI g3985952
BLAST score 149
E value 3.0e-78
Match length 276
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 171360

Seq. ID jC-atX22009Q1E1B03a1

Method BLASTN
NCBI GI g3172156
BLAST score 169
E value 3.0e-90
Match length 229
% identity 93

NCBI Description Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171361

Seq. ID jC-atX22009Q1E1B11a1

Method BLASTN
NCBI GI g2760829
BLAST score 158
E value 1.0e-83
Match length 348
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F18A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171362

Seq. ID jC-atX22009Q1E1C12b1

Method BLASTX
NCBI GI 94581856
BLAST score 581
E value 3.0e-60
Match length 130
% identity 90

NCBI Description (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase

[Mentha x piperita]



```
Seq. No.
                  171363
Seq. ID
                  jC-atX22011Q1K1B09a1
                  BLASTN
Method
NCBI GI
                  q4467131
BLAST score
                  186
E value
                  1.0e-100
Match length
                  282
                  91
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                  (ESSA project)
Seq. No.
                  171364
Seq. ID
                  jC-atX22011Q1K1D08a1
Method
                  BLASTN
NCBI GI
                  g2584827
BLAST score
                  162
E value
                  5.0e-86
Match length
                  293
                  92
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  171365
Seq. ID
                  jC-atX22012Q1E1C01a1
Method
                  BLASTX
NCBI GI
                  g4098968
BLAST score
                  167
E value
                   4.0e-12
                  35
Match length
                  94
% identity
NCBI Description (U81294) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  171366
                  jC-atX22012Q1E1C12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4115912
BLAST score
                  178
                  1.0e-95
E value
Match length
                  262
                  92
% identity
NCBI Description Arabidopsis thaliana BAC F3H7
                  171367
Seq. No.
                  jC-atX22012Q1E1F07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3335331
BLAST score
                  65
E value
                  2.0e-28
Match length
                  113
                   77
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
```

Seq. No. 171368

Seq. ID jC-atX22012Q1E1F07b2

Method BLASTX

23402

complete sequence [Arabidopsis thaliana]



```
NCBI GI
                  g3080374
BLAST score
                  200
                  2.0e-15
E value
Match length
                  138
% identity
                  3
                  (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171369
Seq. ID
                  jC-atX22013Q1E1A04a1
                  BLASTN
Method
NCBI GI
                  g2351064
BLAST score
                  121
E value
                  8.0e-62
Match length
                  173
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171370
                  jC-atX22013Q1E1C02a1
```

Seq. ID BLASTN Method g2618602 NCBI GI BLAST score 266 E value 1.0e-148 270 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 171371 jC-atX22013Q1E1D06a1 Seq. ID Method BLASTX q3461821 NCBI GI BLAST score 153 5.0e-10 E value

51 Match length 61 % identity

(AC004138) putative nucleoside triphosphatase [Arabidopsis NCBI Description

thaliana]

Seq. No. 171372

jC-atX22013Q1E1G06a1 Seq. ID

Method BLASTN NCBI GI q3869067 BLAST score 261 1.0e-145 E value 357 Match length 92 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCK7, complete sequence [Arabidopsis thaliana]

Seq. No. 171373

jC-atX22013Q1E1G06a2 Seq. ID

Method BLASTN NCBI GI g3869069 98 BLAST score E value 5.0e-48



```
Match length
                  230
% identity
                  85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171374
Seq. ID
                  jC-atX22014Q1E1A02a1
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  82
                  1.0e-38
E value
Match length
                  150
% identity
                  89
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  171375
Seq. ID
                  jC-atX22014Q1E1C04a1
Method
                  BLASTN
NCBI GI
                  g1839239
BLAST score
                  281
E value
                  1.0e-157
Match length
                  313
% identity
                  97
NCBI Description
                 Arabidopsis thaliana aVps41p (AVPS41) gene, partial cds
                  171376
Seq. No.
Seq. ID
                  jC-atX22014Q1E1D04a1
Method
                  BLASTN
NCBI GI
                  g4415928
BLAST score
                  122
E value
                  2.0e-62
Match length
                  199
                  93
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171377
                  jC-atX22016Q1E1C01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589438
BLAST score
                  119
E value
                  1.0e-60
Match length
                  205
% identity
                  88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ2, complete sequence
Seq. No.
                  171378
Seq. ID
                  jC-atX22016Q1E1D10a1
```

Method BLASTX NCBI GI g2827710 BLAST score 196 E value 6.0e-25Match length 76 % identity 84

NCBI Description (AL021684) lysosomal Pro-X carboxypeptidase - like protein

NCBI Description



[Arabidopsis thaliana]

```
Seq. No.
                  171379
                  jC-atX22017Q1E1C04b1
Seq. ID
Method
                  BLASTX
                  g2129532
NCBI GI
BLAST score
                  89
                  7.0e-24
E value
Match length
                  81
                  74
% identity
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
NCBI Description
                  Arabidopsis thaliana >gi 1107507 emb CAA63746 (X93461)
                  acyl-[acyl-carrier protein] desaturase [Arabidopsis
                  thaliana]
Seq. No.
                  171380
                  jC-atX22017Q1E1H03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264321
BLAST score
                  43
                  2.0e-15
E value
Match length
                  69
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171381
Seq. ID
                  jC-atX22018Q1E1D11b1
Method
                  BLASTN
NCBI GI
                  q4586349
BLAST score
                  62
                  9.0e-27
E value
                  86
Match length
                  93
% identity
                  Arabidopsis thaliana DNA for glucose-1-phosphate
NCBI Description
                  adenylyltransferase, complete cds
Seq. No.
                  171382
                  jC-atX22019Q1E1H05a1
Seq. ID
Method
                  BLASTN
                  g2191126
NCBI GI
BLAST score
                  124
E value
                  2.0e-63
                  277
Match length
                  94
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  171383
Seq. ID
                   jC-atX22020Q1E1F05a1
Method
                  BLASTN
NCBI GI
                  g3292807
BLAST score
                  88
E value
                   3.0e-42
Match length
                  156
                  89
% identity
```

23405

(ESSAII project)

Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19



Seq. No. 171384

Seq. ID jC-atX22020Q1E1F09a1

Method BLASTX
NCBI GI g2674203
BLAST score 138
E value 1.0e-17
Match length 88
% identity 57

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

Seq. No. 171385

Seq. ID jC-atX22022Q1E1B07b1

Method BLASTN
NCBI GI g2246379
BLAST score 323
E value 0.0e+00
Match length 399
% identity 97

NCBI Description A.thaliana mRNA for peptidyl-prolyl cis-trans isomerase

Seq. No. 171386

Seq. ID jC-atX22022Q1E1C09a1

Method BLASTN
NCBI GI g3449330
BLAST score 113
E value 6.0e-57
Match length 219
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No. 171387

Seq. ID jC-atX22022Q1E1F02a1

Method BLASTN
NCBI GI 94678705
BLAST score 193
E value 1.0e-104
Match length 423
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7

(ESSA project)

Seq. No. 171388

Seq. ID jC-atX22022Q1E1F05a1

Method BLASTN
NCBI GI g3695386
BLAST score 230
E value 1.0e-126
Match length 246
% identity 98

NCBI Description Arabidopsis thaliana BAC T2L5

Seq. No. 171389

Seq. ID jC-atX22022Q1E1F08a1

Method BLASTN



NCBI GI g4589412 BLAST score 293 E value 1.0e-164 Match length 293 % identity 64

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F6N7, complete sequence

Seq. No. 171390

Seq. ID jC-atX22023Q1E1A09a1

Method BLASTN
NCBI GI g4678258
BLAST score 86
E value 3.0e-41
Match length 106

% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F617 (ESSA project)

Seq. No. 171391

Seq. ID jC-atX22023Q1E1G03a1

Method BLASTN
NCBI GI 93242700
BLAST score 254
E value 1.0e-141
Match length 295
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F26B6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171392

Seq. ID jC-atX22024Q1E1E01b1

Method BLASTN
NCBI GI g2618602
BLAST score 57
E value 9.0e-24
Match length 61
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 171393

Seq. ID jC-atX22024Q1E1G02a1

Method BLASTN
NCBI GI g2351062
BLAST score 302
E value 1.0e-169
Match length 340
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 171394

Seq. ID jC-atX22024Q1E1H04a1

Method BLASTX NCBI GI g1706738 BLAST score 194



E value 8.0e-15 Match length 71 % identity 51

NCBI Description FLAVONOL 3-SULFOTRANSFERASE (F3-ST) >gi_498645 (U10275)

flavonol 3-sulfotransferase [Flaveria bidentis]

Seq. No. 171395

Seq. ID jC-atX22025Q1E1C04a1

Method BLASTX
NCBI GI g2739373
BLAST score 96
E value 2.0e-13
Match length 110
% identity 39

NCBI Description (AC002505) putative flavonol 3-o-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 171396

Seq. ID jC-atX22025Q1E1H10a1

Method BLASTX
NCBI GI g3193297
BLAST score 430
E value 2.0e-42
Match length 81
% identity 100

NCBI Description (AF069298) similar to epoxide hydrolases [Arabidopsis

thaliana]

Seq. No. 171397

Seq. ID jC-atX22026Q1E1B04a1

Method BLASTN
NCBI GI 94589969
BLAST score 102
E value 2.0e-50
Match length 166
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F1P15 genomic

sequence, complete sequence

Seq. No. 171398

Seq. ID jC-atX22026Q1E1B07a1

Method BLASTN
NCBI GI g3395421
BLAST score 53
E value 2.0e-21
Match length 85
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC T19C21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171399

Seq. ID jC-atX22026Q1E1E01a1

Method BLASTN
NCBI GI g4757410
BLAST score 125
E value 3.0e-64
Match length 153



% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVE11, complete sequence

Seq. No. 171400

Seq. ID jC-atX22026Q1E1E03a1

Method BLASTN
NCBI GI g2342717
BLAST score 247
E value 1.0e-136
Match length 420
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T14G11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171401

Seq. ID jC-atX22027Q1E1E02a1

Method BLASTN
NCBI GI g1707006
BLAST score 45
E value 2.0e-16

E value 2.0e-Match length 109 % identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171402

Seq. ID jC-atX22027Q1E1F07a1

Method BLASTX
NCBI GI g4006871
BLAST score 510
E value 7.0e-52
Match length 104
% identity 100

NCBI Description (Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No. 171403

Seq. ID jC-atX22027Q1E1F10a1

Method BLASTX
NCBI GI g2129899
BLAST score 205
E value 4.0e-16
Match length 80
% identity 49

NCBI Description chalcone reductase homolog - Sesbania rostrata (fragment)

>gi_899483_emb_CAA88591_ (Z48672) chalcone reductase

homologue [Sesbania rostrata]

Seq. No. 171404

Seq. ID jC-atX22028Q1E1F08a1

Method BLASTX
NCBI GI 94490750
BLAST score 162
E value 3.0e-11
Match length 32
% identity 100

NCBI Description (AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]



```
Seq. No.
                  171405
                  jC-atX22028Q1E1H09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194119
                  193
BLAST score
                  1.0e-14
E value
Match length
                  66
                  53
% identity
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                  171406
Seq. No.
Seq. ID
                  jC-atX22029Q1E1F02a1
Method
                  BLASTX
                  q4008012
NCBI GI
                  269
BLAST score
E value
                  8.0e-24
                  53
Match length
% identity
                  98
                  (AF084037) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  171407
Seq. No.
Seq. ID
                   jC-atX22030Q1E1B05a1
Method
                  BLASTX
                  q99772
NCBI GI
BLAST score
                  372
E value
                  1.0e-35
Match length
                   95
% identity
                  78
                  ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana
NCBI Description
                  >gi 166936 (J05540) ubiquitin extension protein (UBQ6)
                   [Arabidopsis thaliana] >gi 3522953 (AC004411) ubiquitin
                  extension protein (UBQ6) [Arabidopsis thaliana]
Seq. No.
                   171408
                   jC-atX22030Q1E1E07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g499046
BLAST score
                   128
E value
                  9.0e-66
                  160
Match length
                   95
% identity
NCBI Description A.thaliana (CDNA4) myosin heavy chain mRNA
                   171409
Seq. No.
                   jC-atX22031Q1E1A06a1
Seq. ID
                   BLASTN
Method
                   q4587986
NCBI GI
                  54
BLAST score
E value
                   1.0e-21
                   174
Match length
                  82
% identity
NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete
```

sequence

171410

Seq. No.



Seq. ID jC-atX22031Q1E1D06a1 Method BLASTN NCBI GI g3779020 BLAST score 158 1.0e-83 E vâlue Match length 275 89 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 171411 Seq. ID jC-atX22031Q1E1F11a1 Method BLASTX NCBI GI g3924613 BLAST score 289 E value 6.0e-26Match length 66 % identity 88 (AF069442) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein [Arabidopsis thaliana] Seq. No. 171412 Seq. ID jC-atX22032Q1E1A08a1 Method BLASTN NCBI GI g3047060 BLAST score 513 E value 0.0e + 00Match length 535 99 % identity NCBI Description Arabidopsis thaliana BAC F7N22 Seq. No. 171413 Seq. ID jC-atX22032Q1E1C02a1 Method BLASTX NCBI GI g4160532 BLAST score 144 E value 4.0e-09 69 Match length % identity 49 (AJ011304) sphingosine-1-phosphate lyase [Homo sapiens] NCBI Description Seq. No. 171414 jC-atX22032Q1E1G09b1 Seq. ID BLASTN Method NCBI GI g2618602 BLAST score 82 E value 2.0e-38

Match length 158 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 171415

Seq. ID jC-atX22032Q1E1H09b1

Method BLASTN NCBI GI g4490291



```
BLAST score
                  83
                   5.0e-39
E value
Match length
                   253
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                   (ESSA project)
Seq. No.
                  171416
Seq. ID
                   jC-atX22032Q1E1H11a1
Method
                  BLASTN
NCBI GI
                  g4159705
BLAST score
                   458
E value
                   0.0e + 00
Match length
                   461
                   100
% identity
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                   171417
Seq. ID
                  jC-atX22033Q1E1F04a1
Method
                  BLASTN
NCBI GI
                  q4757678
BLAST score
                   211
E value
                   1.0e-115
Match length
                   395
                   90
% identity
                  Arabidopsis thaliana chromosome I BAC F9H16 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  171418
Seq. ID
                   jC-atX22033Q1E1F05a1
Method
                  BLASTN
NCBI GI
                  q2477521
BLAST score
                   416
                  0.0e+00
E value
Match length
                   441
                   98
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171419
Seq. ID
                   jC-atX22033Q1E2A09a1
Method
                  BLASTX
NCBI GI
                  q2979566
BLAST score
                  121
                  3.0e-06
E value
                  70
Match length
                   94
% identity
NCBI Description
                 (AC003680) MADS box protein AGL20 [Arabidopsis thaliana]
```

Seq. No. 171420

Seq. ID jC-atX22033Q1E2C04a1

Method BLASTN
NCBI GI g3860242
BLAST score 134
E value 3.0e-69
Match length 162



```
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome I BAC T13M11 genomic
                - sequence, complete sequence
Seq. No.
                  171421
Seq. ID
                  jC-atX22033Q1E2C12a1
Method
                  BLASTN
NCBI GI
                  q2570223
BLAST score
                  130
E value
                  6.0e-67
Match length
                  294
                  93
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  171422
Seq. ID
                  jC-atX22034Q1E2G03a2
Method
                  BLASTX
NCBI GI
                  q4588002
BLAST score
                  162
E value
                  2.0e-41
Match length
                  91
% identity
                  90
NCBI Description
                  (AF085279) hypothetical ankyrin-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  171423
Seq. ID
                  jC-atX22034Q1E2H10b1
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  239
                  4.0e-20
E value
Match length
                  78
% identity
                  58
NCBI Description
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
                  [Nicotiana tabacum]
Seq. No.
                  171424
Seq. ID
                  jC-atX22035Q1E1D03b1
Method
                  BLASTN
NCBI GI
                  g3176693
BLAST score
                  132
E value
                  5.0e-68
Match length
                  366
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC T27I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171425
Seq. No.
Seq. ID
                  jC-atX22039Q1E1B06b1
Method
                  BLASTX
                  q2246621
                  259
```

NCBI GI BLAST score 7.0e-23 E value Match length 64 % identity 83

(AF004393) salt-stress induced tonoplast intrinsic protein NCBI Description



[Arabidopsis thaliana]

```
Seq. No.
                   171426
Seq. ID
                   jC-atX22039Q1E1H01034a1
Method
                   BLASTX
NCBI GI
                  q2895510
BLAST score
                   390
                   6.0e-38
E value
Match length
                   72
                   100
% identity
                  (AF033204) putative pectin methylesterase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   171427
Seq. ID
                   jC-atX22044Q1E1B01019a1
                  BLASTX
Method
NCBI GI
                  q4454049
BLAST score
                   225
E value
                   1.0e-18
Match length
                   60
                   80
% identity
                  (AL035394) 98b like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   171428
Seq. ID
                   jC-atX22046Q1E1G01005a1
                   BLASTN
Method
NCBI GI
                  q3869075
BLAST score
                   98
E value
                   3.0e-48
Match length
                   146
% identity
                   92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171429
                   jC-atX22051Q1E1A09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2244788
BLAST score
                   454
                   0.0e+00
E value
                   454
Match length
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   171430
Seq. No.
                   jC-atX22051Q1E1C11a1
Seq. ID
Method
                   {\tt BLASTN}
NCBI GI
                   g4567259
BLAST score
                   35
E value
                   3.0e-10
                   108
Match length
                   88
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3K23 genomic
```

Seq. No. 171431

sequence, complete sequence



```
Seq. ID
                  jC-atX22051Q1E1D08b1
Method
                  BLASTN
NCBI GI
                  q4587986
BLAST score
                  48
E value
                  2.0e-18
                  96
Match length
                  88
% identity
NCBI Description
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
                  sequence
                  171432
Seq. No.
Seq. ID
                  jC-atX22052Q1E1A07a1
Method
                  BLASTN
NCBI GI
                  g4753645
BLAST score
                  166
                  2.0e-88
E value
Match length
                  234
% identity
                  93
NCBI Description
                 Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
                  (ESSA project)
Seq. No.
                  171433
Seq. ID
                  jC-atX22052Q1E1B04a1
Method
                  BLASTN
NCBI GI
                  g2351061
BLAST score
                  158
                  8.0e-84
E value
Match length
                  187
% identity
                  95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171434
Seq. ID
                  jC-atX22052Q1E1B09a1
Method
                  BLASTN
NCBI GI
                  g16188
BLAST score
                  39
E value
                  8.0e-13
Match length
                  47
% identity
                  96
NCBI Description A.thaliana mRNA ATR2 for NADPH-cytochrome P450 reductase
Seq. No.
                  171435
Seq. ID
                  jC-atX22052Q1E1C06a1
Method
                  BLASTN
NCBI GI
                  q3582315
BLAST score
                  132
E value
                  3.0e-68
Match length
                  263
% identity
                  87
                  Arabidopsis thaliana chromosome II BAC T27A16 genomic
NCBI Description
```

NCBI Description Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171436

Seq. ID jC-atX22052Q1E1E12b1

Method BLASTX NCBI GI q1363489



BLAST score 467 E value 8.0e-47 Match length 86 % identity 100

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No. 171437

Seq. ID jC-atX22052Q1E1G10a1

Method BLASTN
NCBI GI g4558590
BLAST score 70
E value 4.0e-31
Match length 157
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC T17C22 genomic

sequence, complete sequence

Seq. No. 171438

Seq. ID jC-atX22052Q1E1H04a1

Method BLASTN
NCBI GI 94468103
BLAST score 39
E value 8.0e-13
Match length 143
% identity 80

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)

Seq. No. 171439

Seq. ID jC-atX22053Q1E1A09b1

Method BLASTX
NCBI GI g4539307
BLAST score 291
E value 1.0e-26
Match length 69
% identity 81

NCBI Description (AL049480) putative acidic ribosomal protein [Arabidopsis

thaliana]

Seq. No. 171440

Seq. ID jC-atX22055Q1E1A09a1

Method BLASTN
NCBI GI g3859658
BLAST score 109
E value 1.0e-54
Match length 162
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 171441

Seq. ID jC-atX22055Q1E1D06a1

Method BLASTN NCBI GI g4678258 BLAST score 134



```
E value
                  1.0e-69
Match length
                  193
                  91
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F617
NCBI Description
                   (ESSA project)
Seq. No.
                  171442
                  jC-atX22056Q1E1G10b1
Seq. ID
                  BLASTN
Method
                  g2262135
NCBI GI
BLAST score
                   361
E value
                  0.0e+00
Match length
                  385
% identity
                  98
NCBI Description
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                  cM, complete sequence
Seq. No.
                  171443
                  jC-atX22058Q1E1F03a1
Seq. ID
Method
                  BLASTX
                  g2244792
NCBI GI
                   395
BLAST score
E value
                  3.0e - 38
Match length
                  88
                  91
% identity
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171444
                  jC-atX22059Q1E1A02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589430
BLAST score
                  263
E value
                  1.0e-146
                  263
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLD14, complete sequence
                  171445
Seq. No.
                  jC-atX22059Q1E1H09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519193
                  134
BLAST score
E value
                   2.0e-69
Match length
                  246
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDC11, complete sequence
```

Seq. No. 171446

Seq. ID jC-atX22060Q1E1D10a1

Method BLASTN
NCBI GI g3449334
BLAST score 218
E value 1.0e-119
Match length 234
% identity 98



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana] Seq. No. 171447 Seq. ID jC-atX22061Q1E2A02a1 Method BLASTX NCBI GI q3785986 BLAST score 150 E value 5.0e-10 Match length 27 % identity 100 NCBI Description (AC005560) RGA1 protein [Arabidopsis thaliana] Seq. No. 171448 Seq. ID jC-atX22061Q1E2B08a1 Method BLASTN NCBI GI g3702737 BLAST score 132 E value 4.0e-68 Match length 262 90 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana] Seq. No. 171449 jC-atX22061Q1E2E01a1 Seq. ID Method BLASTN NCBI GI q4314374 BLAST score 43 3.0e-15 E value 95 Match length 93 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana] 171450 Seq. No. jC-atX22061Q1E2E06a1 Seq. ID Method BLASTX g4490704 NCBI GI BLAST score 217 E value 6.0e-18 Match length 43 % identity 100 (AL035680) putative protein [Arabidopsis thaliana] NCBI Description 171451 Seq. No. jC-atX22062Q1E1E06a1 Seq. ID Method BLASTX NCBI GI g2129727

93 BLAST score 6.0e-03 E value Match length 46 % identity 27

RNA-binding protein 37 - Arabidopsis thaliana >gi 1174153 NCBI Description

(U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 171452



Seq. ID jC-atX22063Q1E1B04a1

Method BLASTN
NCBI GI g3522932
BLAST score 210
E value 1.0e-115
Match length 252
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171453

Seq. ID jC-atX22065Q1E1F08a1

Method BLASTN
NCBI GI g4455339
BLAST score 184
E value 3.0e-99
Match length 259
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5

(ESSAII project)

Seq. No. 171454

Seq. ID jC-atX22065Q1E1G01a1

Method BLASTX
NCBI GI g2982444
BLAST score 396
E value 1.0e-38
Match length 79
% identity 99

NCBI Description (AL022224) CLV1 receptor kinase like protein [Arabidopsis

thaliana]

Seq. No. 171455

Seq. ID jC-atX22065Q1E1G05a1

Method BLASTN
NCBI GI g3269280
BLAST score 210
E value 1.0e-114
Match length 260
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22

(ESSAII project)

Seq. No. 171456

Seq. ID jC-atX22067Q1E1A07a1

Method BLASTN
NCBI GI g4733957
BLAST score 207
E value 1.0e-113
Match length 262
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T26C18 genomic

sequence, complete sequence

Seq. No. 171457

Seq. ID jC-atX22067Q1E1F01a1

Method BLASTN



NCBI GI g472876
BLAST score 191
E value 1.0e-103
Match length 236
% identity 96

NCBI Description A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No. 171458

Seq. ID jC-atX22067Q1E1G11b1

Method BLASTN
NCBI GI g2828186
BLAST score 126
E value 9.0e-65
Match length 166
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 171459

Seq. ID jC-atX22067Q1E1H04a1

Method BLASTX
NCBI GI g4027891
BLAST score 226
E value 6.0e-19
Match length 66
% identity 58

NCBI Description (AF049350) alpha-expansin precursor [Nicotiana tabacum]

Seq. No. 171460

Seq. ID jC-atX22068Q1E1G05a1

Method BLASTN
NCBI GI g3702722
BLAST score 262
E value 1.0e-146
Match length 262
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K12B20, complete sequence [Arabidopsis thaliana]

Seq. No. 171461

Seq. ID jC-atX22069Q1E1B01a1

Method BLASTX
NCBI GI g3461846
BLAST score 352
E value 1.0e-33
Match length 95
% identity 33

NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis

thaliana]

Seq. No. 171462

Seq. ID jC-atX22069Q1E1F09a1

Method BLASTN
NCBI GI g2584827
BLAST score 240
E value 1.0e-132
Match length 256



% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171463

Seq. ID jC-atX22069Q1E1G12a1

Method BLASTN
NCBI GI 94510408
BLAST score 230
E value 1.0e-126
Match length 262
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T1E2 genomic

sequence, complete sequence

Seq. No. 171464

Seq. ID jC-atX22070Q1E1C05a1

Method BLASTN
NCBI GI g2252823
BLAST score 106
E value 1.0e-52
Match length 167
% identity 94

NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 171465

Seq. ID jC-atX22070Q1E1D10a1

Method BLASTN
NCBI GI g2337888
BLAST score 247
E value 1.0e-137

E value 1.00-1
Match length 263
% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 171466

Seq. ID jC-atX22072Q1E1A10a1

Method BLASTN
NCBI GI g1498063
BLAST score 238
E value 1.0e-131
Match length 262
% identity 98

NCBI Description Arabidopsis thaliana AtE1 (atE1) mRNA, complete cds

Seq. No. 171467

Seq. ID jC-atX22072Q1E1C04a1

Method BLASTN
NCBI GI g2351065
BLAST score 35
E value 2.0e-10
Match length 119
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]



Seq. No. 171468

Seq. ID jC-atX22072Q1E1D06a1

Method BLASTN
NCBI GI g3869069
BLAST score 198
E value 1.0e-107
Match length 222
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 171469

Seq. ID jC-atX22072Q1E1F07a1

Method BLASTN
NCBI GI g3985931
BLAST score 133
E value 5.0e-69
Match length 156
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21H1, complete sequence [Arabidopsis thaliana]

Seq. No. 171470

Seq. ID jC-atX22072Q1E1F12a1

Method BLASTX
NCBI GI g3859659
BLAST score 157
E value 8.0e-11
Match length 36
% identity 83

NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)

[Arabidopsis thaliana]

Seq. No. 171471

Seq. ID jC-atX22072Q1E1H08a1

Method BLASTX
NCBI GI g99677
BLAST score 298
E value 4.0e-27
Match length 65
% identity 97

NCBI Description chaperonine 60K beta chain - Arabidopsis thaliana

(fragment) >gi_553036 (M35598) 60-kDa chaperonin-60

beta-polypeptide [Arabidopsis thaliana]

Seq. No. 171472

Seq. ID jC-atX22073Q1E1B05a1

Method BLASTN
NCBI GI g2062153
BLAST score 268
E value 1.0e-149
Match length 268
% identity 64

NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171473



jC-atX22073Q1E1C05b1

Method BLASTX
NCBI GI g119350
BLAST score 289
E value 6.0e-26
Match length 57
% identity 100

Seq. ID

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase);identical to P25696

[Arabidopsis thaliana]

Seq. No. 171474

Seq. ID jC-atX22073Q1E1G11a1

Method BLASTN
NCBI GI g4454447
BLAST score 53
E value 2.0e-21
Match length 109
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171475

Seq. ID jC-atX22074Q1E1A02a1

Method BLASTN
NCBI GI g4079614
BLAST score 249
E value 1.0e-138
Match length 249
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171476

Seq. ID jC-atX22074Q1E1F03a1

Method BLASTN
NCBI GI g3869069
BLAST score 177
E value 3.0e-95
Match length 177
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 171477

Seq. ID jC-atX22074Q1E1H08a1

Method BLASTX
NCBI GI g3548801
BLAST score 226
E value 8.0e-19
Match length 54
% identity 81



(AC005313) putative transmembrane protein [Arabidopsis NCBI Description thaliana] >gi_4335768 gb AAD17445 (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No. 171478

Seq. ID jC-atX22075Q1E1C06a1

Method BLASTN NCBI GI g3150396 BLAST score 264 E value 1.0e-147 Match length 288 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

171479 Seq. No.

Seq. ID jC-atX22075Q1E1C12b1

Method BLASTN NCBI GI g2281081 BLAST score 250 E value 1.0e-138 Match length 456 98 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171480

Seq. ID jC-atX22076Q1E1E01a1

Method BLASTX g4585882 NCBI GI BLAST score 320 E value 1.0e-29 Match length 78

85 % identity

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 171481

jC-atX22076Q1E1F07a1 Seq. ID

Method BLASTN NCBI GI q4662609 BLAST score 139 E value 2.0e-72 Match length 227 % identity 89

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 171482

Seq. ID C-atX22076Q1E1F11a1

Method BLASTN NCBI GI q4567259 BLAST score 236 E value 1.0e-130 Match length 278 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic



sequence, complete sequence

```
Seq. No.
                  171483
                  jC-atX22078Q1E1C10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159701
BLAST score
                  327
                  0.0e+00
E value
Match length
                  420
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K22G18, complete sequence
                  171484
Seq. No.
Seq. ID
                  jC-atX22078Q1E1D05a1
Method
                  BLASTN
                  q4263694
NCBI GI
BLAST score
                  221
                  1.0e-121
E value
Match length
                  233
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171485
                  jC-atX22078Q1E1D10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244795
BLAST score
                  179
                  5.0e-13
E value
                  49
Match length
                  73
% identity
                 (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  171486
Seq. No.
Seq. ID
                  jC-atX22079Q1E1B12a1
Method
                  BLASTX
                  q3868859
NCBI GI
BLAST score
                  393
E value
                  3.0e - 38
Match length
                  131
% identity
NCBI Description
                 (AB013887) RAV2 [Arabidopsis thaliana]
                  171487
Seq. No.
Seq. ID
                  jC-atX22080Q1E1F09a1
Method
                  BLASTX
NCBI GI
                  q4826972
BLAST score
                  144
E value
                  7.0e-09
Match length
                  48
% identity
NCBI Description RNA binding motif protein 8 >qi 4455129 qb AAD21089.1
                   (AF127761) ribonucleoprotein RBM8 [Homo sapiens]
```

Seq. No. 171488

Seq. ID jC-atX22080Q1E2C04a1



Method BLASTN
NCBI GI g4680765
BLAST score 43
E value 2.0e-15
Match length 123
% identity 84

NCBI Description Arabidopsis thaliana BAC F14I23 from chromosome V near 69

cM, complete sequence

Seq. No. 171489

Seq. ID jC-atX22080Q1E2G09b1

Method BLASTX
NCBI GI g3152600
BLAST score 216
E value 5.0e-18
Match length 52
% identity 77

NCBI Description (AC002986) Contains similarity to S. cerevisiae

hypothetical protein YOR197w, gb Z75105. ESTs gb H37409,

gb AA395290, and gb T43907 come from this gene.

[Arabidopsis thaliana]

Seq. No. 171490

Seq. ID jC-atX22081Q1E2B12a1

Method BLASTN
NCBI GI 94510392
BLAST score 151
E value 2.0e-79
Match length 347
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic

sequence, complete sequence

Seq. No. 171491

Seq. ID jC-atX22081Q1E2D05b1

Method BLASTN
NCBI GI g2462780
BLAST score 272
E value 1.0e-151
Match length 324
% identity 96

NCBI Description Arabidopsis thaliana carbamoyl phosphate synthetase small

subunit mRNA (carA), complete cds

Seq. No. 171492

Seq. ID jC-atX22082Q1E1D09a1

Method BLASTN
NCBI GI g3046847
BLAST score 39
E value 5.0e-13
Match length 135
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 171493

Seq. ID jC-atX22083Q1E1E08a1

E value

Match length

% identity

1.0e-167

323

98



```
Method
                   BLASTN
NCBI GI
                   q4680765
BLAST score
                   113
                   4.0e-57
E value
Match length
                   165
% identity
                   92
NCBI Description
                   Arabidopsis thaliana BAC F14I23 from chromosome V near 69
                   cM, complete sequence
                   171494
Seq. No.
                   jC-atX22084Q1E1B02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4103963
BLAST score
                   215
E value
                   3.0e-17
Match length
                   42
                   100
% identity
NCBI Description (AF030035) calmodulin [Phaseolus vulgaris]
Seq. No.
                   171495
                   jC-atX22084Q1E1B11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3912927
BLAST score
                   236
E value
                   2.0e-20
                   51
Match length
% identity
                   47
NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   171496
                   jC-atX22084Q1E1G10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4210448
                   55
BLAST score
E value
                   1.0e-22
                   95
Match length
                   89
% identity
NCBI Description Arabidopsis thaliana gene for ARR1 protein, complete cds
                   171497
Seq. No.
                   jC-atX22084Q1E2C09a1
Seq. ID
Method
                   BLASTX
                   g1871180
NCBI GI
BLAST score
                   314
E value
                   3.0e-29
Match length
                   92
% identity
                   73
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]
Seq. No.
                   171498
Seq. ID
                   jC-atX22085Q1E2F05a1
Method
                   BLASTN
NCBI GI
                   q4519194
BLAST score
                   298
```



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No. 171499

Seq. ID jC-atX22086Q1E1B03a1

Method BLASTN
NCBI GI g3319359
BLAST score 259
E value 1.0e-144
Match length 363
% identity 100

NCBI Description Arabidopsis thaliana BAC T7M24

Seq. No. 171500

Seq. ID jC-atX22086Q1E1C10a1

Method BLASTN
NCBI GI g4539309
BLAST score 218
E value 1.0e-119
Match length 254
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22

(ESSA project)

Seq. No. 171501

Seq. ID jC-atX22087Q1E1A06a1

Method BLASTN
NCBI GI g4582444
BLAST score 40
E value 2.0e-13
Match length 48
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T9H9 genomic

sequence, complete sequence

Seq. No. 171502

Seq. ID jC-atX22088Q1E1E06a1

Method BLASTX
NCBI GI g3702323
BLAST score 272
E value 4.0e-24
Match length 53
% identity 92

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 171503

Seq. ID jC-atX22088Q1E1E12a1

Method BLASTX
NCBI GI g4455206
BLAST score 258
E value 2.0e-22
Match length 51
% identity 94

NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis

thaliana]

Seq. No. 171504



Seq. ID jC-atX22088Q1E1E12b1 BLASTX Method NCBI GI g4455206 BLAST score 626 2.0e-65 E value Match length 131 95 % identity (AL035440) putative beta-1, 3-glucanase [Arabidopsis NCBI Description thaliana] Seq. No. 171505 Seq. ID jC-atX22089Q1E1F02a2 Method BLASTN NCBI GI g3250673 BLAST score 68 2.0e-30 E value Match length 92 % identity 93 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project) 171506 Seq. No. Seq. ID jC-atX22089Q1E1F02b2 Method BLASTN NCBI GI g3250673 BLAST score 110 2.0e-55 E value Match length 131 % identity 95 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project) Seq. No. 171507 jC-atX23001Q1E1A09a1 Seq. ID BLASTN Method NCBI GI g2244870 50 BLAST score E value 2.0e-19 Match length 146 % identity 89 Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No 171508 Seq. No. jC-atX23002Q1E1A12b1 Seq. ID Method BLASTX NCBI GI g4262236 BLAST score 171

2.0e-17 E value 90 Match length 60 % identity

(AC006200) putative ribose 5-phosphate isomerase NCBI Description

[Arabidopsis thaliana]

171509 Seq. No.

jC-atX23003Q1E1G11b1 Seq. ID

BLASTN Method



NCBI GI g3252804 BLAST score 35 E value 2.0e-10 Match length 111 % identity 42

NCBI Description Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171510

Seq. ID jC-atX23004Q1E1D04a1

Method BLASTN
NCBI GI g2598228
BLAST score 117
E value 1.0e-59
Match length 121
% identity 99

NCBI Description A.thaliana mRNA for Rab11 protein

Seq. No. 171511

Seq. ID jC-atX23004Q1E1E04a1

Method BLASTN
NCBI GI g3046854
BLAST score 112
E value 1.0e-56
Match length 116
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No. 171512

Seq. ID jC-atX23004Q1E1H08a1

Method BLASTN
NCBI GI g4263642
BLAST score 84
E value 7.0e-40
Match length 128
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T13H18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171513

Seq. ID jC-atX23005Q1E1B06b1

Method BLASTN
NCBI GI 94580365
BLAST score 62
E value 1.0e-26
Match length 154
% identity 90

NCBI Description Arabidopsis thaliana chromosome I BAC F3F20 genomic

sequence, complete sequence

Seq. No. 171514

Seq. ID jC-atX23005Q1E1E09a1

Method BLASTN
NCBI GI g4691223
BLAST score 146
E value 8.0e-77



```
150
Match length
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
                   171515
Seq. No.
Seq. ID
                   jC-atX23005Q1E1F01a1
Method
                   BLASTN
NCBI GI
                   g2760167
BLAST score
                   144
E value
                   1.0e-75
Match length
                   144
% identity
                   100
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MCO15, complete sequence [Arabidopsis thaliana]

171516 Seq. No. Seq. ID jC-atX23005Q1E1G06a1 Method BLASTX NCBI GI g3776581 BLAST score 527 E value 6.0e-54

Match length 106 % identity 95

NCBI Description (AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 171517 jC-atX23006Q1E1D08a1 Seq. ID Method BLASTX

NCBI GI g1170921 BLAST score 264 E value 4.0e-23 Match length 117 % identity 42

NCBI Description S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE

> METHYLTRANSFERASE >gi_1074428_pir__G64153 hypothetical protein HI0508 - Haemophilus influenzae (strain Rd KW20)

>gi 1573489 (U32732)

S-adenosylmethionine: 2-demethylmenaquinone

methyltransferase (menG) [Haemophilus influenzae Rd]

Seq. No. 171518

Seq. ID jC-atX23007Q1E1H07a1

Method BLASTN NCBI GI g2673901 BLAST score 152 E value 5.0e-80 Match length 350 97 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171519

Seq. ID jC-atX23008Q1E1C02a1

Method BLASTN NCBI GI g2252848



BLAST score 122 E value 2.0e-62 Match length 142 % identity 96

NCBI Description Arabidopsis thaliana BAC TM018A10

Seq. No. 171520

Seq. ID jC-atX23010Q1E2C09a1

Method BLASTN
NCBI GI g4159700
BLAST score 134
E value 1.0e-69
Match length 138
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1L20, complete sequence

Seq. No. 171521

Seq. ID jC-atX23011Q1E1B03a1

Method BLASTN
NCBI GI g4468976
BLAST score 139
E value 2.0e-72
Match length 209
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18

(ESSA project)

Seq. No. 171522

Seq. ID jC-atX23012Q1E1A05b1

Method BLASTX
NCBI GI g115783
BLAST score 618
E value 2.0e-64
Match length 116
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 171523

Seq. ID jC-atX23013Q1E1D09a1

Method BLASTN
NCBI GI g2244991
BLAST score 117
E value 3.0e-59
Match length 225
% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 171524

Seq. ID jC-atX23013Q1E1H02a1

Method BLASTN NCBI GI g1777311 BLAST score 117



E value 3.0e-59
Match length 292
% identity 85

NCBI Description Arabidopsis thaliana mRNA for novel serine/threonine

protein kinase, complete cds

Seq. No. 171525

Seq. ID jC-atX23013Q1E1H09a1

Method BLASTN
NCBI GI g4646229
BLAST score 195
E value 1.0e-106
Match length 251
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F27A10 genomic

sequence, complete sequence

Seq. No. 171526

Seq. ID jC-atX23014Q1E1A04a1

Method BLASTN
NCBI GI g4662609
BLAST score 247
E value 1.0e-137

E value 1.0e-1
Match length 247
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 171527

Seq. ID jC-atX23015Q1E1G12a1

Method BLASTN
NCBI GI 94454022
BLAST score 84
E value 1.0e-39
Match length 184
% identity 84

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16

(ESSAII project)

Seq. No. 171528

Seq. ID jC-atX23016Q1E1C06b1

Method BLASTN
NCBI GI g2160155
BLAST score 112
E value 4.0e-56
Match length 325
% identity 97

NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 171529

Seq. ID jC-atX23017Q1E1C10a1

Method BLASTN
NCBI GI g4263774
BLAST score 93
E value 3.0e-45
Match length 123

NCBI Description



```
% identity
                  93
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171530
Seq. ID
                  jC-atX23017Q1E1D10b2
Method
                  BLASTN
NCBI GI
                  g4092471
BLAST score
                  52
E value
                  2.0e-20
Match length
                  103
% identity
                  88
NCBI Description
                  Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5
                  cM, complete sequence
Seq. No.
                  171531
                  jC-atX23018Q1E1D12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3293582
BLAST score
                  158
E value
                  1.0e-83
Match length
                  311
                  87
% identity
NCBI Description Arabidopsis thaliana BAC T15F16
Seq. No.
                  171532
Seq. ID
                  jC-atX23020Q1E1F10a1
Method
                  BLASTN
NCBI GI
                  q4757401
BLAST score
                  375
E value
                  0.0e+00
Match length
                  412
% identity
                  49
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGH6, complete sequence
Seq. No.
                  171533
Seq. ID
                  jC-atX23021Q2E1E05a1
Method
                  BLASTN
NCBI GI
                  q2564047
BLAST score
                  250
E value
                  1.0e-138
                  258
Match length
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJB21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171534
Seq. ID
                  jC-atX23021Q2E1F04a1
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  65
E value
                  1.0e-28
Match length
                  105
% identity
                  90
```

MDC11, complete sequence

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:



```
171535
 Seq. No.
 Seq. ID
                    jC-atX23022Q2E1F04b1
 Method
                    BLASTN
                    g4725940
 NCBI GI
BLAST score
                    74
                    9.0e-34
 E value
 Match length
                    179
                    57
 % identity
 NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17
                    (ESSA project)
                    171536
 Seq. No.
 Seq. ID
                    jC-atX23025Q1E1A05a1
 Method
                    BLASTN
 NCBI GI
                    g3608126
                    279
 BLAST score
                    1.0e-156
 E value
                    353
 Match length
                    100
 % identity
                    Arabidopsis thaliana chromosome II BAC T32F12 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    171537
                    jC-atX23025Q1E1B01a1
 Seq. ID
 Method
                    BLASTN
                    g4733953
 NCBI GI
                    90
 BLAST score
                    2.0e-43
 E value
 Match length
                    130
                    92
 % identity
 NCBI Description Arabidopsis thaliana chromosome I BAC F13011 genomic
                    sequence, complete sequence
                    171538
 Seq. No.
 Seq. ID
                    jC-atX23025Q1E1F12a1
 Method
                    BLASTN
 NCBI GI
                    g4519193
 BLAST score
                    39
 E value
                    4.0e-13
 Match length
                    103
 % identity
                    84
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                    MDC11, complete sequence
                    171539
 Seq. No.
 Seq. ID
                    jC-atX23026Q1E1E07a1
 Method
                    BLASTN
```

NCBI GI g3269280

BLAST score 52 E value 1.0e-20 Match length 184

% identity 82

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22

(ESSAII project)

Seq. No. 171540



Seq. ID jC-atX23026Q1E1G11b2

Method BLASTX
NCBI GI 94455033
BLAST score 200
E value 1.0e-15
Match length 120
% identity 38

NCBI Description (AF116237) pseudouridine synthase 1 [Mus musculus]

Seq. No. 171541

Seq. ID jC-atX23026Q1E1H05a1

Method BLASTN
NCBI GI g3327922
BLAST score 274
E value 1.0e-152
Match length 447
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171542

Seq. ID jC-atX24001Q1E1B02b1

Method BLASTN
NCBI GI g4510360
BLAST score 51

E value 5.0e-20 Match length 151 83

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 171543

Seq. ID jC-atX24003Q1E1B02b1

Method BLASTN
NCBI GI g3046847
BLAST score 60
E value 2.0e-25
Match length 100
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 171544

Seq. ID jC-atX24003Q1E1E05a1

Method BLASTX
NCBI GI g3334441
BLAST score 196
E value 6.0e-15
Match length 102
% identity 37

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II

>gi 2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 171545

Seq. ID jC-atX24003Q1E1E12a1

Method BLASTN



```
NCBI GI
                  g2213606
BLAST score
                  63
                  3.0e-27
E value
                  115
Match length
                  89
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
                  171546
Seq. No.
                  jC-atX24004Q1E1F11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  115
                  5.0e-58
E value
                  270
Match length
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171547
Seq. No.
                  jC-atX24005Q1E1C05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462780
BLAST score
                  317
                  1.0e-178
E value
Match length
                  329
% identity
                  99
NCBI Description Arabidopsis thaliana carbamoyl phosphate synthetase small
                  subunit mRNA (carA), complete cds
                  171548
Seq. No.
Seq. ID
                   jC-atX24005Q1E1D08a1
Method
                  BLASTX
NCBI GI
                  g4056502
BLAST score
                  442
E value
                  6.0e-44
Match length
                  91
                  100
% identity
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                   171549
Seq. No.
Seq. ID
                   jC-atX24005Q1E1D08b1
Method
                  BLASTX
NCBI GI
                  q4056502
BLAST score
                  435
E value
                   4.0e-43
Match length
                  91
% identity
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                   171550
Seq. ID
                   jC-atX24005Q1E1G12b1
```

Method BLASTX NCBI GI g4103963 BLAST score 198 E value 3.0e-15 Match length 41



% identity

NCBI Description (AF030035) calmodulin [Phaseolus vulgaris]

171551 Seq. No.

jC-atX24005Q1E1H05a1 Seq. ID

Method BLASTN NCBI GI q2795802 35 BLAST score 1.0e-10 E value 68 Match length 97

NCBI Description Arabidopsis thaliana chromosome II BAC F17A14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171552

% identity

Seq. ID jC-atX24005Q1E1H06a1

Method BLASTN NCBI GI q3335331 BLAST score 152 3.0e-80 E value Match length 225 % identity 94

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171553

jC-atX24005Q1E1H11a1 Seq. ID

Method BLASTN g298035 NCBI GI BLAST score 94 7.0e-46E value Match length 134 93 % identity

NCBI Description A.thaliana Lhcb4 gene

171554 Seq. No.

Seq. ID jC-atX24005Q1E1H12a1

Method BLASTN NCBI GI q2832639 BLAST score 263 E value 1.0e-146 Match length 275 99 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. No. 171555

Seq. ID jC-atX24006Q1E1A02a1

Method BLASTN NCBI GI q4063737 BLAST score 107 E value 3.0e-53 Match length 235 % identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic

sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 171556

Seq. ID jC-atX24010Q1E1A04b1

Method BLASTX
NCBI GI g232031
BLAST score 149
E value 5.0e-10
Match length 62
% identity 47

NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224

translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'

[Oryza sativa]

Seq. No. 171557

Seq. ID jC-atX24010Q1E1A10a1

Method BLASTN
NCBI GI g3228516
BLAST score 67
E value 1.0e-29
Match length 95
% identity 93

NCBI Description Arabidopsis thaliana ETTIN gene, complete cds

Seq. No. 171558

Seq. ID jC-atX24011Q1E1A07a1

Method BLASTN
NCBI GI g2264313
BLAST score 131
E value 1.0e-67
Match length 235
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOP10, complete sequence [Arabidopsis thaliana]

Seq. No. 171559

Seq. ID jC-atX24014Q1E1D01a1

Method BLASTX
NCBI GI g2129742
BLAST score 327
E value 2.0e-30
Match length 78
% identity 76

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 171560

Seq. ID jC-atX24014Q1E1D04a1

Method BLASTX
NCBI GI g4105782
BLAST score 278
E value 1.0e-24
Match length 63
% identity 78

% identity

NCBI Description

100

thaliana]





```
NCBI Description
                 (AF049922) PGP169-12 [Petunia x hybrida]
                   171561
Seq. No.
                   jC-atX24015Q1E1F09a1
Seq. ID
Method
                  BLASTN
                  g3985952
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
                   98
Match length
                   84
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MRC8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171562
Seq. ID
                   jC-atX24015Q1E1G10a1
Method
                  BLASTN
NCBI GI
                  g2584827
BLAST score
                   68
                   3.0e-30
E value
                  144
Match length
                   84
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                   171563
                   jC-atX24015Q1E1H03a1
Seq. ID
Method
                  BLASTX
                  g464720
NCBI GI
BLAST score
                   247
E value
                   6.0e-21
Match length
                   50
% identity
                   96
NCBI Description 40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) ribosomal
                  protein S28 [Arabidopsis thaliana]
Seq. No.
                   171564
Seq. ID
                   jC-atX24015Q1E1H07a1
Method
                   BLASTN
NCBI GI
                   q4581138
BLAST score
                   434
E value
                   0.0e+00
Match length
                   434
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
                   sequence, complete sequence
Seq. No.
                   171565
Seq. ID
                   jC-atX24016Q1E1B10a1
Method
                  BLASTX
NCBI GI
                   q4468805
BLAST score
                   486
E value
                   4.0e-49
Match length
                   94
```

(AL035601) auxin-responsive GH3-like protein [Arabidopsis



```
Seq. No.
                   171566
                   jC-atX24016Q1E1H09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3341671
                   435
BLAST score
                   0.0e + 00
E value
                   435
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC F16B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171567
                   jC-atX24018Q1E1A08a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4262221
                   81
BLAST score
                   6.0e - 38
E value
Match length
                   145
                   89
% identity
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171568
                   jC-atX24018Q1E1B11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4584531
                   78
BLAST score
E value
                   3.0e-36
Match length
                   142
                   89
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
NCBI Description
                   (ESSA project)
                   171569
Seq. No.
                   jC-atX24019Q1E1C01a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4325365
BLAST score
                   117
                   3.0e-59
E value
                   258
Match length
                   86
% identity
NCBI Description Arabidopsis thaliana BAC T3H13
                   171570
Seq. No.
                   jC-atX24019Q1E1F06a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2924729
BLAST score
                   84
```

7.0e-40 E value 88 Match length 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MNA5, complete sequence [Arabidopsis thaliana]

171571 Seq. No.

jC-atX24020Q1E1H10a1 Seq. ID

Method BLASTN



NCBI GI g2154716
BLAST score 160
E value 7.0e-85
Match length 272
% identity 89

NCBI Description A.thaliana mRNA for Kap alpha protein

Seq. No. 171572

Seq. ID jC-atX24023Q1E1E09a1

Method BLASTN
NCBI GI g2827513
BLAST score 149
E value 4.0e-78
Match length 408
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16

(ESSAII project)

Seq. No. 171573

Seq. ID jC-atX24023Q1E1F01a1

Method BLASTN
NCBI GI g2570223
BLAST score 110
E value 3.0e-55
Match length 182
% identity 90

NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171574

Seq. ID jC-atX24023Q1E1H06b1

Method BLASTN
NCBI GI g4589435
BLAST score 50
E value 2.0e-19
Match length 154

% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOE17, complete sequence

Seq. No. 171575

Seq. ID jC-atX24024Q1E1F03a1

Method BLASTN
NCBI GI 94589438
BLAST score 83
E value 5.0e-39
Match length 192
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ2, complete sequence

Seq. No. 171576

Seq. ID jC-atX24024Q1E1F11a1

Method BLASTN
NCBI GI g3046852
BLAST score 192
E value 1.0e-104

23442

E value

Match length

% identity

0.0e+00

368

94



```
232
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MQJ16, complete sequence [Arabidopsis thaliana]
                   171577
Seq. No.
Seq. ID
                   jC-atX24025Q1E1A03a1
Method
                  BLASTX
NCBI GI
                  g4006934
BLAST score
                   356
E value
                   8.0e - 34
Match length
                   68
% identity
                   100
NCBI Description
                 (AJ012571) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  171578
                   jC-atX24025Q1E1G08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2795802
BLAST score
                   159
E value
                   3.0e-84
                   303
Match length
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F17A14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171579
Seq. ID
                   jC-atX24026Q1E1C01a1
Method
                  BLASTN
NCBI GI
                   q4741941
BLAST score
                   112
E value
                   2.0e-56
Match length
                   208
% identity
                  88
NCBI Description
                  Arabidopsis thaliana Lhca5 protein (Lhca5) mRNA, complete
Seq. No.
                   171580
Seq. ID
                   jC-atX24026Q1E1F07a1
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  214
E value
                  1.0e-117
Match length
                  226
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
Seq. No.
                  171581
Seq. ID
                   jC-atX24026Q1E1G02a1
Method
                  BLASTN
NCBI GI
                  g3449327
BLAST score
                  360
```

23443

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 171582 Seq. ID jC-atX24026Q1E1G07a1 Method BLASTN g3510345 NCBI GI BLAST score 18 E value 3.5e + 00Match length 268 82 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana] Seq. No. 171583 jC-atX24026Q1E1H03a1 Seq. ID Method BLASTN g3687221 NCBI GI BLAST score 159 3.0e-84 E value 255 Match length 91 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 171584 Seq. ID jC-atX24027Q1E1F03a1 Method BLASTX NCBI GI g4335719 BLAST score 169 6.0e-12 E value Match length 45 % identity 58 NCBI Description (AC006248) putative RING-H2 finger protein RHG1a [Arabidopsis thaliana] Seq. No. 171585 Seq. ID jC-atX24027Q1E1G01a1 Method BLASTN NCBI GI q4455339 BLAST score 446 E value 0.0e+00Match length 446 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project) Seq. No. 171586 Seq. ID jC-atX24028Q1E1C12a1 Method BLASTN NCBI GI q2828184 BLAST score 133 E value 8.0e-69 Match length 181

% identity 93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MSN9, complete sequence [Arabidopsis thaliana]



Seq. No. 171587

Seq. ID jC-atX24029Q1E1H03a1

Method BLASTN
NCBI GI 94753195
BLAST score 335
E value 0.0e+00
Match length 359
% identity 98

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 171588

Seq. ID jC-atX24030Q1E1F08a1

Method BLASTN
NCBI GI g2264367
BLAST score 56
E value 6.0e-23

Match length 155 % identity 92

NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 171589

Seq. ID , jC-atX24032Q1E1B04a1

Method BLASTN
NCBI GI g4218109
BLAST score 90
E value 4.0e-43
Match length 250
% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16

(ESSAII project)

Seq. No. 171590

Seq. ID jC-atX24033Q1E1A11a1

Method BLASTN
NCBI GI g3366536
BLAST score 424
E value 0.0e+00
Match length 424
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T25N2O,

complete sequence [Arabidopsis thaliana]

Seq. No. 171591

Seq. ID jC-atX24034Q1E1E09a1

Method BLASTN
NCBI GI g2264314
BLAST score 137
E value 3.0e-71
Match length 230
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 171592

Seq. ID jC-atX24036Q1E1H01b1



Method BLASTN
NCBI GI g3228389
BLAST score 46
E value 6.0e-17
Match length 170
% identity 82

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 171593

Seq. ID jC-atX24037Q1E1F10b1

Method BLASTX
NCBI GI 94432832
BLAST score 576
E value 1.0e-59
Match length 148
% identity 80

NCBI Description (AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No. 171594

Seq. ID jC-atX24038Q1E1A02a1

Method BLASTN
NCBI GI g2337888
BLAST score 234
E value 1.0e-129
Match length 274

% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 171595

Seq. ID jC-atX24038Q1E1A08b1

Method BLASTN
NCBI GI g2618683
BLAST score 56
E value 8.0e-23
Match length 182

% identity 86
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171596

Seq. ID jC-atX24038Q1E1D03a1

Method BLASTN
NCBI GI g2494106
BLAST score 366
E value 0.0e+00
Match length 397
% identity 97

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171597

Seq. ID jC-atX24038Q1E1G07a1

Method BLASTN NCBI GI g3702735 BLAST score 371



```
E value
                   0.0e + 00
Match length
                   383
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQL5, complete sequence [Arabidopsis thaliana]
                   171598
Seq. No.
                   jC-atX24040Q1E1B12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4406752
BLAST score
                   354
                   0.0e + 00
E value
                   408
Match length
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F19B11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   171599
Seq. No.
                   jC-atX24040Q1E1D06a2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4063735
BLAST score
                   121
E value
                   1.0e-61
Match length
                  236
                   90
% identity
                  Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
                   171600
Seq. No.
Seq. ID
                   jC-atX24041Q1E1A09a1
Method
                  BLASTX
NCBI GI
                   g4006898
BLAST score
                   267
E value
                   1.0e-23
Match length
                   68
% identity
                   78
NCBI Description
                  (Z99708) splicing factor-like protein [Arabidopsis
                  thalianal
Seq. No.
                   171601
Seq. ID
                   jC-atX24041Q1E1G07a1
Method
                  BLASTN
NCBI GI
                   g4519183
BLAST score
                   348
E value
                   0.0e+00
Match length
                   364
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15C23, complete sequence
Seq. No.
                   171602
Seq. ID
                   jC-atX24043Q1E1C12b1
```

Method BLASTN NCBI GI g4589436 BLAST score 40 E value 4.0e-13 Match length 140



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPA22, complete sequence
Seq. No.
                   171603
Seq. ID
                   jC-atX24043Q1E1G11a1
Method
                  BLASTN
NCBI GI
                  g2351068
BLAST score
                  155
E value
                   8.0e-82
Match length
                   351
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRH10, complete sequence [Arabidopsis thaliana]
                   171604
Seq. No.
Seq. ID
                   jC-atX24044Q1E1B02a1
Method
                  BLASTN
NCBI GI
                  q2264302
BLAST score
                   345
E value
                   0.0e+00
Match length
                   357
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171605
Seq. ID
                   jC-atX24044Q1E1C04a1
Method
                  BLASTX
NCBI GI
                  g2129517
BLAST score
                  455
E value
                   2.0e-45
Match length
                  85
% identity
                  100
NCBI Description
                  24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis
                  thaliana
Seq. No.
                   171606
Seq. ID
                   jC-atX24045Q1E1B03a1
Method
                  BLASTX
NCBI GI
                  q2827714
BLAST score
                  553
E value
                   7.0e-57
Match length
                  104
% identity
                   100
NCBI Description
                  (AL021684) receptor protein kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                  171607
```

Seq. ID jC-atX24045Q1E1C06a1

Method BLASTN
NCBI GI g4314354
BLAST score 412
E value 0.0e+00
Match length 412
% identity 57

NCBI Description Arabidopsis thaliana chromosome II BAC T9I22 genomic

NCBI Description



```
sequence, complete sequence [Arabidopsis thaliana]
```

```
171608
Seq. No.
                  jC-atX24045Q1E1D01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589439
BLAST score
                  272
                  1.0e-151
E value
                  308
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQM1, complete sequence
                  171609
Seq. No.
                  jC-atX24046Q1E1H03b1
Seq. ID
                  BLASTX
Method
                  g3193292
NCBI GI
BLAST score
                  140
                   4.0e-09
E value
                  56
Match length
                  54
% identity
                  (AF069298) similar to ATPases associated with various
NCBI Description
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                  [Arabidopsis thaliana]
Seq. No.
                  171610
Seq. ID
                  jC-atX24046Q1E1H07b1
Method
                  BLASTX
NCBI GI
                  q2335099
BLAST score
                  203
E value
                   4.0e-16
                  72
Match length
% identity
                   54
                 (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171611
Seq. ID
                   jC-atX24047Q1E1C07b1
Method
                  BLASTX
NCBI GI
                   q2129604
BLAST score
                   294
E value
                   4.0e-27
Match length
                   60
                   97
% identity
NCBI Description
                  GTP-binding protein 1 - Arabidopsis thaliana
                   >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -
                  Arabidopsis thaliana >gi 1184981 (U46924) ATGB1
                   [Arabidopsis thaliana]
Seq. No.
                   171612
Seq. ID
                   jC-atX24048Q1E2A06a1
Method
                  BLASTX
NCBI GI
                   g4455367
                  772
BLAST score
E value
                  1.0e-82
Match length
                  153
% identity
```

(AL035524) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  171613
                  jC-atX24048Q1E2C12b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2264314
BLAST score
                  134
                  2.0e-69
E value
                  264
Match length
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
                   171614
Seq. No.
                   jC-atX24048Q1E2G07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  273
                   1.0e-152
E value
                   309
Match length
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   171615
Seq. No.
                   jC-atX24048Q1E2G10a1
Seq. ID
Method
                  BLASTN
                   g3445196
NCBI GI
BLAST score
                   76
                   5.0e - 35
E value
                   168
Match length
                   86
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20K9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   171616
Seq. No.
Seq. ID
                   jC-atX24049Q1E1A01a1
Method
                   BLASTN
NCBI GI
                   q3600062
BLAST score
                   169
E value
                   2.0e-90
Match length
                   169
% identity
                   100
NCBI Description Arabidopsis thaliana BAC T25C13
                   171617
Seq. No.
Seq. ID
                   jC-atX24049Q1E1D04a1
Method
                   BLASTX
NCBI GI
                   q99749
BLAST score
                   482
```

E value 1.0e-48 Match length 121 % identity

probable serine/threonine-specific protein kinase ATPK64 NCBI Description

(EC 2.7.1.-) - Arabidopsis thaliana

>gi 217843 dbj BAA01731 (D10937) protein kinase

[Arabidopsis thaliana]



```
Seq. No.
                  171618
                  jC-atX24049Q1E2C09b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2373405
BLAST score
                  169
                  2.0e-12
E value
                  46
Match length
% identity
                  44
                  (D85194) no known genes showing a high homology to 4B-1
NCBI Description
                  clone sequence were found in the EMBL database. Orf was 640
                  amino acid long and contained a proline and alanine repeat
                   [Arabidopsis thaliana]
Seq. No.
                  171619
                  jC-atX24050Q1E1B05a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3046850
BLAST score
                  101
E value
                  1.0e-49
Match length
                  260
                  85
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24G6, complete sequence [Arabidopsis thaliana]
                  171620
Seq. No.
Seq. ID
                  jC-atX24050Q1E1D07b1
Method
                  BLASTN
NCBI GI
                  g2854069
                  69
BLAST score
                  7.0e-31
E value
Match length
                  121
                  89
% identity
NCBI Description
                  Arabidopsis thaliana putative histone deacetylase (HD2)
                  mRNA, complete cds
Seq. No.
                  171621
Seq. ID
                  jC-atX24050Q1E1F10a2
Method
                  BLASTN
NCBI GI
                  q4249393
BLAST score
                  98
                  5.0e-48
E value
Match length
                  200
                  85
% identity
                  Arabidopsis thaliana chromosome II BAC T9J23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171622
Seq. ID
                  jC-atX24052Q1E2B11a1
```

Method BLASTN NCBI GI g2264320 BLAST score 130 E value 2.0e-67 Match length 130 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXI10, complete sequence [Arabidopsis thaliana]



Seq. No. 171623 Seq. ID jC-atX24053Q1E1B04a1 Method BLASTN NCBI GI q4510360 BLAST score 105 E value 4.0e-52 219 Match length 85 % identity Arabidopsis thaliana chromosome II BAC F11F19 genomic NCBI Description sequence, complete sequence Seq. No. 171624 jC-atX24053Q1E1E03a1 Seq. ID Method BLASTN NCBI GI g4220643 BLAST score 263 E value 1.0e-146 371 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MWD22, complete sequence [Arabidopsis thaliana] Seq. No. 171625 jC-atX24054Q1E1C09a1 Seq. ID Method BLASTN NCBI GI g1236618 BLAST score 76 E value 9.0e - 35208 Match length % identity 84 Arabidopsis thaliana glutamate decarboxylase (GAD2) mRNA, NCBI Description complete cds 171626 Seq. No. jC-atX24054Q1E1D02b1 Seq. ID Method BLASTN NCBI GI g4757411 83 3.0e-39 111 95 % identity MXC7, complete sequence Seq. No. 171627

BLAST score

E value Match length

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

jC-atX24055Q1E1F05a1 Seq. ID

Method BLASTN NCBI GI g3250673 BLAST score 83 3.0e - 39E value Match length 107 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5

(ESSAII project)

Seq. No. 171628

Seq. ID jC-atX24055Q1E1F05b1



Method BLASTN
NCBI GI g3250673
BLAST score 109
E value 8.0e-55
Match length 130
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5

(ESSAII project)

Seq. No. 171629

Seq. ID jC-atX24056Q1E1C01a2

Method BLASTN
NCBI GI g1399182
BLAST score 62
E value 2.0e-26
Match length 114

% identity 89

NCBI Description Arabidosis thaliana lycopene beta cyclase mRNA, complete

cds

Seq. No. 171630

Seq. ID jC-atX24056Q1E1E06b1

Method BLASTN
NCBI GI g2914688
BLAST score 81
E value 5.0e-38
Match length 125
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171631

Seq. ID jC-atX24056Q1E2D11a1

Method BLASTN
NCBI GI g4199934
BLAST score 86
E value 4.0e-41
Match length 126
% identity 92

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 171632

Seq. ID jC-atX24056Q1E2E07a1

Method BLASTN
NCBI GI g2351062
BLAST score 366
E value 0.0e+00
Match length 390
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 171633

Seq. ID jC-atX24056Q1E2G06a1

Method BLASTN NCBI GI 94185128



```
140
BLAST score
                   4.0e-73
E value
                   168
Match length
                   96
% identity
                  Arabidopsis thaliana chromosome II P1 MSF3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171634
Seq. No.
                   jC-atX24058Q1E1D11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3451055
BLAST score
                   284
E value
                   1.0e-159
                   365
Match length
% identity
                   94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20
                   (ESSAII project)
Seq. No.
                   171635
Seq. ID
                   jC-atX24058Q1E1E02a1
Method
                   BLASTN
NCBI GI
                   g2264306
                   52
BLAST score
                   3.0e-20
E value
Match length
                   224
                   89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
                   171636
Seq. No.
                   jC-atX24058Q1E1E07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4589443
BLAST score
                   405
E value
                   0.0e+00
Match length
                   452
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MVP7, complete sequence
                   171637
Seq. No.
Seq. ID
                   jC-atX24058Q1E1H06a1
Method
                   BLASTN
NCBI GI
                   g3150395
BLAST score
                   433
E value
                   0.0e + 00
Match length
                   462
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9D9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 171638

Seq. ID jC-atX24059Q1E1D01a1

Method BLASTN NCBI GI g3643588 BLAST score 261 E value 1.0e-145



```
Match length 301 % identity 97 NCBI Description Ara seq Seq. No. 171 Seq. ID jC-Method BLA NCBI GI g46 BLAST score 191
```

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

171639 jC-atX24059Q1E1D07a1

Method BLASTN
NCBI GI 94662609
BLAST score 191
E value 1.0e-103
Match length 332
% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 171640

Seq. ID jC-atX24059Q1E1D07b1

Method BLASTN
NCBI GI 94662609
BLAST score 285
E value 1.0e-159
Match length 402
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 171641

Seq. ID jC-atX24059Q1E1G04b1

Method BLASTX
NCBI GI g1255951
BLAST score 149
E value 4.0e-10
Match length 41
% identity 66

NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 171642

Seq. ID jC-atX24060Q1E1C08a1

Method BLASTX
NCBI GI g119143
BLAST score 169
E value 6.0e-12
Match length 33
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 171643



jC-atX24060Q1E1C09a1 Seq. ID Method BLASTN g3133272 NCBI GI BLAST score 228 E value 1.0e-125 308 Match length 93 % identity Genomic sequence for Arabidopsis thaliana BAC T17H7, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 171644 jC-atX24060Q1E1C10a1 Seq. ID Method BLASTX g1653665 NCBI GI 151 BLAST score 1.0e-09 E value Match length 112 % identity 30 (D90915) peptide chain release factor [Synechocystis sp.] NCBI Description Seq. No. 171645 Seq. ID jC-atX24060Q1E1D07a1 Method BLASTN NCBI GI g2815519 BLAST score 394 0.0e+00E value Match length 461 % identity 100 Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 171646 jC-atX24061Q1E1B04a1 Seq. ID Method BLASTN NCBI GI q3941423 BLAST score 201 E value 1.0e-109 Match length 277 % identity 93 NCBI Description Arabidopsis thaliana putative transcription factor (MYB17) mRNA, partial cds 171647 Seq. No. Seq. ID jC-atX24062Q1E1A04b1 Method BLASTN NCBI GI q3366536 284 E value 1.0e-158 Match length 488 100 % identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC T25N2O, complete sequence [Arabidopsis thaliana]

BLAST score

171648 Seq. No.

Seq. ID jC-atX24062Q1E1F09a1

BLASTN Method NCBI GI g2618683

23456

E value

Match length

97



```
BLAST score
                  138
E value
                  5.0e-72
                  154
Match length
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  jC-atX24063Q1E1A04a1
Seq. ID
                  BLASTX
Method
                  g3128188
NCBI GI
                  271
BLAST score
                  8.0e-24
E value
                  76
Match length
                  62
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171650
Seq. ID
                  jC-atX24063Q1E1G08b1
Method
                  BLASTN
NCBI GI
                  q3406034
                  308
BLAST score
E value
                  1.0e-173
Match length
                  308
                  100
% identity
NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  171651
Seq. ID
                   jC-atX24064Q1E1D05a1
Method
                  BLASTX
NCBI GI
                  q3617741
BLAST score
                  249
E value
                  2.0e-21
Match length
                  51
% identity
                  100
                  (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   171652
Seq. ID
                   jC-atX24064Q1E1D05b1
Method
                  BLASTX
                  g3617741
NCBI GI
                   249
BLAST score
                   2.0e-21
E value
Match length
                   51
                   100
% identity
                  (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                   171653
Seq. No.
                   jC-atX24064Q1E1G08a1
Seq. ID
                   BLASTX
Method
                  g2618686
NCBI GI
                   235
BLAST score
                   1.0e-19
```



% identity 46
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 171654
Seq. ID jC-atX24065Q1E1C04a1
Method BLASTN

NCBI GI g4558586
BLAST score 309
E value 1.0e-173
Match length 325
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence,

complete sequence

Seq. No. 171655

Seq. ID jC-atX24066Q1E1A03a1

Method BLASTX
NCBI GI g544424
BLAST score 204
E value 6.0e-16
Match length 39
% identity 97

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi 4567224 gb AAD23639.1_AC007119_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 171656

Seq. ID jC-atX24066Q1E1A03b1

Method BLASTX
NCBI GI g544424
BLAST score 204
E value 6.0e-16
Match length 39
% identity 97

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755 pir S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301 emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 171657

Seq. ID jC-atX24066Q1E1B01b1

Method BLASTX
NCBI GI g2244784
BLAST score 351
E value 1.0e-33
Match length 155
% identity 53

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 171658



Seq. ID jC-atX24066Q1E1B11a1

Method BLASTN
NCBI GI g3445196
BLAST score 291
E value 1.0e-163
Match length 307
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171659

Seq. ID jC-atX24066Q1E1D09b1

Method BLASTX
NCBI GI g2317905
BLAST score 426
E value 6.0e-42
Match length 137
% identity 67

NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 171660

Seq. ID jC-atX24066Q1E1E11a1

Method BLASTN
NCBI GI 94220640
BLAST score 191
E value 1.0e-103
Match length 329
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 171661

Seq. ID jC-atX24067Q1E1C09a1

Method BLASTX
NCBI GI g3702333
BLAST score 232
E value 2.0e-19
Match length 49
% identity 88

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 171662

Seq. ID jC-atX24069Q1E1A01a1

Method BLASTN
NCBI GI g3282170
BLAST score 98
E value 4.0e-48
Match length 130
% identity 94

NCBI Description Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171663

Seq. ID jC-atX24069Q1E1D05a1

Method BLASTN NCBI GI g2656029 BLAST score 242



```
E value
                  1.0e-134
Match length
                  322
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
Seq. No.
                  171664
Seq. ID
                  jC-atX24071Q1E1B04a1
Method
                  BLASTN
NCBI GI
                  q4757662
BLAST score
                  364
E value
                  0.0e + 00
Match length
                  382
                  99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
NCBI Description
                  chromosome I, complete sequence
                  171665
Seq. No.
Seq. ID
                  jC-atX24071Q1E1B04b1
Method
                  BLASTX
NCBI GI
                  q4522009
BLAST score
                  326
E value
                  4.0e-30
Match length
                  78
% identity
                  81
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  171666
                  jC-atX24071Q1E1B12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241939
BLAST score
                  346
E value
                  0.0e + 00
Match length
                  380
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T26J13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171667
Seq. No.
Seq. ID
                  jC-atX24071Q1E1F01a1
Method
                  BLASTN
NCBI GI
                  g3510345
BLAST score
                  254
E value
                  1.0e-141
                  403
Match length
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ8, complete sequence [Arabidopsis thaliana]
                  171668
Seq. No.
Seq. ID
                  jC-atX24072Q1E1E08a1
Method
                  BLASTN
NCBI GI
                  g3790590
BLAST score
                  245
E value
                  1.0e-135
```

348

95

Match length % identity



```
NCBI Description Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA,
                  partial cds
                  171669
Seq. No.
Seq. ID
                  jC-atX24074Q1E1D08a1
                  BLASTX
Method
                  g2497486
NCBI GI
                  413
BLAST score
                  2.0e-40
E value
                  82
Match length
                  99
% identity
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                  KINASE) >qi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                  thaliana]
                  171670
Seq. No.
                  jC-atX24075Q1E1G12b1
Seq. ID
                  BLASTX
Method
                  g4314359
NCBI GI
BLAST score
                  428
E value
                  4.0e-42
                  98
Match length
                  88
% identity
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
                  171671
Seq. No.
Seq. ID
                  jC-atX24076Q1E1D04b1
                  BLASTN
Method
                  g4539353
NCBI GI
BLAST score
                  60
E value
                  1.0e-25
Match length
                  116
                  88
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F25I24
                  (ESSA project)
                  171672
Seq. No.
Seq. ID
                  jC-atX24076Q1E1G07b1
                  BLASTN
Method
NCBI GI
                  q2407799
BLAST score
                  34
E value
                  4.0e-10
Match length
                  62
% identity
                  89
NCBI Description Arabidopsis thaliana mRNA for histone H2A.F/Z
                  171673
Seq. No.
                  jC-atX24078Q1E1B01b1
Seq. ID
```

Method BLASTX q4586062 NCBI GI BLAST score 191 4.0e-15 E value 55 Match length % identity

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 171674

23461



jC-atX24078Q1E1H03a1 Seq. ID BLASTX Method g3047086 NCBI GI BLAST score 244 9.0e-21 E value 68 Match length 63 % identity (AF058914) similar to reverse transcriptase (Pfam: NCBI Description transcript fact.hmm, score: 72.31) [Arabidopsis thaliana] 171675 Seq. No. Seq. ID jC-atX24081Q1E1H09a1 BLASTX Method g3367522 NCBI GI BLAST score 426 5.0e-42E value 81 Match length 100 % identity (AC004392) EST gb T04691 comes from this gene. [Arabidopsis NCBI Description thaliana] 171676 Seq. No. jC-atX24083Q1E1D11a1 Seq. ID BLASTN Method q509418 NCBI GI BLAST score 205 1.0e-111 E value 290 Match length 92 % identity NCBI Description A.thaliana (Landsberg erecta) ABI1 gene 171677 Seq. No. jC-atX24088Q1E1B01b1 Seq. ID BLASTX Method NCBI GI q4240122 BLAST score 165 5.0e-12 E value 40 Match length 80 % identity NCBI Description (AB007802) cytochrome b5 [Arabidopsis thaliana] 171678 Seq. No. jC-atX24095Q1E1D10b1 Seq. ID Method BLASTX q3643611 NCBI GI BLAST score 337 5.0e-62 E value 150 Match length 75 % identity NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. ID jC-atX24099Q1E1B12b1

171679

Method BLASTN
NCBI GI g4544435
BLAST score 47
E value 1.0e-17

Seq. No.

23462



107 Match length 87 % identity

Arabidopsis thaliana chromosome II BAC F14M13 genomic NCBI Description

sequence, complete sequence

171680 Seq. No.

Seq. ID jC-atX24099Q1E1D06b1

Method BLASTN g3643588 NCBI GI 53

BLAST score

3.0e-21 E value 182 Match length 92 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

171681 Seq. No.

Seq. ID jC-atX24101Q1E1C02b1

Method BLASTX NCBI GI g2935342 692 BLAST score 4.0e-73 E value 163 Match length 87 % identity

(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 NCBI Description

[Arabidopsis thaliana]

171682 Seq. No.

Seq. ID jC-atX24102Q1E1E03a1

Method BLASTN NCBI GI g2656029 BLAST score 64 E value 5.0e-28 124 Match length 88 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQB2

171683 Seq. No.

Seq. ID jC-atX24102Q1E1F02a1

Method BLASTN NCBI GI g1483214 BLAST score 116 1.0e-58 E value Match length 231 % identity 87

NCBI Description A.thaliana mRNA for chloroplast FtsH protease

Seq. No. 171684

Seq. ID jC-atX24102Q1E1F12a1

Method BLASTN NCBI GI g3445415 BLAST score 442 0.0e+00E value Match length 446 % identity 100

NCBI Description Arabidopsis thaliana mRNA for DEAD box-like RNA helicase,



partial

```
171685
Seq. No.
Seq. ID
                  jC-atX24102Q1E1H03a1
Method
                  BLASTN
                  g4580365
NCBI GI
BLAST score
                  386
                  0.0e+00
E value
                  390
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome I BAC F3F20 genomic
NCBI Description
                  sequence, complete sequence
                  171686
Seq. No.
Seq. ID
                  jC-atX24102Q1E1H09a1
Method
                  BLASTN
                  g4757678
NCBI GI
                  35
BLAST score
                  2.0e-10
E value
Match length
                  163
% identity
                  80
NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic
                  sequence, complete sequence
                  171687
Seq. No.
Seq. ID
                  jC-atX24103Q1E1D08b1
Method
                  BLASTX
                  g3511223
NCBI GI
BLAST score
                  787
                  3.0e-84
E value
Match length
                  159
% identity
                  96
NCBI Description (AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]
                  171688
Seq. No.
Seq. ID
                  jC-atX24103Q1E1E06a1
                  BLASTN
Method
NCBI GI
                  g2656027
BLAST score
                  45
                  1.0e-16
E value
Match length
                  85
% identity
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJH22
Seq. No.
                  171689
Seq. ID
                   jC-atX24103Q1E1E07a2
                  BLASTX
Method
NCBI GI
                  g115470
BLAST score
                  50
E value
                  2.0e-25
Match length
                   63
                  98
% identity
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                  DEHYDRATASE) >gi_320554_pir__$28412 carbonate dehydratase
```

(EC 4.2.1.1) precursor - Arabidopsis thaliana

>gi 14343 emb CAA46508 (X65541) carbonic anhydrase



[Arabidopsis thaliana]

171690 Seq. No. Seq. ID jC-atX24103Q1E2B09a1 Method BLASTN g2924733 NCBI GI 312 BLAST score 1.0e-175 E value Match length 332 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 171691

Seq. ID jC-atX24103Q1E2H09b1

Method BLASTN
NCBI GI g3643588
BLAST score 478
E value 0.0e+00
Match length 486
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171692

Seq. ID jC-atX24103Q1E2H12b1

Method BLASTX
NCBI GI g2119846
BLAST score 733
E value 6.0e-78
Match length 139
% identity 99

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 171693

Seq. ID jC-atX24104Q1E2G08a1

Method BLASTN
NCBI GI g3241926
BLAST score 261
E value 1.0e-145
Match length 452
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 171694

Seq. ID jC-atX24105Q1E1E07a1

Method BLASTN
NCBI GI g4406752
BLAST score 347
E value 0.0e+00



```
Match length
                  351
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F19B11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171695
Seq. No.
Seq. ID
                  jC-atX24106Q1E1A01a1
                  BLASTN
Method
                  g3193282
NCBI GI
BLAST score
                  318
                  1.0e-179
E value
                  395
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana BAC T14P8
                  171696
Seq. No.
Seq. ID
                  jC-atX24106Q1E1A01b1
Method
                  BLASTN
                  g3193282
NCBI GI
BLAST score
                  280
E value
                  1.0e-156
                  478
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana BAC T14P8
                  171697
Seq. No.
Seq. ID
                  jC-atX24106Q1E1F07a1
Method
                  BLASTN
NCBI GI
                  g4415905
BLAST score
                  220
E value
                  1.0e-120
                  268
Match length
                  96
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171698
Seq. No.
Seq. ID
                  jC-atX24106Q1E1F08a1
                  BLASTN
Method
NCBI GI
                  q1916911
BLAST score
                  398
E value
                  0.0e + 00
Match length
                  402
                  100
% identity
NCBI Description Arabidopsis thaliana transcription factor inhibitor I kappa
                  B homolog (nim1) gene, complete cds
Seq. No.
                  171699
Seq. ID
                  jC-atX24107Q1E1E08a1
Method
                  BLASTN
```

Method BLASTN
NCBI GI g4049332
BLAST score 365
E value 0.0e+00
Match length 373
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4

(ESSAII project)



Seq. No. 171700 Seq. ID jC-atX

jC-atX24107Q1E1H05a1

Method BLASTN
NCBI GI 94249393
BLAST score 206
E value 1.0e-112
Match length 338
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171701

Seq. ID jC-atX24109Q1E1D07a1

Method BLASTN
NCBI GI g642161
BLAST score 48
E value 3.0e-18
Match length 107
% identity 94

NCBI Description A.thaliana gene for chloroplast ribosomal protein S13

Seq. No. 171702

Seq. ID jC-atX24109Q1E1D07b1

Method BLASTN
NCBI GI g642161
BLAST score 48
E value 3.0e-18
Match length 107
% identity 94

NCBI Description A.thaliana gene for chloroplast ribosomal protein S13

Seq. No. 171703

Seq. ID jC-atX24109Q1E1F05a2

Method BLASTN
NCBI GI g3985934
BLAST score 176
E value 2.0e-94
Match length 265
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 171704

Seq. ID jC-atX24109Q1E1G11a1

Method BLASTN
NCBI GI 94733952
BLAST score 308
E value 1.0e-173
Match length 348
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No. 171705

Seq. ID jC-atX24110Q1E1B07b1

Method BLASTN



NCBI GI g3046847 BLAST score 278 E value 1.0e-155 Match length 462 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 171706

Seq. ID jC-atX24110Q1E1D06a1

Method BLASTN
NCBI GI g473258
BLAST score 61
E value 5.0e-26
Match length 152

% identity 84
NCBI Description Arabidopsis thaliana Ser/Thr protein phosphatase mRNA,

complete cds

Seq. No. 171707

Seq. ID jC-atX24110Q1E1D07a1

Method BLASTN
NCBI GI g2264303
BLAST score 237
E value 1.0e-131
Match length 318
% identity 78

% identity 78
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBB18, complete sequence [Arabidopsis thaliana]

Seq. No. 171708

Seq. ID jC-atX24113Q1E1A03a1

Method BLASTN
NCBI GI g2618605
BLAST score 453
E value 0.0e+00
Match length 453
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 171709

Seq. ID jC-atX24113Q1E1E07b1

Method BLASTN
NCBI GI g4406752
BLAST score 410
E value 0.0e+00
Match length 465
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F19B11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171710

Seq. ID jC-atX24115Q1E1C05a1

Method BLASTN NCBI GI g3449334

BLAST score 77

E value

Match length

6.0e-12

78



```
3.0e-35
E value
                  312
Match length
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                  171711
Seq. No.
                  jC-atX24115Q1E1H01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4490734
BLAST score
                  365
                  0.0e+00
E value
                  418
Match length
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
                                                                      (ESSA
NCBI Description
                  project)
                  171712
Seq. No.
                  jC-atX24116Q1E1B12a1
Seq. ID
                  BLASTX
Method
                  g4325375
NCBI GI
                  236
BLAST score
                  8.0e-20
E value
                  52
Match length
                  92
% identity
                  (AF128396) similar to arginases (Pfam: PF00491,
NCBI Description
                  Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]
Seq. No.
                  171713
                  jC-atX24120Q1E1H03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3133272
BLAST score
                  41
                  5.0e-14
E value
                  129
Match length
                  81
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T17H7,
                  complete sequence [Arabidopsis thaliana]
                  171714
Seq. No.
Seq. ID
                   jC-atX24121Q1E1C10a1
Method
                  BLASTX
NCBI GI
                  g4115364
BLAST score
                   243
E value
                   7.0e-21
Match length
                   53
% identity
                   85
                  (AC005957) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   171715
Seq. ID
                   jC-atX24126Q1E1A02a1
                  BLASTN
Method
                  g4115352
NCBI GI
                   37
BLAST score
```

23469



% identity 44

NCBI Description Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171716

Seq. ID jC-atX24128Q1E1B02b1

Method BLASTN
NCBI GI g2264317
BLAST score 85
E value 2.0e-40
Match length 165
% identity 44

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 171717

Seq. ID jC-atX24134Q1E1D04b1

Method BLASTN
NCBI GI g3461810
BLAST score 92
E value 3.0e-44

Match length 308 % identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T17M13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171718

Seq. ID jC-atX24135Q1E1G03b1

Method BLASTX
NCBI GI g3687243
BLAST score 260
E value 1.0e-22
Match length 63
% identity 81

NCBI Description (AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No. 171719

Seq. ID jC-atX24137Q1E1F06a1

Method BLASTN
NCBI GI g3805839
BLAST score 329
E value 0.0e+00
Match length 341
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14

(ESSAII project)

Seq. No. 171720

Seq. ID jC-atX25001Q1E2A05a1

Method BLASTN
NCBI GI g2584827
BLAST score 245
E value 1.0e-135
Match length 300
% identity 95

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,

% identity

NCBI Description

100



complete sequence [Arabidopsis thaliana]

Seq. No. 171721 jC-atX25001Q1E2A06b1 Seq. ID BLASTX Method NCBI GI q1076427 BLAST score 206 7.0e-24E value 66 Match length 73 % identity ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis NCBI Description thaliana 171722 Seq. No. Seq. ID jC-atX25001Q1E2B09b1 Method BLASTN q3046851 NCBI GI BLAST score 255 1.0e-141 E value 255 Match length 100 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana] 171723 Seq. No. jC-atX25002Q1E1B06a1 Seq. ID Method BLASTN NCBI GI g3021263 BLAST score 103 5.0e-51E value 176 Match length 92 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 NCBI Description (ESSAII project) 171724 Seq. No. Seq. ID jC-atX25002Q1E1C11b1 Method BLASTN g4691223 NCBI GI 283 BLAST score 1.0e-158 E value Match length 456 % identity 98 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 NCBI Description (ESSA project) Seq. No. 171725 Seq. ID jC-atX25003Q1E1C02b1 Method BLASTN NCBI GI q3212846 BLAST score 247 E value 1.0e-137 247 Match length

23471

Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
171726
Seq. No.
                  jC-atX25003Q1E1C10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377507
BLAST score
                  197
                  7.0e-23
E value
                  79
Match length
                  71
% identity
                  (AF056026) auxin transport protein EIR1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3661620 (AF093241) putative auxin efflux
                  carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459)
                  polar-auxin-transport efflux component AGRAVITROPIC 1
                  [Arabidopsis thaliana] >gi 4206709 (AF086906) root
                  gravitropism control protein [Arabidopsis thaliana]
Seq. No.
                  171727
                  jC-atX25003Q1E1F12b1
Seq. ID
Method
                  BLASTN
                  g3643191
NCBI GI
BLAST score
                  212
E value
                  1.0e-116
                  233
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana unknown mRNA
Seq. No.
                  171728
Seq. ID
                  jC-atX25004Q1E1C01a1
                  BLASTX
Method
NCBI GI
                  g1518540
BLAST score
                  391
E value
                  7.0e-38
Match length
                  83
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  171729
Seq. ID
                  jC-atX25004Q1E1G03b1
Method
                  BLASTX
NCBI GI
                  q4204265
BLAST score
                  220
E value
                  8.0e-18
Match length
                  85
% identity
                  52
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  171730
Seq. ID
                  jC-atX25004Q1E1G08b1
Method
                  BLASTX
NCBI GI
                  g1209703
BLAST score
                  366
E value
                  6.0e - 35
Match length
                  69
```

% identity 97

NCBI Description (U40489) maize gll homolog [Arabidopsis thaliana]

Seq. No. 171731

Seq. ID jC-atX25006Q1E1D07b1

BLAST score

Match length

E value

118

212

8.0e-60



```
Method
                  BLASTX
NCBI GI
                  q535780
BLAST score
                  429
                  9.0e-43
E value
                  82
Match length
                  100
% identity
                 (D26609) transmembrane protein [Arabidopsis thaliana]
NCBI Description
                  171732
Seq. No.
                  jC-atX25006Q1E2D01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1931636
                  239
BLAST score
                  1.0e-132
E value
                  239
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
                  171733
Seq. No.
                  jC-atX25006Q1E2G06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618602
                  49
BLAST score
                  7.0e-19
E value
                  83
Match length
                  90
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  171734
Seq. No.
                  jC-atX25006Q1E2H01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264320
BLAST score
                  136
E value
                  7.0e-71
Match length
                  140
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXI10, complete sequence [Arabidopsis thaliana]
                  171735
Seq. No.
Seq. ID
                  jC-atX25007Q1E1C09a1
Method
                  BLASTN
NCBI GI
                  q2098816
BLAST score
                  160
E value
                  6.0e-85
Match length
                  228
% identity
                  93
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
Seq. No.
                  171736
Seq. ID
                  jC-atX25007Q1E1F06b1
Method
                  BLASTN
NCBI GI
                  g4191771
```

23473

% identity



97 % identity Arabidopsis thaliana chromosome II BAC F3P11 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171737 Seq. No. iC-atX25007Q1E1H10b1 Seq. ID BLASTN Method g2618602 NCBI GI BLAST score 216 E value 1.0e-118 216 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSJ1, complete sequence [Arabidopsis thaliana] 171738 Seq. No. jC-atX25008Q1E1A01b1 Seq. ID BLASTN Method g4589410 NCBI GI 135 BLAST score 5.0e-70E value 212 Match length 97 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: F2015, complete sequence Seq. No. 171739 jC-atX25008Q1E1E04b1 Seq. ID Method BLASTX g1418319 NCBI GI BLAST score 335 5.0e-35 E value 83 Match length % identity NCBI Description (X95965) CER1-like [Arabidopsis thaliana] Seq. No. 171740 Seq. ID jC-atX25008Q1E1F06a1 Method BLASTX NCBI GI q3334756 BLAST score 184 E value 4.0e-14Match length 62 % identity (Y16672) putative arginine/serine-rich splicing factor NCBI Description [Medicago sativa] 171741 Seq. No. jC-atX25008Q1E1H02b1 Seq. ID BLASTX Method NCBI GI g2245118 BLAST score 186 E value 2.0e-14 34 Match length 100

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

NCBI Description

171747

Seq. No.



```
171742
Seq. No.
                  jC-atX25008Q1E1H04b1
Seq. ID
Method
                  BLASTN
                  g4220631
NCBI GI
BLAST score
                  132
E value
                  3.0e-68
                  249
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5J14, complete sequence [Arabidopsis thaliana]
                  171743
Seq. No.
                  jC-atX25009Q1E1A01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3287862
BLAST score
                   428
E value
                  1.0e-42
                  79
Match length
                  100
% identity
                  PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >qi 2289007
NCBI Description
                   (AC002335) trypsin inhibitor 2 precursor isolog
                   [Arabidopsis thaliana]
                  171744
Seq. No.
                  jC-atX25009Q1E1A07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3269280
BLAST score
                  140
                   6.0e-73
E value
Match length
                  264
                  88
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
                   (ESSAII project)
Seq. No.
                  171745
Seq. ID
                   jC-atX25009Q1E1C02b1
Method
                  BLASTX
NCBI GI
                  a585421
BLAST score
                   431
                   5.0e-43
E value
Match length
                   77
% identity
                   100
NCBI Description
                  LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi 541879 pir JQ2391
                   lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana
                  >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]
Seq. No.
                  171746
Seq. ID
                   jC-atX25009Q1E1C04b1
Method
                  BLASTX
NCBI GI
                  q2281095
BLAST score
                  238
E value
                   2.0e-20
Match length
                  67
                   73
% identity
```

(AC002333) cysteine synthase, cpACS1 [Arabidopsis thaliana]



Seq. ID jC-atX25009Q1E1C09b1 BLASTN Method NCBI GI q4757392 BLAST score 246 1.0e-136 E value Match length 246 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: NCBI Description K14A17, complete sequence Seq. No. 171748 Seq. ID jC-atX25009Q1E1C11b1 Method BLASTX g4741950 NCBI GI BLAST score 378 E value 8.0e-37 72 Match length % identity 100 (AF134125) Lhcb2 protein [Arabidopsis thaliana] NCBI Description Seq. No. 171749 jC-atX25009Q1E1E01b1 Seq. ID Method BLASTN NCBI GI g4589434 BLAST score 106 5.0e-53 E value Match length 122 % identity 67 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence 171750 Seq. No. jC-atX25009Q1E1F11a1 Seq. ID BLASTX Method g2244933 NCBI GI 305 BLAST score E value 6.0e-28 Match length 73 81 % identity (Z97339) similar to hypothetical protein YPL211w - yeast NCBI Description [Arabidopsis thaliana] Seq. No. 171751 jC-atX25009Q1E1G10b1 Seq. ID Method BLASTX g729406 NCBI GI BLAST score 190 E value 2.0e-14

Match length 59 % identity 59

NCBI Description ELONGATION FACTOR P (EF-P) >gi 421056 pir S34443 translation elongation factor EF-P - Escherichia coli

>gi_433670_emb_CAA43851_ (X61676) elongation factor P
[Escherichia coli] >gi_536991 (U14003) elongation factor P
[Escherichia coli] >gi_1790590 (AE000487) elongation factor

P (EF-P) [Escherichia coli]



109

33

Match length % identity

```
171752
Seq. No.
Seq. ID
                  jC-atX25009Q1E1H03b1
Method
                  BLASTX
NCBI GI
                  g464720
BLAST score
                  247
                  2.0e-21
E value
                  50
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) ribosomal
NCBI Description
                  protein S28 [Arabidopsis thalīana]
                  171753
Seq. No.
Seq. ID
                  jC-atX25010Q1E1A06b1
Method
                  BLASTX
NCBI GI
                  g461550
                  323
BLAST score
                  2.0e-30
E value
Match length
                  68
                  93
% identity
                  ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_81635_pir__B39732 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma-1 chain precursor, chloroplast -
                  Arabidopsis thaliana >qi 166632 (M61741) ATP synthase
                  gamma-subunit [Arabidopsis thaliana]
                  171754
Seq. No.
Seq. ID
                  jC-atX25010Q1E1D08a1
                  BLASTN
Method
NCBI GI
                  q166673
BLAST score
                  76
                  7.0e-35
E value
                  108
Match length
                  94
% identity
NCBI Description
                  Arabidopsis thaliana carboxypeptidase Y-like protein gene,
                  complete cds
Seq. No.
                  171755
                  jC-atX25010Q1E1E08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4581103
BLAST score
                  125
E value
                  3.0e-64
Match length
                  161
                   94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T24I21 genomic
                  sequence, complete sequence
                  171756
Seq. No.
                  jC-atX25011Q1E1A04a1
Seq. ID
Method
                  BLASTX
                  g4220480
NCBI GI
BLAST score
                  169
                  5.0e-12
E value
```

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]



```
171757
Seq. No.
Seq. ID
                  jC-atX25011Q1E1D07a1
Method
                  BLASTN
NCBI GI
                  g4587986
BLAST score
                  331
E value
                  0.0e + 00
                  379
Match length
                  100
% identity
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
NCBI Description
                  sequence
                  171758
Seq. No.
Seq. ID
                  jC-atX25012Q1E1H08a1
                  BLASTX
Method
                  g3914780
NCBI GI
BLAST score
                  158
                  1.0e-10
E value
Match length
                  63
                  52
% identity
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO
                  171759
Seq. No.
Seq. ID
                   jC-atX25013Q1E1A03a1
Method
                  BLASTN
NCBI GI
                  g3482964
BLAST score
                   414
                   0.0e+00
E value
                   418
Match length
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
                   (ESSAII project)
                   171760
Seq. No.
                   jC-atX25013Q1E1B04a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2182287
BLAST score
                   149
                   3.0e-78
E value
Match length
                  297
% identity
                   90
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   171761
Seq. ID
                   jC-atX25013Q1E1D05a1
                   BLASTN
Method
                   g2351071
NCBI GI
                   159
BLAST score
                   3.0e-84
E value
Match length
                   260
                   93
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

Seq. No. 171762

Seq. ID jC-atX25013Q1E1D06b1

Method BLASTX

MVA3, complete sequence [Arabidopsis thaliana]



```
g3024898
NCBI GI
                  391
BLAST score
                  7.0e-39
E value
                  132
Match length
                  62
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE KIAA0224 (HA4657) >gi 1504028 dbj BAA13213
                                                                  elicase
                  (D86977) similar to putative ATP-dependent
                  K03H1.2 of C.elegans(S41025) [Homo sapiens
                                                                  3123906
                  (AF038391) pre-mRNA splicing totor [Homo ...
                  171763
Seq. No.
Seq. ID
                  jC-atX25014Q1E1G01a1
                  BLASTN
Method
NCBI GI
                  g3241923
                  98
BLAST score
                  6.0e-48
E value
Match length
                  202
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5
NCBI Description
                  MMN10, complete sequence [Arabidopsis thalia
                  171764
Seq. No.
Seq. ID
                  jC-atX25014Q1E1G09a1
                  BLASTX
Method
                  q729406
NCBI GI
                  193
BLAST score
                  7.0e-15
E value
                  59
Match length
                  61
% identity
                 ELONGATION FACTOR P (EF-P) >gi 421 - pii S34443
NCBI Description
                  translation elonga or factor EF-P - Escherichia coli
                  (X61676) elongation factor P
                  [Escherichia coll] >gi 536991 (U14003) elongation factor P
                  [Escherichia coli] >qi 1790590 (AE000487) elongation factor
                  P (EF-P) [Escherichia coli]
                  171765
Seq. No.
                  jC-atX25014Q1E1H12a1
Seq. ID
Method
                  BLASTN
                  q2623294
NCBI GI
BLAST score
                  126
                  1.0e-64
E value
                  206
Match length
                  90
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171766
Seq. No.
                  jC-atX25018Q1E1A07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589434
BLAST score
                  115
                  2.0e-58
E value
Match length
                  119
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

54

% identity



MNJ7, complete sequence

Seq. No. 171767 jC-atX25018Q1E1A07b1 Seq. ID Method BLASTX q3309082 NCBI GI 273 BLAST score 4.0e-24 E value 62 Match length % identity (AF076251) calcineurin B-like protein 1 [Arabidopsis NCBI Description thaliana] 171768 Seq. No. jC-atX25018Q1E1D08a1 Seq. ID Method BLASTN NCBI GI g2213606 225 BLAST score 1.0e-123 E value 329 Match length 92 % identity Genomic sequence for Arabidopsis thaliana BAC F21J9, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 171769 Seq. ID jC-atX25019Q1E1B10a1 BLASTN Method NCBI GI g2351062 BLAST score 165 E value 5.0e-88 217 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MAH20, complete sequence [Arabidopsis thaliana] 171770 Seq. No. Seq. ID jC-atX25020Q1E1C08a1 BLASTN Method NCBI GI g2351062 BLAST score 198 1.0e-107 E value Match length 262 94 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana] Seq. No. 171771 jC-atX25020Q1E1C08b1 Seq. ID Method BLASTN NCBI GI g2351062 BLAST score 128

6.0e-66 E value Match length 196 91 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]



```
171772
Seq. No.
Seq. ID
                  jC-atX25020Q1E1F04a1
                  BLASTX
Method
                  g4726118
NCBI GI
                  271
BLAST score
                   4.0e-24
E value
                   46
Match length
                  100
% identity
                   (AC006436) putative somatic embryogenesis receptor-like
NCBI Description
                  kinase [Arabidopsis thaliana]
                  171773
Seq. No.
Seq. ID
                   jC-atX25021Q1E1F02a2
                  BLASTN
Method
                  g3668073
NCBI GI
                   55
BLAST score
                   2.0e-22
E value
                  119
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171774
Seq. No.
Seq. ID
                   jC-atX25021Q1E1F09b1
                   BLASTN
Method
                   g4713943
NCBI GI
BLAST score
                   64
                   2.0e-28
E value
                   64
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
NCBI Description
                   complete sequence
                   171775
Seq. No.
Seq. ID
                   jC-atX25021Q1E1G01a1
Method
                   BLASTN
                   g4220627
NCBI GI
BLAST score
                   284
                   1.0e-159
E value
Match length
                   324
                   97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K20J1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171776
                   jC-atX25021Q1E1G06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g81850
BLAST score
                   279
E value
                   8.0e-25
                   57
Match length
                   98
% identity
                   histone H3 (clone pH3c-1) - alfalfa (fragment)
NCBI Description
```

Seq. No. 171777

[Medicago sativa]

>gi 829279 emb CAA31967 (X13676) histone H3 (AA 1-120)



```
jC-atX25022Q1E1E08a1
Seq. ID
                  BLASTN
Method
                  g4558656
NCBI GI
                  115
BLAST score
                  4.0e-58
E value ·
                  237
Match length
                  91
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T10F5 genomic
                  sequence, complete sequence
                  171778
Seq. No.
                  jC-atX25023Q1E1A07a1
Seq. ID
                  BLASTN
Method
                  q431257
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
                  182
Match length
                   79
% identity
NCBI Description Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds
                   171779
Seq. No.
                   jC-atX25023Q1E1A09a1
Seq. ID
Method
                   BLASTN
                   q4337024
NCBI GI
BLAST score
                   59
                   6.0e-25
E value
                  75
Match length
% identity
NCBI Description Arabidopsis thaliana AIM1 protein (AIM1) gene, complete cds
                   171780
Seq. No.
                   jC-atX25023Q1E1A12b2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3319339
                   119
BLAST score
                   2.0e-60
E value
                   207
Match length
                   91
% identity
NCBI Description Arabidopsis thaliana BAC F9D12
                   171781
Seq. No.
                   jC-atX25026Q1E1A04a1
Seq. ID
Method
                   BLASTN
                   g2477521
NCBI GI
                   59
BLAST score
                   1.0e-24
E value
                   184
Match length
                   90
 % identity
                  Arabidopsis thaliana chromosome I BAC F22K20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171782
 Seq. No.
                   jC-atX25026Q1E1A11b1
 Seq. ID
                   BLASTN
 Method
                   q3779020
 NCBI GI
```

243

1.0e-134

BLAST score

E value



Match length 263 % identity

Arabidopsis thaliana chromosome II BAC T4E14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

171783 Seq. No.

jC-atX25026Q1E1C10a1 Seq. ID

Method BLASTN q16371 NCBI GI BLAST score 32 E value 9.0e-09 Match length 44 93 % identity

A.thaliana gene (LHCP AB 180) for chlorophyll a/b binding NCBI Description

protein

Seq. No. 171784

jC-atX25026Q1E1C10b1 Seq. ID

BLASTX Method q115767 NCBI GI BLAST score 331 E value 5.0e-31 Match length 108 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-165/180) (LHCP) >qi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

171785 Seq. No.

Seq. ID jC-atX25027Q1E1H09b1

BLASTN Method g3128137 NCBI GI BLAST score 61 7.0e-26 E value 235 Match length 88 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K9I9, complete sequence [Arabidopsis thaliana]

171786 Seq. No.

jC-atX25029Q1E1E01a1 Seq. ID

BLASTN Method g2351065 NCBI GI BLAST score 251 1.0e-139 E value 304 Match length 95 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 171787

jC-atX25029Q1E1G01a1 Seq. ID

Method BLASTN



NCBI GI g4519188 BLAST score 107 E value 2.0e-53 Match length 155 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L19, complete sequence

Seq. No. 171788

Seq. ID jC-atX25030Q1E1D04a1

Method BLASTN
NCBI GI g3492855
BLAST score 281
E value 1.0e-157
Match length 313
% identity 92

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2,

complete sequence [Arabidopsis thaliana]

Seq. No. 171789

Seq. ID jC-atX25030Q1E1H01a1

Method BLASTN
NCBI GI g2642427
BLAST score 95
E value 4.0e-46
Match length 224
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC T20D16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171790

Seq. ID jC-atX25033Q1E1H04a1

Method BLASTN
NCBI GI g2494110
BLAST score 298
E value 1.0e-167
Match length 451
% identity 100

NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 171791

Seq. ID jC-atX25034Q1E1H03a1

Method BLASTN
NCBI GI g3047074
BLAST score 247
E value 1.0e-136
Match length 392
% identity 90

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 171792

Seq. ID jC-atX25034Q1E1H03b1

Method BLASTN
NCBI GI g3047074
BLAST score 221
E value 1.0e-121



```
Match length 261 % identity 96
```

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 171793

Seq. ID jC-atX25035Q1E1D03a1

Method BLASTX
NCBI GI g2228773
BLAST score 286
E value 1.0e-25
Match length 65
% identity 88

NCBI Description (AF001454) Dc3 promoter-binding factor-2 [Helianthus

annuus]

Seq. No. 171794

Seq. ID jC-atX25037Q1E1C03a1

Method BLASTX
NCBI GI g4314378
BLAST score 496
E value 3.0e-50
Match length 133
% identity 66

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 171795

Seq. ID jC-atX25037Q1E1C11a1

Method BLASTN
NCBI GI g1244741
BLAST score 265
E value 1.0e-147
Match length 265
% identity 100

NCBI Description Arabidopsis thaliana nuclear ribosomal ITS-1, 5.8S

ribosomal RNA, and ITS-2. >gi_1245679_gb_U52185_ASU52185 Arabidopsis suecica nuclear ribosomal ITS-1, 5.8S ribosomal

RNA, and ITS-2

Seq. No. 171796

Seq. ID jC-atX25037Q1E1C11b1

Method BLASTN
NCBI GI g1244741
BLAST score 261
E value 1.0e-145
Match length 261
% identity 100

NCBI Description Arabidopsis thaliana nuclear ribosomal ITS-1, 5.8S

ribosomal RNA, and ITS-2. >gi_1245679_gb_U52185_ASU52185 Arabidopsis suecica nuclear ribosomal ITS-1, 5.8S ribosomal

RNA, and ITS-2

Seq. No. 171797

Seq. ID jC-atX25037Q1E1E04a1

Method BLASTN
NCBI GI g3241926
BLAST score 56
E value 3.0e-23

E value

Match length

% identity

1.0e-61

289

67



64 Match length 97 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSG15, complete sequence [Arabidopsis thaliana] 171798 Seq. No. jC-atX25037Q1E1E11a1 Seq. ID Method BLASTN g3241926 NCBI GI BLAST score 45 E value 1.0e-16 Match length 121 84 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSG15, complete sequence [Arabidopsis thaliana] 171799 Seq. No. jC-atX25038Q1E1A09a1 Seq. ID Method BLASTX g4510389 NCBI GI BLAST score 48 E value 2.0e-39 Match length 87 97 % identity (AC007017) putative solute carrier protein [Arabidopsis NCBI Description thaliana] 171800 Seq. No. jC-atX25038Q1E1D02a1 Seq. ID BLASTN Method g4262221 NCBI GI 39 BLAST score 2.0e-12 E value 87 Match length 86 % identity Arabidopsis thaliana chromosome II BAC F10A8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171801 Seq. No. Seq. ID jC-atX25038Q1E1E11a2 Method BLASTN g2351071 NCBI GI BLAST score 104 1.0e-51 E value 172 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MVA3, complete sequence [Arabidopsis thaliana] 171802 Seq. No. Seq. ID jC-atX25039Q1E1H07b1 BLASTN Method g2281081 NCBI GI BLAST score 121

23486



```
NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171803
Seq. No.
                  jC-atX25040Q1E1B06a1
Seq. ID
                  BLASTN
Method
                  g3660464
NCBI GI
                  109
BLAST score
E value
                  2.0e-54
                  269
Match length
% identity
                  85
                  Arabidopsis thaliana mRNA for Inositol 1,3,4-Trisphosphate
NCBI Description
                  5/6 Kinase
                  171804
Seq. No.
                   jC-atX25040Q1E1E01a1
Seq. ID
                  BLASTN
Method
                   g2262135
NCBI GI
                   150
BLAST score
                   7.0e-79
E value
Match length
                   286
% identity
                   94
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                   cM, complete sequence
                   171805
Seq. No.
                   jC-atX25041Q1E1B02a1
Seq. ID
                   BLASTN
Method
                   g3702729
NCBI GI
                   314
BLAST score
                   1.0e-176
E value
Match length
                   381
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K2A11, complete sequence [Arabidopsis thaliana]
                   171806
Seq. No.
                   jC-atX25041Q1E1B04a1
Seq. ID
                   BLASTN
Method
                   g4159707
NCBI GI
BLAST score
                   181
                   2.0e-97
E value
Match length
                   313
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MJK13, complete sequence
                   171807
Seq. No.
Seq. ID
                   jC-atX25041Q1E1B11b1
                   BLASTN
Method
NCBI GI
                   q2656026
BLAST score
                   93
                   2.0e-45
E value
Match length
                   97
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

23487

```
171808
Seq. No.
                  jC-atX25045Q1E1A03a1
Seq. ID
                  BLASTN
Method
                  g4544435
NCBI GI
                  382
BLAST score
                  0.0e + 00
E value
                  398
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                  sequence, complete sequence
                  171809
Seq. No.
                  jC-atX25047Q1E1A06a1
Seq. ID
                  BLASTX
Method
                  g3688186
NCBI GI
                  324
BLAST score
                  4.0e-30
E value
                  81
Match length
                  79
% identity
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                  171810
Seq. No.
                  jC-atX25049Q1E1E08a1
Seq. ID
Method
                  BLASTN
                  q2281081
NCBI GI
                  105
BLAST score
                  3.0e-52
E value
                  185
Match length
                  88
% identity
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171811
Seq. No.
Seq. ID
                   jC-atX25050Q1E1C07b1
Method
                  BLASTX
                  g586078
NCBI GI
                   258
BLAST score
                   6.0e-23
E value
                   54
Match length
                   89
% identity
                  TUBULIN BETA CHAIN >gi 1076736 pir JC2518 beta-tubulin
NCBI Description
                  pTUB22 - rice >gi 303842 dbj BAA02505 (D13224)
                   beta-tubulin [Oryza sativa]
                   171812
Seq. No.
Seq. ID
                   jC-atX25051Q1E1G12a1
                   BLASTN
Method
                   g3449334
NCBI GI
BLAST score
                   81
E value
                   7.0e-38
                   189
Match length
                   84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYH9, complete sequence [Arabidopsis thaliana]
```

23488

171813

Seq. No.

Seq. ID

Method



```
jC-atX25055P1E1G03a1
Seq. ID
                  BLASTN
Method
                   g2335089
NCBI GI
BLAST score
                   154
                   3.0e-81
E value
                   340
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171814
Seq. No.
                   jC-atX25056Q1E1B06b1
Seq. ID
                   BLASTN
Method
                   g4589435
NCBI GI
                   35
BLAST score
                   1.0e-10
E value
                   91
Match length
                   84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOE17, complete sequence
                   171815
Seq. No.
                   jC-atX25056Q1E1D09a1
Seq. ID
                   BLASTN
Method
                   g4490701
NCBI GI
                   79
BLAST score
                   2.0e-36
E value
                   29
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
NCBI Description
                   (ESSA project)
                   171816
Seq. No.
                   jC-atX25056Q1E1E10b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3869065
                   60
BLAST score
                   1.0e-25
E value
                   110
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24M7, complete sequence [Arabidopsis thaliana]
                   171817
Seq. No.
Seq. ID
                   jC-atX25059Q1E1A01a1
Method
                   BLASTN
NCBI GI
                   g3869075
BLAST score
                   262
                   1.0e-145
E value
Match length
                   307
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXK3, complete sequence [Arabidopsis thaliana]
                   171818
Seq. No.
```

23489

jC-atX25059Q1E1F03a1

BLASTN



NCBI GI g3617740
BLAST score 218
E value 1.0e-119
Match length 301
% identity 96

NCBI Description Arabidopsis thaliana BAC F1I21 from chromosome 1, near 59

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 171819

Seq. ID jC-atX25059Q1E1G06a1

Method BLASTN
NCBI GI g3080352
BLAST score 101
E value 8.0e-50
Match length 161
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18

(ESSAII project)

Seq. No. 171820

Seq. ID jC-atX25059Q1E1H01b1

Method BLASTN
NCBI GI 94204173
BLAST score 156
E value 1.0e-82
Match length 156
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC T2K10 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 171821

Seq. ID jC-atX25060Q1E1G04a1

Method BLASTN
NCBI GI g1872520
BLAST score 140
E value 6.0e-73
Match length 296
% identity 87

NCBI Description Arabidopsis thaliana zinc-finger protein Lsd1 (LSD1) mRNA,

complete cds

Seq. No. 171822

Seq. ID jC-atX25061Q1E1B11a1

Method BLASTN
NCBI GI 94490734
BLAST score 128
E value 7.0e-66
Match length 236
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 171823

Seq. ID jC-atX25061Q1E1C04b1

Method BLASTN
NCBI GI g4262221
BLAST score 172

23490



E value 3.0e-92
Match length 208
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171824
Seq. ID jC-atX25061Q1E1D12a1
Method BLASTN

Method BLASTN
NCBI GI g1009711
BLAST score 143
E value 6.0e-75
Match length 143
% identity 100

NCBI Description Arabidopsis thaliana calreticulin (AtCRTL) mRNA, partial

cds

Seq. No. 171825

Seq. ID jC-atX25062Q1E1E11a1

Method BLASTN
NCBI GI g3510340
BLAST score 187
E value 1.0e-101
Match length 348
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDN11, complete sequence [Arabidopsis thaliana]

Seq. No. 171826

Seq. ID jC-atX25062Q1E1F08a1

Method BLASTN
NCBI GI g3868722
BLAST score 47
E value 3.0e-17
Match length 83
% identity 89

% identity 89
NCBI Description Arabidopsis thaliana BAC T19G15, from chromosome V near

60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 171827

Seq. ID jC-atX25062Q1E1H06a1

Method BLASTX
NCBI GI g1703478
BLAST score 750
E value 6.0e-80
Match length 141
% identity 100

NCBI Description (U40566) ubiquitin activating enzyme 2 [Arabidopsis

thaliana]

Seq. No. 171828

Seq. ID jC-atX25065Q1E1E04b1

Method BLASTN
NCBI GI g3366536
BLAST score 66
E value 4.0e-29
Match length 118

```
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T25N20,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  171829
Seq. No.
                  jC-atX25065Q1E1G11a1
Seq. ID
                  BLASTN
Method
                  g3128143
NCBI GI
                  73
BLAST score
                  3.0e - 33
E value
                  157
Match length
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTI20, complete sequence [Arabidopsis thaliana]
                  171830
Seq. No.
Seq. ID
                   jC-atX25066Q1E1C11b1
                  BLASTN
Method
                  q4757403
NCBI GI
BLAST score
                   153
                   9.0e-81
E value
                   234
Match length
                   91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJL12, complete sequence
                   171831
Seq. No.
                   jC-atX25068Q1E1B02a1
Seq. ID
                   BLASTN
Method
                   g3461834
NCBI GI
                   372
BLAST score
                   0.0e + 00
E value
                   401
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T9I4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171832
Seq. No.
                   jC-atX25068Q1E1B11a1
Seq. ID
Method
                   BLASTN
                   g3046853
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   92
Match length
                   85
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRA19, complete sequence [Arabidopsis thaliana]

171833 Seq. No.

Seq. ID jC-atX25069Q1E1B01a1

Method BLASTX q1931647 NCBI GI BLAST score 385 3.0e-37E value 142 Match length 59 % identity

(U95973) endomembrane protein EMP70 precusor isolog NCBI Description



[Arabidopsis thaliana]

171834 Seq. No. jC-atX25069Q1E1B12a1 Seq. ID BLASTN Method g4572664 NCBI GI BLAST score 81 3.0e-38 E value Match length 105 97 % identity Arabidopsis thaliana chromosome II BAC F25P17 genomic NCBI Description sequence, complete sequence 171835 Seq. No. Seq. ID jC-atX25069Q1E1H07a1 Method BLASTX g4531442 NCBI GI 444 BLAST score 4.0e-44 E value 101 Match length % identity 88 (AC006224) hypothetical protein [Arabidopsis thaliana] NCBI Description 171836 Seq. No. Seq. ID jC-atX25073Q1E1C08b1 BLASTN Method g2244901 NCBI GI 254 BLAST score 1.0e-141 E value 300 Match length 95 % identity Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No 171837 Seq. No. Seq. ID jC-atX25073Q1E1F01a1 Method BLASTX NCBI GI g2347208 229 BLAST score 7.0e-19 E value 80 Match length 49 % identity (AC002338) APG protein isolog [Arabidopsis thaliana] NCBI Description 171838 Seq. No. Seq. ID jC-atX25073Q1E1H06b2 BLASTN Method NCBI GI q4263038 BLAST score 117 4.0e-59E value Match length 165 93 % identity NCBI Description Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 171839

jC-atX25074Q1E1E06b1 Seq. ID

Method

NCBI GI

E value,

BLAST score

BLASTN q2618600

5.0e-49

99

```
BLASTN
Method
                  g4235150
NCBI GI
                  511
BLAST score
                  0.0e+00
E value
                  523
Match length
% identity
                  62
                  Arabidopsis thaliana chromosome I BAC T25B24 genomic
NCBI Description
                  sequence, complete sequence
                  171840
Seq. No.
                  jC-atX25074Q1E1G10b1
Seq. ID
                  BLASTX
Method
                  q3184281
NCBI GI
                  257
BLAST score
                  4.0e-22
E value
                  70
Match length
                  70
% identity
                  (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  171841
Seq. No.
                   jC-atX25074Q1E2A01a1
Seq. ID
Method
                  BLASTN
                  g2245031
NCBI GI
                  272
BLAST score
                  1.0e-151
E value
                   348
Match length
                   95
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   171842
                   jC-atX25074Q1E2A05b1
Seq. ID
                   BLASTX
Method
                   q2569931
NCBI GI
BLAST score
                   176
                   8.0e-13
E value
                   49
Match length
                   73
% identity
                  (AJ002280) shaggy-like kinase beta [Arabidopsis thaliana]
NCBI Description
                   171843
Seq. No.
Seq. ID
                   jC-atX25074Q1E2A06b1
                   BLASTX
Method
NCBI GI
                   q3660467
BLAST score
                   657
E value
                   4.0e-74
Match length
                   158
% identity
                   92
                  (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   171844
Seq. No.
Seq. ID
                   jC-atX25076Q1E1A06a1
```

23494

% identity

79

```
99
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDC12, complete sequence [Arabidopsis thaliana]
                  171845
Seq. No.
Seq. ID
                  jC-atX25076Q1E1B04a1
Method
                  BLASTX
NCBI GI
                  g2983277
                  169
BLAST score
                  8.0e-12
E value
                  90
Match length
                  40
% identity
                   (AE000702) 3-deoxy-manno-octulosonate cytidylyltransferase
NCBI Description
                   [Aquifex aeolicus]
                  171846
Seq. No.
Seq. ID
                  jC-atX25076Q1E1H09b1
Method
                  BLASTN
NCBI GI
                  q4038029
BLAST score
                  139
                  2.0e-72
E value
                  203
Match length
                  92
% identity
                  Arabidopsis thaliana chromosome II BAC F504 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171847
Seq. No.
                  jC-atX25077Q1E1C01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4582451
BLAST score
                  215
                  2.0e-27
E value
Match length
                  75
                  91
% identity
NCBI Description (AC007071) unknown protein [Arabidopsis thaliana]
                  171848
Seq. No.
                   jC-atX25077Q1E1C02a1
Seq. ID
Method
                  BLASTN
                  g2618599
NCBI GI
BLAST score
                  222
                  1.0e-122
E value
                  222
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171849
Seq. ID
                  jC-atX25077Q1E1C07a1
Method
                  BLASTN
NCBI GI
                  g2832667
BLAST score
                  326
                  0.0e+00
E value
                  446
Match length
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14

Seq. ID



(ESSAII project)

```
171850
Seq. No.
                  jC-atX25077Q1E1H08b1
Seq. ID
                  BLASTX
Method
                  g1354510
NCBI GI
                  360
BLAST score
                  2.0e-34
E value
                  72
Match length
                  99
% identity
                  (U55205) HAL2-like protein [Arabidopsis thaliana]
NCBI Description
                  171851
Seq. No.
                  jC-atX25078Q1E1B02a1
Seq. ID
                  BLASTN
Method
                  g3702735
NCBI GI
                  312
BLAST score
                  1.0e-175
E value
                  316
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQL5, complete sequence [Arabidopsis thaliana]
                  171852
Seq. No.
Seq. ID
                  jC-atX25078Q1E1B02b1
                  BLASTX
Method
                  g2245037
NCBI GI
                  205
BLAST score
                  4.0e-16
E value
                  91
Match length
                  56
% identity
NCBI Description (Z97342) nuclear antigen homolog [Arabidopsis thaliana]
                  171853
Seq. No.
Seq. ID
                  jC-atX25079Q1E1C09a1
Method
                  BLASTX
                  g3482933
NCBI GI
                  290
BLAST score
                   3.0e-26
E value
Match length
                   68
% identity
                   85
                  (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                  thaliana]
                   171854
Seq. No.
Seq. ID
                   jC-atX25079Q1E1C09b1
                   BLASTX
Method
NCBI GI
                   g3482933
BLAST score
                   669
                   1.0e-70
E value
Match length
                   123
                   100
% identity
                  (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   171855
```

23496

jC-atX25080Q1E1C10a1

Seq. ID

Method

NCBI GI

BLAST score

```
BLASTN
Method
NCBI GI
                  q2264313
BLAST score
                  372
                  0.0e + 00
E value
Match length
                  396
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171856
                  jC-atX25080Q1E1E12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  213
                  1.0e-116
E value
Match length
                  277
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171857
                  jC-atX25081Q1E1B09a1
Seq. ID
Method
                  BLASTN
                  q1305456
NCBI GI
                  150
BLAST score
                   5.0e-79
E value
                   234
Match length
                   91
% identity
                  Arabidopsis thaliana cytosolic cyclophilin (ROC2) gene,
NCBI Description
                   complete cds
                   171858
Seq. No.
                   jC-atX25081Q1E1C02a1
Seq. ID
                   BLASTN
Method
                   g3327922
NCBI GI
BLAST score
                   95
                   5.0e-46
E value
                   296
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171859
Seq. No.
                   jC-atX25081Q1E1D08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3402703
                   543
BLAST score
                   9.0e-56
E value
                   137
Match length
% identity
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   171860
Seq. No.
```

23497

jC-atX25081Q1E1F09a1

BLASTN

160

q2737903



E value 5.0e-85 Match length 204 % identity 95

NCBI Description Arabidopsis thaliana retrotransposon TSCL genomic sequence

Seq. No. 171861

Seq. ID jC-atX25090Q1E1E10b1

Method BLASTN
NCBI GI g3668073
BLAST score 92
E value 2.0e-44
Match length 276
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171862

Seq. ID jC-atX25091Q1E1D08a1

Method BLASTN
NCBI GI g4584519
BLAST score 70
E value 2.0e-31
Match length 130
% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18

(ESSA project)

Seq. No. 171863

Seq. ID jC-atX25091Q1E1F03a1

Method BLASTN
NCBI GI 94469002
BLAST score 103
E value 3.0e-51
Match length 118
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 171864

Seq. ID jC-atX25091Q1E1F03b1

Method BLASTN
NCBI GI g4469002
BLAST score 97
E value 2.0e-47
Match length 205
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 171865

Seq. ID jC-atX25092Q1E1D09a1

Method BLASTN
NCBI GI g2351063
BLAST score 227
E value 1.0e-124
Match length 446
% identity 100

23498

```
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCL19, complete sequence [Arabidopsis thaliana]
                  171866
Seq. No.
                  jC-atX25093Q1E1D05a1
Seq. ID
                  BLASTN
Method
                  q4581138
NCBI GI
                  58
BLAST score
                  1.0e-24
E value
                  74
Match length
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
NCBI Description
                  sequence, complete sequence
                  171867
Seq. No.
Seq. ID
                  jC-atX25094Q1E1E10b1
                  BLASTN
Method
                  g3461834
NCBI GI
                  93
BLAST score
                  3.0e-45
E value
Match length
                  141
% identity
                  91
                  Arabidopsis thaliana chromosome II BAC T9I4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171868
Seq. No.
Seq. ID
                   jC-atX25095Q1E1E02b1
                  BLASTN
Method
                   g2924651
NCBI GI
BLAST score
                   80
E value
                   2.0e-37
Match length
                   108
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K2A18, complete sequence [Arabidopsis thaliana]
                   171869
Seq. No.
Seq. ID
                   jC-atX25095Q1E1E09a2
                   BLASTN
Method
NCBI GI
                   g4159703
BLAST score
                   46
                   6.0e-17
E value
Match length
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K5F14, complete sequence
                   171870
Seq. No.
                   jC-atX25096Q1E1G10b1
Seq. ID
                   BLASTN
Method
```

NCBI GI g3785992
BLAST score 90
E value 1.0e-43
Match length 98
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]



```
171871
Seq. No.
                  jC-atX25097Q1E1C03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678380
BLAST score
                  384
                  3.0e-37
E value
                  92
Match length
                  84
% identity
                  (ALO49656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  171872
                  jC-atX25097Q1E1F10b1
Seq. ID
                  BLASTX
Method
                  g115767
NCBI GI
BLAST score
                  238
                  8.0e-38
E value
                  102
Match length
                  87
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                   171873
Seq. No.
                   jC-atX25098Q1E1A05a1
Seq. ID
                   {\tt BLASTN}
Method
                   g2252639
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
                   308
Match length
                   95
% identity
                  Genomic sequence of Arabidopsis BAC F8A5, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                   171874
Seq. No.
Seq. ID
                   jC-atX25098Q1E1A05b1
Method
                   BLASTX
NCBI GI
                   g2462748
                   701
BLAST score
                   3.0e-74
E value
                   143
Match length
% identity
                   (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   171875
                   jC-atX25098Q1E1C09a1
Seq. ID
                   BLASTN
Method
```

NCBI GI g2656028
BLAST score 315
E value 1.0e-177
Match length 359
% identity 100

% identity

NCBI Description

31

thalianal



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNF13
                  171876
Seq. No.
                  jC-atX25099Q1E1C11b1
Seq. ID
Method
                  BLASTN
                  g430946
NCBI GI
                  145
BLAST score
E value
                  3.0e-76
Match length
                  145
% identity
                  100
                 Arabidopsis thaliana PSI type III chlorophyll a/b-binding
NCBI Description
                  protein (Lhca3*1) mRNA, complete cds
                  171877
Seq. No.
Seq. ID
                  jC-atX25100Q1E1A01a1
Method
                  BLASTX
NCBI GI
                  g2191187
                  226
BLAST score
                  1.0e-18
E value
                  74
Match length
% identity
                 . 58
                  (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
                  171878
Seq. No.
Seq. ID
                  jC-atX25100Q1E1C06b1
                  BLASTN
Method
                  g3282170
NCBI GI
                  331
BLAST score
E value
                  0.0e+00
                  372
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,
                  complete sequence [Arabidopsis thaliana]
                  171879
Seq. No.
Seq. ID
                  jC-atX25100Q1E1G12a1
                  BLASTN
Method
NCBI GI
                  q4757414
BLAST score
                   114
E value
                   1.0e-57
Match length
                  182
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
                   171880
Seq. No.
Seq. ID
                   jC-atX25101Q1E1C03a1
Method
                   BLASTX
NCBI GI
                  g4582435
BLAST score
                   249
E value
                  1.0e-21
Match length
                  95
```

(AC007196) putative selenium-binding protein [Arabidopsis

NCBI Description

Seq. No.

171886



```
171881
Seq. No.
                  jC-atX25101Q1E1D03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1403138
BLAST score
                  566
E value
                  2.0e-58
                  106
Match length
                  100
% identity
                  (X98190) peroxidase ATP2a [Arabidopsis thaliana]
NCBI Description
                  >qi 4371288 qb AAD18146 (AC006260) putative peroxidase
                  ATPZa [Arabidopsis thaliana]
                  171882
Seq. No.
Seq. ID
                  jC-atX25101Q1E1G05a1
                  BLASTN
Method
                  g2160155
NCBI GI
BLAST score
                  46
E value
                  6.0e-17
Match length
                  136
                  92
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  171883
Seq. No.
                   jC-atX25101Q1E1G11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4376087
BLAST score
                  137
E value
                   3.0e-71
                  205
Match length
                   93
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
Seq. No.
                   171884
Seq. ID
                   jC-atX25102Q1E1C09a1
Method
                   BLASTN
NCBI GI
                   g2264302
BLAST score
                   373
E value
                   0.0e + 00
                   444
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC12, complete sequence [Arabidopsis thaliana]
                   171885
Seq. No.
                   jC-atX25102Q1E1C11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4417283
                   294
BLAST score
                   1.0e-26
E value
                   71
Match length
                   75
% identity
```

23502

(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

NCBI GI



```
jC-atX25102Q1E1E10a1
Seq. ID
Method
                   BLASTX
                   g4567231
NCBI GI
BLAST score
                   262
E value
                   8.0e-23
                   52
Match length
                   100
% identity
NCBI Description
                   (AC007119) putative glucose-1-phosphate adenylyltransferase
                   [Arabidopsis thaliana]
                   171887
Seq. No.
                   jC-atX25103Q1E1G03a1
Seq. ID
Method
                   BLASTX
                   q3668082
NCBI GI
                   146
BLAST score
                   2.0e-09
E value
Match length
                   45
% identity
                   60
                  (AC004667) putative DAL1 protein [Arabidopsis thaliana]
NCBI Description
                   171888
Seq. No.
                   jC-atX25103Q1E1G07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3395421
BLAST score
                   146
E value
                   2.0e-76
                   278
Match length
% identity
                   96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T19C21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   171889
Seq. No.
Seq. ID
                   jC-atX25106Q1E1H06a1
                   BLASTN
Method
NCBI GI
                   g2252848
BLAST score
                   188
E value
                   1.0e-101
Match length
                   212
% identity
                   98
NCBI Description Arabidopsis thaliana BAC TM018A10
                   171890
Seq. No.
                   jC-atX25107Q1E1B09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2493964
                   180
BLAST score
                   4.0e-13
E value
                   74
Match length
                   51
% identity
                   XANTHINE DEHYDROGENASE (XD) (ROSY LOCUS PROTEIN)
NCBI Description
                   >gi_1743224_emb_CAA69405_ (Y08237) xanthine dehydrogenase
                   [Drosophila subobscura]
                   171891
Seq. No.
                   jC-atX25108Q1E1H12a1
Seq. ID
Method
                   BLASTN
```

g2924734



BLAST score 52 E value 2.0e-20 Match length 121 % identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXE10, complete sequence [Arabidopsis thaliana]

Seq. No. 171892

Seq. ID jC-atX25109Q1E1B01a1

Method BLASTN
NCBI GI g2160155
BLAST score 34
E value 9.0e-10
Match length 38

% identity 97
NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 171893

Seq. ID jC-atX25112Q1E1A12a1

Method BLASTN
NCBI GI g3299824
BLAST score 219
E value 1.0e-120
Match length 267
% identity 96

NCBI Description Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,

near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 171894

Seq. ID jC-atX25112Q1E1C10b1

Method BLASTN
NCBI GI g3135610
BLAST score 50
E value 1.0e-19
Match length 126
% identity 85

NCBI Description Arabidopsis thaliana cellulose synthase mRNA, partial cds

Seq. No. 171895

Seq. ID jC-atX25113Q1E1F09a1

Method BLASTX
NCBI GI g3047082
BLAST score 429
E value 1.0e-42
Match length 94
% identity 85

NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase

precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No. 171896

Seq. ID jC-atX25114Q1E1C10a1

Method BLASTN
NCBI GI g2660661
BLAST score 202
E value 1.0e-110
Match length 226



```
% identity
                  Arabidopsis thaliana chromosome V BAC T19K24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171897
Seq. No.
                  jC-atX25115Q1E1E04a1
Seq. ID
                  BLASTX
Method
                  q3367528
NCBI GI
BLAST score
                  207
                  1.0e-16
E value
                  41
Match length
                  100
% identity
                  (AC004392) Strong similarity to gi_2160138 F19K23.6 gene
NCBI Description
                  product from A. thaliana BAC gb_ACO00375. [Arabidopsis
                  thaliana]
                  171898
Seq. No.
                  jC-atX25116Q1E1B04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3668073
                  194
BLAST score
                  1.0e-105
E value
                  262
Match length
                  94
% identity
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  171899
Seq. No.
                   jC-atX25116Q1E1D03a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1143389
                   50
BLAST score
                   1.0e-19
E value
                   110
Match length
% identity
                   86
NCBI Description A.thaliana mRNA for 3-hydroxy-3-methylglutaryl-CoA synthase
                   171900
Seq. No.
                   jC-atX25116Q1E1D10a1
Seq. ID
Method
                   BLASTN
                   q2760165
NCBI GI
BLAST score
                   331
                   0.0e + 00
E value
Match length
                   355
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAC9, complete sequence [Arabidopsis thaliana]
                   171901
Seq. No.
Seq. ID
                   jC-atX25117Q1E1D05a1
Method
                   BLASTN
                   g3927822
NCBI GI
BLAST score
                   113
                   6.0e-57
E value
```

23505

Arabidopsis thaliana chromosome II BAC F8N16 genomic

201

89

Match length % identity

NCBI Description

Method

BLASTN



sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  171902
Seq. ID
                  jC-atX35007Q1E1D10a1
                  BLASTN
Method
NCBI GI
                  g3449334
BLAST score
                  89
E value
                  1.0e-42
Match length
                  161
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                  171903
Seq. No.
Seq. ID
                  jC-atX35009Q1E1F09a1
                  BLASTN
Method
NCBI GI
                  g16229
BLAST score
                  82
E value
                  1.0e-38
Match length
                  130
                  92
% identity
NCBI Description A.thaliana cor6.6 mRNA
                  171904
Seq. No.
Seq. ID
                   jC-atX35010Q1E1E04a1
                  BLASTX
Method
                  g2821961
NCBI GI
BLAST score
                  281
E value
                   5.0e-25
Match length
                   64
% identity
                   86
                  (AB006693) spermidine synthase [Arabidopsis thaliana]
NCBI Description
                  171905
Seq. No.
Seq. ID
                   jC-atX35015Q1E1A06b1
                   BLASTN
Method
NCBI GI
                   g3212846
BLAST score
                   146
                   1.0e-76
E value
Match length
                   191
                   94
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   171906
                   jC-atX35015Q1E1E12a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3859590
BLAST score
                   81
E value
                   5.0e-38
Match length
                   152
% identity
                   90
NCBI Description Arabidopsis thaliana BAC T15B16
                   171907
Seq. No.
                   jC-atX35018Q1E1A12a1
Seq. ID
```

23506



NCBI GI g2564049
BLAST score 73
E value 4.0e-33
Match length 161
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE2, complete sequence [Arabidopsis thaliana]

Seq. No. 171908

Seq. ID jC-atX35019Q1E1D0330a1

Method BLASTN
NCBI GI g2264317
BLAST score 173
E value 1.0e-92
Match length 285
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 171909

Seq. ID jC-atX35020Q1E1B08b1

Method BLASTN
NCBI GI g4235150
BLAST score 90
E value 2.0e-43
Match length 181
% identity 88

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic

sequence, complete sequence

Seq. No. 171910

Seq. ID jC-atX35020Q1E1E02a1

Method BLASTN
NCBI GI g3582315
BLAST score 43
E value 3.0e-15
Match length 67
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T27A16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171911

Seq. ID jC-atX35039Q1E1E04a1

Method BLASTN
NCBI GI g3869252
BLAST score 69
E value 1.0e-30
Match length 189
% identity 84

NCBI Description Arabidopsis thaliana ferredoxin-dependent glutamate

synthase precursor (GLU2) mRNA, complete cds

Seq. No. 171912

Seq. ID jC-atX35040Q1E1C10a1

Method BLASTN NCBI GI g259446 BLAST score 79



4.0e-37 E value 83 Match length 99 % identity glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, NCBI Description C24, mRNA, 680 nt] 171913 Seq. No. Seq. ID jC-atX35042Q1E1A07a1 Method BLASTN q2815519 NCBI GI BLAST score 100 4.0e-49 E value 260 Match length % identity 53 Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 171914 Seq. ID jC-atX35044Q1E1E11b1 Method BLASTX NCBI GI q3687243 BLAST score 260 2.0e-22 · E value 66 Match length 80 % identity (AC005169) putative ribosomal protein [Arabidopsis NCBI Description thaliana] Seq. No. Seq. ID 171915 jC-atX35049Q1E1E05a1 BLASTN Method g1532162 NCBI GI 175 BLAST score 9.0e-94 E value 328 Match length 98 % identity NCBI Description Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I 171916 Seq. No. jC-atX35050Q1E1G05b1 Seq. ID Method BLASTX NCBI GI g3135256 BLAST score 760 E value 2.0e-82 152 Match length 97 % identity NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID jC-atX35051Q1E1G08a1

171917

Method BLASTN
NCBI GI g2642152
BLAST score 353
E value 0.0e+00



```
373
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T5I7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  jC-atX35052Q1E1H04a1
Seq. ID
Method
                  BLASTN
                  a4757662
NCBI GI
                  233
BLAST score
                  1.0e-128
E value
                  253
Match length
                  98
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
NCBI Description
                  chromosome I, complete sequence
```

 Seq. No.
 171919

 Seq. ID
 jC-atX35054Q1E1A01a1

 Method
 BLASTN

 NCBI GI
 g16367

 BLAST score
 58

 E value
 5.0e-24

E value 5.0e-24
Match length 118
% identity 87

NCBI Description A.thaliana gene (LHCP AB 165) for chlorophyll a/b binding

protein

 Seq. No.
 171920

 Seq. ID
 jC-atX35054Q1E1G05b2

 Method
 BLASTX

 NCBT CI
 g115783

NCBI GI g115783
BLAST score 458
E value 7.0e-46
Match length 86
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 171921 jC-atXA12a2 Seq. ID BLASTN Method q58201 NCBI GI BLAST score 44 3.0e-15 E value 52 Match length 96 % identity

NCBI Description Cloning vector pGEM-3Z

Seq. No. 171922
Seq. ID jC-atXA34a2
Method BLASTN
NCBI GI g4314336
BLAST score 55
E value 7.0e-22
Match length 55



```
% identity
NCBI Description
                  Homo sapiens chromosome 10 clone CIT987SK-101106 map 10q25,
                  complete sequence [Homo sapiens]
                  171923
Seq. No.
                   jC-atXA34f2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g619522
                  50
BLAST score
                  7.0e-19
E value
Match length
                   57
                   98
% identity
                  Synechococcus PCC 6301 genomic DNA (clone PJRSY01)
NCBI Description
                  171924
Seq. No.
Seq. ID
                   jC-atXB632f2
                  BLASTN
Method
                  g507770
NCBI GI
BLAST score
                   33
E value
                  1.0e-08
                   65
Match length
                   89
% identity
NCBI Description
                  Zea mays D3L H(+)-transporting ATPase (Mhal) gene, complete
                  cds
                  171925
Seq. No.
Seq. ID
                   jC-atXB810a2
                  BLASTX
Method
NCBI GI
                  g3482928
BLAST score
                   58
                   2.0e-12
E value
                   58
Match length
                   86
% identity
                   (AC003970) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3929586 (AF100166) phytochrome interacting factor 3
                   [Arabidopsis thaliana]
                   171926
Seq. No.
Seq. ID
                   jC-atXB810f2
Method
                   BLASTX
NCBI GI
                   g3482928
BLAST score
                   107
E value
                   2.0e-09
Match length
                   44
                   84
% identity
NCBI Description
                  (AC003970) Unknown protein [Arabidopsis thaliana]
                   >gi 3929586 (AF100166) phytochrome interacting factor 3
                   [Arabidopsis thaliana]
Seq. No.
                   171927
                   jC-atXL1023Q1B1D07b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2264314
BLAST score
                   228
                   1.0e-125
E value
Match length
                   228
```

23510

100

% identity



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 171928
Seq. ID jC-atXL1025Q1B1G02b1

Method BLASTN
NCBI GI g4585890
BLAST score 213
E value 1.0e-116
Match length 237
% identity 97

NCBI Description Arabidopsis thalia. Thromosome II BAT T3G21 Conomic

sequence, complete seq

Seq. No. 171929

Seq. ID jC-atXL1026Q1B1D11b1

Method BLASTN
NCBI GI g2264318
BLAST score 166
E value 2.0e-88
Match length 325
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUP24, complete sequence [Arabidopsis thaliana]

Seq. No. 171930

Seq. ID jC-atXL1028Q1B1C11b1

Method BLASTN
NCBI GI g3068702
BLAST score 105
E value 4.0e-52
Match length 129
% identity 95

NCBI Description Arabidopsis thaliana putative transmembrane probein Glp

(AtG1), putative nuclear DNA-binding protein (AtG2), Em1 protein (ATEM1), putative chlorophy tase (AtG4), putative transmembrane protein G5p (AtG4), put

Seq. No. 171931

Seq. ID jC-atXL1028Q1B1H05b1

Method BLASTN
NCBI GI 94519191
BLAST score 70
E value 3.0e-31
Match length 287
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9P8, complete sequence

Seq. No. 171932

Seq. ID jC-atXL1029Q1B1C07b1

Method BLASTN
NCBI GI g2618683
BLAST score 88
E value 3.0e-42

Match length 128 % identity 92



NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana] 171933 Seq. No. Seq. ID jC-atXL102Q1B1A10b1 Method BLASTN NCBI GI g2564048 BLAST score 139 E value 1.0e-72 Match length 139 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MKD15, complete sequence [Arabidopsis thaliana] Seq. No. 171934 Seq. ID jC-atXL102Q1E1F03b1 Method BLASTN NCBI GI g4159705 BLAST score 139 E value 2.0e-72 195 Match length 93 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MGD8, complete sequence 171935 Seq. No. jC-atXL1031Q1E1E04a1 Seq. ID Method BLASTN NCBI GI q4519195 BLAST score 118 1.0e-59 E value Match length 281 100 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MQC12, complete sequence Seq. No. 171936 Seq. ID jC-atXL1034Q1E1C09a1 Method BLASTN NCBI GI g4204173 BLAST score 90 E value 3.0e-43Match length 146 % identity 90 NCBI Description Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

171937 Seq. No.

Seq. ID jC-atXL1036Q1E1C03a1

Method BLASTN NCBI GI g4587641 BLAST score 121 E value 9.0e-62 Match length 157 94 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence



Seq. No. Seq. ID

171938

jC-atXL1038Q1E1F05a1

```
BLASTN
Method
                  g11957
NCBI GI
BLAST score
                  71
                  3.0e - 32
E value
                  83
Match length
                  48
% identity
NCBI Description Rice complete chloroplast genome
                  171939
Seq. No.
Seq. ID
                  jC-atXL103Q1B1H06b1
                  BLASTN
Method
NCBI GI
                  g2244747
BLAST score
                  132
                  3.0e-68
E value
                  208
Match length
                  91
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  171940
Seq. No.
Seq. ID
                  jC-atXL1040Q1E1A05b1
Method
                  BLASTN
NCBI GI
                  g2864607
                  195
BLAST score
                  1.0e-105
E value
                  255
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                  (ESSAII project)
Seq. No.
                  171941
Seq. ID
                  jC-atXL1040Q1E1D11b1
Method
                  BLASTN
                  g4510323
NCBI GI
                  138
BLAST score
                  7.0e-72
E value
Match length
                  150
                  98
% identity
NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                  cM, complete sequence
Seq. No.
                  171942
Seq. ID
                  jC-atXL1040Q1E1H05b1
Method
                  BLASTX
NCBI GI
                  g2129772
BLAST score
                  234
E value
                  9.0e-20
                  49
Match length
                  88
% identity
                  xyloglucan endotransglycosylase-related protein XTR-7 -
NCBI Description
                  Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  171943
Seq. No.
```



jC-atXL1040Q1E1H09a1 Seq. ID Method BLASTN q3608126 NCBI GI BLAST score 369 0.0e+00E value Match length 369 100 % identity Arabidopsis thaliana chromosome II BAC T32F12 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171944 Seq. No. Seq. ID jC-atXL1043Q1E1A10a1 BLASTN Method g4589410 NCBI GI 63 BLAST score 2.0e-27 E value 83 Match length 94 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description F2015, complete sequence 171945 Seq. No. jC-atXL1043Q1E1B10b1 Seq. ID Method BLASTN NCBI GI g3449323 250 BLAST score 1.0e-138 E value 250 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MZA15, complete sequence [Arabidopsis thaliana] Seq. No. 171946 Seq. ID jC-atXL1043Q1E1F03b1 Method BLASTN NCBI GI g603055 BLAST score 36 E value 6.0e-11 Match length 36 % identity 100 NCBI Description Arabidopsis thaliana inner mitochondrial membrane protein mRNA, complete cds 171947 Seq. No. Seq. ID jC-atXL1044Q1E1F03a1 BLASTN Method NCBI GI g2244747 71 BLAST score 3.0e-32 E value Match length 91 100 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

171948 Seq. No.

jC-atXL1044Q1E1G06a1 Seq. ID

Method BLASTN

NCBI GI

E value

BLAST score



```
g3367500
NCBI GI
                  50
BLAST score
                  2.0e-19
E value
                  108
Match length
                  91
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
                  171949
Seq. No.
                  jC-atXL1044Q1E1G06b1
Seq. ID
Method
                  BLASTN
                  g3367500
NCBI GI
                  199
BLAST score
                  1.0e-108
E value
                   371
Match length
                  100
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
                   171950
Seq. No.
                   jC-atXL1044Q1E1G11a1
Seq. ID
                   BLASTX
Method
                   g3319341
NCBI GI
                   333
BLAST score
                   4.0e-31
E value
                   67
Match length
                   82
% identity
                   (AF077407) similar to Medicago sativa nucleic acid binding
NCBI Description
                   protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
Seq. No.
                   171951
                   jC-atXL1047Q1E1D04b1
Seq. ID
                   BLASTX
Method
                   q2911078
NCBI GI
BLAST score
                   516
                   1.0e-52
E value
                   105
Match length
                   99
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   171952
Seq. No.
Seq. ID
                   jC-atXL1047Q1E1F04a1
                   BLASTN
Method
                   q3738275
NCBI GI
BLAST score
                   72
                   7.0e-33
E value
Match length
                   96
                   95
% identity
                   Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   171953
Seq. No.
Seq. ID
                   jC-atXL105Q1B1F12b1
Method
                   BLASTX
```

q114718

1.0e-10



```
Match length
                  49
                  57
% identity
                  PROBABLE COPPER-TRANSPORTING ATPASE SYNA
NCBI Description
                  >gi 79650 pir S10839 hypothetical protein 5 -
                  Synechococcus sp. (PCC 6301) (fragment)
                  >gi 48026 emb CAA29364 (X05925) VRF 5 (293 AA)
                  [Synechococcus PCC6301]
                  171954
Seq. No.
Seq. ID
                  jC-atXL106Q1B1A05b1
                  BLASTX
Method
                  q4580389
NCBI GI
                  140
BLAST score
                  4.0e-09
E value
Match length
                  33
                  76
% identity
                 (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
                  171955
Seq. No.
Seq. ID
                  jC-atXLI11Q1B1A03a1
Method
                  BLASTX
                  q2462745
NCBI GI
                  111
BLAST score
                  2.0e-20
E value
                  92
Match length
% identity
                  45
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  171956
Seq. No.
Seq. ID
                  jC-atXLI12Q1B1D03b1
Method
                  BLASTN
NCBI GI
                  q4582437
                  126
BLAST score
                  8.0e-65
E value
Match length
                  146
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7024 genomic
                  sequence, complete sequence
Seq. No.
                  171957
Seq. ID
                  jC-atXLI12Q1B1D08b1
Method
                  BLASTN
NCBI GI
                  g1617267
BLAST score
                  54
E value
                  1.0e-21
Match length
                  163
% identity
                  88
NCBI Description B.napus mRNA for acyl CoA synthetase
Seq. No.
                  171958
                  jC-atXLI13Q1B1C03b1
Seq. ID
Method
                  BLASTX
```

NCBI GI g2494125
BLAST score 295
E value 9.0e-27
Match length 56
% identity 100



74

% identity

NCBI Description

```
(AC002376) Strong similarity to Cucumis acetyl-CoA
NCBI Description
                  acyltransferase (gb_D70895). [Arabidopsis thaliana]
                  171959
Seq. No.
Seq. ID
                  jC-atXLI13Q1B1C08b1
                  BLASTX
Method
                  g3786025
NCBI GI
BLAST score
                  174
E value
                  1.0e-12
                  48
Match length
                  73
% identity
                  (AC005499) putative DNA-binding protein, 5' partial
NCBI Description
                  [Arabidopsis thaliana]
                  171960
Seq. No.
Seq. ID
                  jC-atXLIB327401P1c07a1
Method
                  BLASTN
                  g4454022
NCBI GI
                  56
BLAST score
E value
                  2.0e-22
                  85
Match length
                  89
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
                  (ESSAII project)
Seq. No.
                  171961
Seq. ID
                  jC-atXLIB327401P2d05a1
                  BLASTN
Method
                  g2290120
NCBI GI
BLAST score
                  53
E value
                  9.0e-21
Match length
                  64
% identity
                  95
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  171962
Seq. No.
                  jC-atXLIB327401P3b09b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3367500
BLAST score
                  94
E value
                  3.0e-45
Match length
                  142
% identity
                  92
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEO CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.
                  171963
Seq. ID
                  jC-atXLIB327401P3b11b2
Method
                  BLASTX
NCBI GI
                  g2129578
BLAST score
                  315
                  6.0e-29
E value
Match length
                  89
```

dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi 928932 emb CAA89205 (Z49239) homolog of



dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No. 171964

Seq. ID jC-atXLIB327401P3b12b2

Method BLASTN NCBI GI q2582640 BLAST score 54 2.0e-21 E value Match length 58 % identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171965

Seq. ID jC-atXLIB327401P3c02b2

Method BLASTN NCBI GI g2656030 91 BLAST score 2.0e-43 E value 223 Match length

93 % identity

Seq. No. 171966

NCBI Description

Seq. ID jC-atXLIB327401P3c03b2

Method BLASTN NCBI GI g3241939 BLAST score 75 E value 5.0e-34 Match length 103

% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T26J13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

171967 Seq. No.

Seq. ID jC-atXLIB327401P3e03b2

Method BLASTN g2582640 NCBI GI BLAST score 57

E value 4.0e-23 Match length 65 97 % identity

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

Seq. No. 171968

Seq. ID jC-atXLIB327401P3e12b2

Method BLASTN NCBI GI g2582640 BLAST score 36 E value 1.0e-10 Match length 56 91 % identity

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

NCBI Description

thalianal



factor, RSp40

```
171969
Seq. No.
                  jC-atXLIB327401P3f08b2
Seq. ID
Method
                  BLASTN
                  g2245031
NCBI GI
                  264
BLAST score
                  1.0e-146
E value
Match length
                  367
% identity
                  93
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  171970
Seq. No.
Seq. ID
                  jC-atXLIB327401P3g06b2
Method
                  BLASTN
                  g2264318
NCBI GI
                  92
BLAST score
                  5.0e-44
E value
                  306
Match length
% identity
                  89
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
                  171971
Seq. No.
Seq. ID
                  jC-atXLIB327401P3g11b2
Method
                  BLASTN
                  g2582640
NCBI GI
                  37
BLAST score
                  3.0e-11
E value
Match length
                  69
% identity
                  88
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171972
Seq. No.
                  jC-atXLIB327401P3h07b2
Seq. ID
                  BLASTN
Method
                  g3367500
NCBI GI
BLAST score
                  108
                  1.0e-53
E value
Match length
                  192
                  89
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
                   171973
Seq. No.
Seq. ID
                   jC-atXLIB327401P4a03a2
                  BLASTX
Method
NCBI GI
                  g3033375
BLAST score
                  226
                  3.0e-19
E value
Match length
                  139
% identity
                   42
```

23519

(AC004238) putative berberine bridge enzyme [Arabidopsis



171974 Seq. No. Seq. ID jC-atXLIB327401P4a06a2 Method BLASTN NCBI GI g2462264 39 BLAST score E value 2.0e-12 43 Match length 98 % identity Cucumis sativus mRNA for patatin-like protein, partial NCBI Description 171975 Seq. No. jC-atXLIB327401P4a06b2 Seq. ID BLASTN Method g2880038 NCBI GI BLAST score 40 4.0e-13 E value 48 Match length % identity 96 Arabidopsis thaliana chromosome II BAC T11J7 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 171976 Seq. No. jC-atXLIB327401P4a09a2 Seq. ID Method BLASTN NCBI GI g3702733 BLAST score 64 E value 2.0e-27 Match length 192 86 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJP23, complete sequence [Arabidopsis thaliana] Seq. No. 171977 Seq. ID jC-atXLIB327401P4a11b2 Method BLASTN NCBI GI g2351068 BLAST score 69 2.0e-30 E value Match length 172 % identity 86 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana] 171978 Seq. No. Seq. ID jC-atXLIB327401P4b04a2 Method BLASTN g2462264 NCBI GI

50 BLAST score 5.0e-19 E value 50 Match length 100 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

171979 Seq. No.

jC-atXLIB327401P4b05a2 Seq. ID

Method BLASTN NCBI GI g2462264



38

100

Match length

% identity

```
BLAST score
                  2.0e-15
E value
Match length
                  44
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171980
Seq. No.
Seq. ID
                  jC-atXLIB327401P4b07b2
Method
                  BLASTN
                  g2582640
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                  58
Match length
                  98
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171981
Seq. No.
                  jC-atXLIB327401P4b10a2
Seq. ID
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  51
E value
                  1.0e-19
                  51
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171982
Seq. No.
Seq. ID
                  jC-atXLIB327401P4b11a2
Method
                  BLASTN
                  g2462264
NCBI GI
                  37
BLAST score
                  4.0e-11
E value
                  53
Match length
% identity
                  92
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  171983
Seq. No.
                  jC-atXLIB327401P4b12a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g540252
BLAST score
                  35
                  2.0e-10
E value
Match length
                  56
% identity
                   95
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  171984
Seq. No.
                   jC-atXLIB327401P4c02a2
Seq. ID
Method
                  BLASTN
                  g540252
NCBI GI
BLAST score
                   38
                   8.0e-12
E value
```

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.

Seq. ID

Method

171990

BLASTN

jC-atXLIB327401P4c08a2



```
171985
Seq. No.
                  jC-atXLIB327401P4c02b2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  54
                  2.0e-21
E value
                  70
Match length
                  94
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171986
Seq. No.
                  jC-atXLIB327401P4c03b2
Seq. ID
                  BLASTN
Method
                  g3941523
NCBI GI
                  36
BLAST score
                  2.0e-10
E value
                  48
Match length
                  94
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  171987
Seq. No.
                  jC-atXLIB327401P4c04a2
Seq. ID
                  BLASTX
Method
                  q3928543
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
                  93
Match length
                  46
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  171988
Seq. No.
                  jC-atXLIB327401P4c06a1
Seq. ID
                  BLASTN
Method
                  q2702261
NCBI GI
                  119
BLAST score
                  4.0e-60
E value
Match length
                  199
                  95
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T21L14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  171989
Seq. No.
Seq. ID
                   jC-atXLIB327401P4c06b1
Method
                  BLASTX
                  q2702274
NCBI GI
BLAST score
                   349
                   4.0e-38
E value
Match length
                  117
% identity
                  (AC003033) unknown protein [Arabidopsis thaliana]
NCBI Description
```



NCBI GI g4757678 BLAST score 153 E value 2.0e-80 Match length 349 % identity 85

NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic

sequence, complete sequence

Seq. No. 171991

Seq. ID jC-atXLIB327401P4c09a1

Method BLASTN
NCBI GI g2914688
BLAST score 120
E value 1.0e-60
Match length 450
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171992

Seq. ID jC-atXLIB327401P4c09b1

Method BLASTN
NCBI GI g2914688
BLAST score 35
E value 4.0e-10
Match length 80
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 171993

Seq. ID jC-atXLIB327401P4c11b1

Method BLASTN
NCBI GI g531828
BLAST score 39
E value 2.0e-12
Match length 51
% identity 94

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 171994

Seq. ID jC-atXLIB327401P4c12b2

Method BLASTN
NCBI GI g2582640
BLAST score 66
E value 1.0e-28
Match length 66
% identity 100

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 171995

Seq. ID jC-atXLIB327401P4d04b2

Method BLASTN
NCBI GI g2582640
BLAST score 46
E value 1.0e-16



```
58
Match length
                  95
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  171996
Seq. No.
Seq. ID
                  jC-atXLIB327401P4e02a1
                  BLASTN
Method
                  g2462264
NCBI GI
                  45
BLAST score
                  6.0e-16
E value
                  53
Match length
                  96
% identity
                 Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  171997
Seq. No.
Seq. ID
                  jC-atXLIB327401P4e02b2
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                  43
E value
                  3.0e-15
Match length
                  61
                  95
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  171998
Seq. No.
Seq. ID
                   jC-atXLIB327401P4e03a1
                  BLASTN
Method
NCBI GI
                  g3978257
BLAST score
                  91
                  2.0e-43
E value
                   99
Match length
                   98
% identity
                  Arabidopsis thaliana endo-1,4-beta-D-glucanase KORRIGAN
NCBI Description
                   (KOR) gene, KOR-1 allele, complete cds
                  171999
Seq. No.
                   jC-atXLIB327401P4e03a2
Seq. ID
Method
                   BLASTN
                  g3978257
NCBI GI
BLAST score
                   63
                   9.0e-27
E value
                  87
Match length
                   93
% identity
NCBI Description Arabidopsis thaliana endo-1,4-beta-D-glucanase KORRIGAN
                   (KOR) gene, KOR-1 allele, complete cds
                   172000
Seq. No.
Seq. ID
                   jC-atXLIB327401P4e03b1
Method
                   BLASTN
NCBI GI
                  g2687441
```

Method BLASTN
NCBI GI g2687441
BLAST score 48
E value 9.0e-18
Match length 64
% identity 94

NCBI Description Lithophragma trifoliata large subunit 26S ribosomal RNA



gene, partial sequence

```
Seq. No.
                  172001
Seq. ID
                  jC-atXLIB327401P4e04b2
Method
                  BLASTN
NCBI GI
                  g2582640
                  43
BLAST score
                  6.0e-15
E value
Match length
                  51
% identity
                  96
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172002
                  jC-atXLIB327401P4e05a1
Seq. ID
Method
                  BLASTN
                  g4454022
NCBI GI
BLAST score
                  78
                  1.0e-35
E value
Match length
                  173
% identity
                  88
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
                  (ESSAII project)
                  172003
Seq. No.
                  jC-atXLIB327401P4e08a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
                  42
BLAST score
                  3.0e-14
E value
Match length
                  50
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172004
Seq. No.
Seq. ID
                  jC-atXLIB327401P4e09a2
                  BLASTN
Method
NCBI GI
                  g3643588
                  35
BLAST score
                  5.0e-10
E value
Match length
                  162
                  84
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172005
                  jC-atXLIB327401P4e12a2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3702724
BLAST score
                  203
E value
                  1.0e-110
Match length
                  416
                  95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K17N15, complete sequence [Arabidopsis thaliana]
```

23525

172006

Seq. No.



73

1.0e-32

BLAST score

E value

```
jC-atXLIB327401P4e12b2
Seq. ID
Method
                  BLASTN
                  g3702724
NCBI GI
                  82
BLAST score
                  3.0e-38
E value
Match length
                  339
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172007
                  jC-atXLIB327401P4f02a1
Seq. ID
Method
                  BLASTN
                  q2462264
NCBI GI
                  48
BLAST score
                  5.0e-18
E value
Match length
                  52
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172008
Seq. No.
                  jC-atXLIB327401P4f02a2
Seq. ID
Method
                  BLASTX
                  q2262103
NCBI GI
                  382
BLAST score
                   9.0e-37
E value
                  96
Match length
% identity
                   69
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                  172009
Seq. No.
                   jC-atXLIB327401P4f07a1
Seq. ID
Method
                  BLASTN
                   g531828
NCBI GI
                   42
BLAST score
                   4.0e-14
E value
Match length
                   66
% identity
                   92
NCBI Description Cloning vector pSport1, complete cds
                   172010
Seq. No.
                   jC-atXLIB327401P4f12b2
Seq. ID
                   BLASTN
Method
                   g2149639
NCBI GI
BLAST score
                   116
                   2.0e-58
E value
                   233
Match length
                   89
% identity
NCBI Description Arabidopsis thaliana Argonaute protein (AGO1) mRNA,
                   complete cds
                   172011
Seq. No.
                   jC-atXLIB327401P4g01a1
Seq. ID
                   BLASTN
Method
                   q16491
NCBI GI
```



```
116
Match length
% identity
                  A. thaliana mRNA for root-specific gene
NCBI Description
Seq. No.
                  172012
Seq. ID
                  jC-atXLIB327401P4g02b2
                  BLASTN
Method
NCBI GI
                  q2582640
                  56
BLAST score
                  1.0e-22
E value
                  56
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  172013
Seq. No.
Seq. ID
                  jC-atXLIB327401P4g04a2
Method
                  BLASTN
NCBI GI
                  g2290120
                  54
BLAST score
E value
                  2.0e-21
                  58
Match length
                  98
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  172014
Seq. No.
                  jC-atXLIB327401P4g08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2290120
BLAST score
                  53
                  9.0e-21
E value
Match length
                  65
                  95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172015
Seq. No.
Seq. ID
                  jC-atXLIB327401P4g08b1
Method
                  BLASTN
                  g2582640
NCBI GI
                  55
BLAST score
                  5.0e-22
E value
Match length
                  63
                  97
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172016
                  jC-atXLIB327401P4h03a2
Seq. ID
```

Method BLASTN
NCBI GI g3128166
BLAST score 95
E value 8.0e-46
Match length 358
% identity 82

NCBI Description Arabidopsis thaliana chromosome II BAC F4I1 genomic



sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172017 Seq. ID jC-atXLIB327401P4h04b1 BLASTX Method NCBI GI g3128190 BLAST score 282 4.0e-27 E value Match length 93 72 % identity (AC004521) putative beta-glucosidase [Arabidopsis thaliana] NCBI Description 172018 Seq. No. Seq. ID jC-atXLIB327401P4h06a2 BLASTN Method NCBI GI g2462264 BLAST score 43 E value 6.0e-15 Match length 47 % identity 98 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172019 Seq. ID jC-atXLIB327401P4h06b2 Method BLASTN NCBI GI g2392762 BLAST score 111 3.0e-55 E value Match length 139 % identity 95 NCBI Description Arabidopsis thaliana BAC T32N15 from chromsome III near 54 cM, complete sequence 172020 Seq. No. Seq. ID jC-atXLIB327401P4h07b1 Method BLASTN

g3869069 NCBI GI BLAST score 87 E value 4.0e-41 Match length 290 89 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 172021

jC-atXLIB327401P4h10a1 Seq. ID

Method BLASTN NCBI GI g3406034 39 BLAST score E value 2.0e-12 Match length 115 % identity 86

NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

172022 Seq. No.

jC-atXLIB327401P4h10b1 Seq. ID



```
BLASTX
Method
NCBI GI
                  q3063691
BLAST score
                  189
                  3.0e-14
E value
                  44
Match length
                  73
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                  172023
Seq. No.
Seq. ID
                  iC-atXLIB327401P4h12a2
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  54
E value
                  2.0e-21
                  66
Match length
                  95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  172024
Seq. ID
                  jC-atXLIB327402P1a03a1
                  BLASTN
Method
                  g1707369
NCBI GI
                  53
BLAST score
                  9.0e-21
E value
                  89
Match length
                  90
% identity
                  A.thaliana mRNA for arginine/serine-rich splicing factor,
NCBI Description
                  RSp41
                  172025
Seq. No.
                  jC-atXLIB327402P1a06a1
Seq. ID
                  BLASTN
Method
                  q4096078
NCBI GI
BLAST score
                  89
                  2.0e-42
E value
                  175
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172026
                  jC-atXLIB327402P1a08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2564051
BLAST score
                  113
                  1.0e-56
E value
Match length
                  311
% identity
                  84
NCBI Description
                  Arabidopsis thaliana genomic ....romosome 5, P1 clone:
                  MWD9, complete sequence [Arabidopsis thaliana]
                  172027
Seq. No.
```

jC-atXLIB327402P1b01a1 Seq. ID

BLASTN Method q4469002 NCBI GI 55 BLAST score



E value 4.0e-22
Match length 111
% identity 87
NCRI Description Arabido

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 172028

Seq. ID jC-atXLIB327402P1b02a1

Method BLASTN
NCBI GI g531828
BLAST score 37
E value 3.0e-11
Match length 45
% identity 96

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172029

Seq. ID jC-atXLIB327402P1b03a1

Method BLASTX
NCBI GI g131398
BLAST score 184
E value 5.0e-20
Match length 80
% identity 71

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 172030

Seq. ID jC-atXLIB327402P1b05a1

Method BLASTN
NCBI GI g2462264
BLAST score 37
E value 3.0e-11
Match length 45
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172031

Seq. ID jC-atXLIB327402P1c01a1

Method BLASTN
NCBI GI g430946
BLAST score 55
E value 5.0e-22
Match length 126
% identity 87

NCBI Description Arabidopsis thaliana PSI type III chlorophyll a/b-binding

protein (Lhca3*1) mRNA, complete cds

Seq. No. 172032

Seq. ID jC-atXLIB327402P1c04a1



BLASTN Method g2290120 NCBI GI 48 BLAST score 8.0e-18 E value 59 Match length 97 % identity NCBI Description

HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

172033 Seq. No.

jC-atXLIB327402Pld01a1 Seq. ID

BLASTN Method q4741184 NCBI GI 66 BLAST score E value 2.0e-28 105 Match length 90 % identity

Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 NCBI Description

(ESSA project)

Seq. No. 172034

Seq. ID jC-atXLIB327402P1d06b1

BLASTN Method g2582640 NCBI GI 67 BLAST score 2.0e-29 E value 75 Match length 97

% identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

172035 Seq. No.

jC-atXLIB327402P1d12a1 Seq. ID

BLASTN Method NCBI GI g2459406 BLAST score 171 3.0e-91 E value 331 Match length 88 % identity

Arabidopsis thaliana chromosome II BAC F4P9 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

172036 Seq. No.

iC-atXLIB327402P1e02a1 Seq. ID

BLASTN Method NCBI GI g4159704 BLAST score 188 1.0e-101 E value Match length 430 90 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MCB17, complete sequence

172037 Seq. No.

jC-atXLIB327402P1e09a1 Seq. ID

Method BLASTN g2462264 NCBI GI

E value Match length



```
BLAST score
                  48
E value
                  7.0e-18
Match length
                  52
                  98
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  172038
Seq. No.
Seq. ID
                  jC-atXLIB327402P1e12a1
Method
                  BLASTN
                  g3608126
NCBI GI
BLAST score
                  194
                  1.0e-105
E value
Match length
                  318
                  90
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  172039
Seq. No.
Seq. ID
                  jC-atXLIB327402P1f02a1
Method
                  BLASTX
NCBI GI
                  g481132
BLAST score
                  305
E value
                  5.0e-34
Match length
                  119
                  74
% identity
                  sucrose transport protein SUC1 - Arabidopsis thaliana
NCBI Description
                  >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter
                  [Arabidopsis thaliana]
Seq. No.
                  172040
                  jC-atXLIB327402P1f03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2618683
BLAST score
                  228
E value
                  1.0e-125
Match length
                  469
                  85
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172041
Seq. ID
                  jC-atXLIB327402P1f06a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  39
E value
                  2.0e-12
                  55
Match length
% identity
                  95
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172042
Seq. No.
                  jC-atXLIB327402P1f09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4263753
BLAST score
                  86
```

23532

2.0e-40



% identity Arabidopsis thaliana chromosome V map near 60.5 cM, NCBI Description complete sequence [Arabidopsis thaliana] 172043 Seq. No. jC-atXLIB327402P1f10b1 Seq. ID BLASTN Method NCBI GI q2618602 46 BLAST score E value 1.0e-16 98 Match length 89 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSJ1, complete sequence [Arabidopsis thaliana] 172044 Seq. No. Seq. ID jC-atXLIB327402P1f11a1 BLASTX Method NCBI GI g872116 BLAST score 144 7.0e-09 E value 68 Match length 47 % identity (X79770) sti (stress inducible protein) [Glycine max] NCBI Description 172045 Seq. No. Seq. ID jC-atXLIB327402P1f12a1 Method BLASTN NCBI GI g3367500 BLAST score 50 E value 6.0e-19 69 Match length 94 % identity REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 NCBI Description TO: 93489, complete sequence [Arabidopsis thaliana] Seq. No. 172046 Seq. ID jC-atXLIB327402P1g04a1 BLASTN Method NCBI GI q2462264 BLAST score 46 E value 1.0e-16 Match length 54 98 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172047 Seq. No. jC-atXLIB327402P1g06a1 Seq. ID Method BLASTN NCBI GI g2462264 BLAST score 41 1.0e-13 E value 56 Match length 93 % identity

Seq. No. 172048

NCBI Description

Cucumis sativus mRNA for patatin-like protein, partial



```
jC-atXLIB327402P1g08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  36
E value
                  1.0e-10
                  40
Match length
                  97
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172049
Seq. No.
Seq. ID
                  jC-atXLIB327402P1g10a1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  53
                  9.0e-21
E value
Match length
                  69
% identity
                  94
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  172050
Seq. ID
                  jC-atXLIB327402P1g11a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  48
                  8.0e-18
E value
Match length
                  64
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172051
Seq. No.
                  jC-atXLIB327402P1h03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2342673
BLAST score
                  116
E value
                  2.0e-58
                  308
Match length
                  86
% identity
                  Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  172052
Seq. No.
                  jC-atXLIB327402P1h04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3941523
BLAST score
                  39
                  2.0e-12
E value
                  50
Match length
% identity
                  94
NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)
                  mRNA, complete cds
```

Seq. No. 172053

Seq. ID jC-atXLIB327402P1h05a1

Method BLASTN
NCBI GI g3608126
BLAST score 103



```
E value
                  8.0e-51
Match length
                  153
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  172054
Seq. No.
Seq. ID
                  jC-atXLIB327402P1h08b1
Method
                  BLASTN
                  q3941523
NCBI GI
BLAST score
                  35
                  1.0e-10
E value
```

Match length 49
% identity 92
NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 172055
Seq. ID jC-atXLIB327402P1h10a1
Method BLASTN
NCBI GI g2462264

BLAST score 36 E value 1.0e-10 Match length 52 % identity 92

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172056

Seq. ID jC-atXLIB327402P1h11a1

Method BLASTN
NCBI GI g4191771
BLAST score 77
E value 4.0e-35

E value 4.0e-Match length 192 % identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172057

Seq. ID jC-atXLIB327402P2b02a1

Method BLASTX
NCBI GI g1169782
BLAST score 426
E value 7.0e-42
Match length 87
% identity 98

NCBI Description FUSCA PROTEIN FUS6 >gi 432446 (L26498) FUS6 [Arabidopsis

thaliana]

Seq. No. 172058

Seq. ID jC-atXLIB327402P2b03a1

Method BLASTN
NCBI GI g2618600
BLAST score 307
E value 1.0e-172
Match length 338
% identity 98



```
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDC12, complete sequence [Arabidopsis thaliana]
                  172059
Seq. No.
Seq. ID
                  jC-atXLIB327402P2b12a1
                  BLASTN
Method
NCBI GI
                  g531828
                  50
BLAST score
                  6.0e-19
E value
                  62
Match length
                  95
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172060
Seq. No.
Seq. ID
                  jC-atXLIB327402P2c12a1
Method
                  BLASTX
                  g4220451
NCBI GI
BLAST score
                  177
                  1.0e-12
E value
Match length
                  72
% identity
                  56
                  (AC006216) Identical to gb AF054906 myrosinase-binding
NCBI Description
                  protein homolog from Arabidopsis thaliana. ESTs gb F15276
                  and qb F15275 come from this gene. [Arabidopsis thaliana]
                  172061
Seq. No.
Seq. ID
                  jC-atXLIB327402P2d07a1
                  BLASTX
Method
                  g1172977
NCBI GI
BLAST score
                  153
E value
                  5.0e-10
                  49
Match length
                  65
% identity
                  60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  172062
Seq. No.
                  jC-atXLIB327402P2d11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656026
BLAST score
                  113
E value
                  1.0e-56
Match length
                  308
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDF20
                  172063
Seq. No.
```

jC-atXLIB327402P2e02a1 Seq. ID

Method BLASTN NCBI GI g2462264 BLAST score 53 9.0e-21 E value 57 Match length 98 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

NCBI GI



```
172064
Seq. No.
Seq. ID
                  jC-atXLIB327402P2e05a1
Method
                  BLASTN
NCBI GI
                  g2290120
                  56
BLAST score
E value
                  1.0e-22
Match length
                  64
                  97
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172065
Seq. No.
Seq. ID
                  jC-atXLIB327402P2f01a1
                  BLASTN
Method
                  g2290120
NCBI GI
                  53
BLAST score
                  9.0e-21
E value
                  61
Match length
                  97
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
Śeq. No.
                  172066
Seq. ID
                  jC-atXLIB327402P2f03a1
                  BLASTN
Method
                  g2462264
NCBI GI
                  57
BLAST score
                  4.0e-23
E value
                  61
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172067
Seq. No.
                  iC-atXLIB327402P2f04a1
Seq. ID
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  57
                  3.0e-23
E value
Match length
                  65
% identity
                  97
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  172068
Seq. ID
                  jC-atXLIB327402P2f05a1
Method
                  BLASTX
NCBI GI
                  g3980413
BLAST score
                  49
                  2.0e-19
E value
Match length
                  141
% identity
                  43
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
                  172069
Seq. No.
                  jC-atXLIB327402P2f11a1
Seq. ID
Method
                  BLASTN
```

23537

q4757662



BLAST score 221 E value 1.0e-121 Match length 435 % identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 172070

Seq. ID jC-atXLIB327402P2f12a1

Method BLASTN
NCBI GI g3885325
BLAST score 92
E value 5.0e-44

Match length 388 % identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172071

Seq. ID jC-atXLIB327402P2g09a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 6.0e-19
Match length 62
% identity 95

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172072

Seq. ID jC-atXLIB327402P2h02a1

Method BLASTN
NCBI GI g2462264
BLAST score 53
E value 9.0e-21
Match length 57
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172073

Seq. ID jC-atXLIB327402P2h04a1

Method BLASTN
NCBI GI g3738275
BLAST score 414
E value 0.0e+00
Match length 438
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172074

Seq. ID jC-atXLIB327402P2h05a1

Method BLASTN
NCBI GI g3449322
BLAST score 300
E value 1.0e-168
Match length 423
% identity 96



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No. 172075

Seq. ID jC-atXLIB327402P2h07a1

Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 2.0e-15

Match length 52 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172076

Seq. ID jC-atXLIB327402P2h09a1

Method BLASTN
NCBI GI g2462264
BLAST score 55
E value 5.0e-22
Match length 55
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172077

Seq. ID jC-atXLIB327402P2h10a1

Method BLASTX
NCBI GI g3851636
BLAST score 246
E value 8.0e-21
Match length 111
% identity 47

NCBI Description (AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 172078

Seq. ID jC-atXLIB327402P2h12a1

Method BLASTN
NCBI GI 94589439
BLAST score 99
E value 3.0e-48
Match length 167
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 172079

Seq. ID jC-atXLIB327402P3a05a1

Method BLASTN
NCBI GI 94519197
BLAST score 52
E value 1.0e-20
Match length 129
% identity 60

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MTC11, complete sequence

Seq. No. 172080

NCBI GI BLAST score



```
jC-atXLIB327402P3a07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4096078
BLAST score
                  72
E value
                  3.0e-32
                  247
Match length
                  83
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  172081
Seq. No.
                  jC-atXLIB327402P3a09a1
Seq. ID
Method
                  BLASTN
                  q2290120
NCBI GI
BLAST score
                  35
                  4.0e-10
E value
Match length
                  39
                  97
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  172082
Seq. No.
                  jC-atXLIB327402P3a11a1
Seq. ID
Method
                  BLASTX
                  g1769905
NCBI GI
                  87
BLAST score
                  3.0e-12
E value
                  79
Match length
% identity
                  56
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
                  172083
Seq. No.
Seq. ID
                  jC-atXLIB327402P3a12a1
Method
                  BLASTN
NCBI GI
                  g540252
                  34
BLAST score
                  2.0e-09
E value
Match length
                  38
% identity
                  97
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  172084
Seq. No.
                  jC-atXLIB327402P3b05a1
Seq. ID
Method
                  BLASTN
                  g531828
NCBI GI
                  40
BLAST score
                  5.0e-13
E value
Match length
                  92
                  91
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172085
Seq. No.
                  jC-atXLIB327402P3b06a1
Seq. ID
                  BLASTN
Method
```

23540

g2290120



```
2.0e-09
E value
Match length
                  34
                  100
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172086
Seq. No.
                   jC-atXLIB327402P3b07a1
Seq. ID
                  BLASTN
Method
                  g2494106
NCBI GI
                  82
BLAST score
                  4.0e-38
E value
                  167
Match length
                   92
% identity
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                   172087
Seq. No.
Seq. ID
                   jC-atXLIB327402P3b07b1
                   BLASTN
Method
                   g2582640
NCBI GI
                   36
BLAST score
                   9.0e-11
E value
                   60
Match length
                   92
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172088
Seq. No.
Seq. ID
                   jC-atXLIB327402P3c02a1
Method
                   BLASTN
                   g3269280
NCBI GI
                   61
BLAST score
                   1.0e-25
E value
Match length
                   247
                   89
% identity
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
NCBI Description
                   (ESSAII project)
Seq. No.
                   172089
                   jC-atXLIB327402P3c03a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2462264
BLAST score
                   49
                   2.0e-18
E value
                   57
Match length
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172090
Seq. No.
                   jC-atXLIB327402P3c05b1
Seq. ID
```

Method BLASTN
NCBI GI g2582640
BLAST score 54
E value 2.0e-21
Match length 74
% identity 93



Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172091 Seq. No. jC-atXLIB327402P3c12b1 Seq. ID BLASTX Method g2129759 NCBI GI BLAST score 199 3.0e-15 E value 140 Match length 36 % identity UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana NCBI Description >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana] 172092 Seq. No. jC-atXLIB327402P3d02a1 Seq. ID BLASTN Method g2160155 NCBI GI BLAST score 210 1.0e-114 E value 442 Match length 92 % identity Sequence of BAC F21M12 from Arabidopsis thaliana chromosome NCBI Description 1, complete sequence [Arabidopsis thaliana] 172093 Seq. No. jC-atXLIB327402P3d04a1 Seq. ID BLASTX Method NCBI GI g4455369 BLAST score 106 5.0e-12 E value 114 Match length 43 % identity (AL035524) hypothetical protein [Arabidopsis thaliana] NCBI Description 172094 Seq. No. jC-atXLIB327402P3d08a1 Seq. ID BLASTN Method NCBI GI g2462264 BLAST score 36 E value 1.0e-10 40 Match length 97 % identity Cucumis sativus mRNA for patatin-like protein, partial NCBI Description

Seq. No. 172095

jC-atXLIB327402P3d09b1 Seq. ID

Method BLASTX NCBI GI g3212879 BLAST score 188 6.0e-14E value Match length 57 74 % identity

(AC004005) putative ribosomal protein L7 [Arabidopsis NCBI Description

thaliana]



```
Seq. No. 172096
Seq. ID jC-atXLIB327402P3d11a1
Method BLASTX
```

NCBI GI g3935158 BLAST score 598 E value 4.0e-62 Match length 149 % identity 82

NCBI Description (AC004557) F17L21.1 [Arabidopsis thaliana]

Seq. No. 172097

Seq. ID jC-atXLIB327402P3d12b1

Method BLASTN
NCBI GI g3080737
BLAST score 50
E value 5.0e-19
Match length 66
% identity 94

NCBI Description Arabidopsis thaliana pasticcino 1-A (PAS1-A) mRNA, complete

cds

Seq. No. 172098

Seq. ID jC-atXLIB327402P3e04b1

Method BLASTN
NCBI GI g2582640
BLAST score 40
E value 5.0e-13
Match length 71
% identity 90

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172099

Seq. ID jC-atXLIB327402P3e06b1

Method BLASTN
NCBI GI g2582640
BLAST score 53
E value 1.0e-20
Match length 77
% identity 92

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172100

Seq. ID jC-atXLIB327402P3e11a1

Method BLASTN
NCBI GI g2289960
BLAST score 38
E value 8.0e-12
Match length 54
% identity 93

NCBI Description Arabidopsis thaliana GTPase AtRAB8 (atrab8) mRNA, complete

cds

Seq. No. 172101

Seq. ID jC-atXLIB327402P3e11b1

Method BLASTX

Match length



```
NCBI GI
                  q1370198
BLAST score
                  339
                  1.0e-31
E value
Match length
                  92
                  76
% identity
                  (Z73948) RAB8E [Lotus japonicus]
NCBI Description
Seq. No.
                  172102
                  jC-atXLIB327402P3e12b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                  53
E value
                  9.0e-21
                  69
Match length
                  94
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172103
                  jC-atXLIB327402P3f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4096078
BLAST score
                  111
E value
                  2.0e-55
                  442
Match length
% identity
                  90
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172104
                  jC-atXLIB327402P3f02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4096078
BLAST score
                  47
                  3.0e-17
E value
Match length
                  95
                  88
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172105
                   jC-atXLIB327402P3f07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2462264
                   42
BLAST score
                  3.0e-14
E value
                  54
Match length
                   94
% identity
NCBI Description
                  Cucumis sativus mRNA for patatin-like protein, partial
                   172106
Seq. No.
                   jC-atXLIB327402P3f07b1
Seq. ID
Method
                  BLASTN
                  g3600062
NCBI GI
                  76
BLAST score
                  2.0e-34
E value
```



```
% identity
                  95
                  Arabidopsis thaliana BAC T25C13
NCBI Description
                  172107
Seq. No.
                  jC-atXLIB327402P3f08b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2582640
                  46
BLAST score
                  1.0e-16
E value
Match length
                  70
                  91
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172108
Seq. ID
                  jC-atXLIB327402P3f10a1
Method
                  BLASTN
                  g4490717
NCBI GI
BLAST score
                  172
                  9.0e-92
E value
Match length
                  442
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                  project)
                  172109
Seq. No.
                  jC-atXLIB327402P3g04a1
Seq. ID
Method
                  BLASTX
                  g1173624
NCBI GI
                  134
BLAST score
                  6.0e-10
E value
                  64
Match length
                   58
% identity
                  (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                  SM9108']
                  172110
Seq. No.
                   jC-atXLIB327402P3g06a1
Seq. ID
Method
                  BLASTN
                  g4415928
NCBI GI
                   223
BLAST score
                  1.0e-122
E value
Match length
                   444
                   98
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172111
                   jC-atXLIB327402P3g08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q531828
                   39
BLAST score
                   2.0e-12
E value
                   59
Match length
                   92
% identity
```

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172112 Seq. ID jC-atXLIB327402P3g10a1 Method BLASTN NCBI GI q2760171 BLAST score 121 2.0e-61 E value Match length 343 % identity 87 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MPA24, complete sequence [Arabidopsis thaliana] 172113 Seq. No. Seq. ID jC-atXLIB327402P3h02a1 BLASTX Method q4204315 NCBI GI BLAST score 226 E value 2.0e-18 Match length 85 % identity 46 NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana] 172114 Seq. No. jC-atXLIB327402P3h06a1 Seq. ID Method BLASTN g3449323 NCBI GI BLAST score 102 5.0e-50 E value Match length 201 % identity 91 MZA15, complete sequence [Arabidopsis thaliana] Seq. No. 172115

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Seq. ID jC-atXLIB327402P3h07a1

Method BLASTX NCBI GI g3451074 BLAST score 109 4.0e-46 E value Match length 136 % identity 67

(AL031326) putative protein [Arabidopsis thaliana] NCBI Description

172116 Seq. No.

jC-atXLIB327402P3h08a1 Seq. ID

Method BLASTN NCBI GI g2462264 56 BLAST score 1.0e-22 E value 60 Match length 98 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

172117 Seq. No.

jC-atXLIB327402P3h09a1 Seq. ID

Method BLASTN NCBI GI q4519192

BLAST score 49



E value 2.0e-18 89 Match length 89 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MBK21, complete sequence Seq. No. 172118 jC-atXLIB327402P3h11a1 Seq. ID BLASTN Method g4027862 NCBI GI 104 BLAST score 3.0e-51 E value Match length 321 % identity 88 Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 172119 jC-atXLIB327402P4b04b1 Seq. ID Method BLASTN NCBI GI g2288979 BLAST score 63 E value 9.0e-27 Match length 118 89 % identity Arabidopsis thaliana chromosome II BAC T01024 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 172120 jC-atXLIB327402P4d07a1 Seq. ID BLASTN Method g2618600 NCBI GI BLAST score 69 2.0e-30 E value 223 Match length 86 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MDC12, complete sequence [Arabidopsis thaliana] Seq. No. 172121 jC-atXLIB327402P4d07b1 Seq. ID BLASTN Method g2618600 NCBI GI 63 BLAST score 1.0e-26 E value 111 Match length 91 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MDC12, complete sequence [Arabidopsis thaliana]

Seq. No. 172122

Seq. ID jC-atXLIB327402P4d10b1

Method BLASTN
NCBI GI g2618602
BLAST score 84
E value 2.0e-39
Match length 142



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  172123
Seq. No.
                  jC-atXLIB327402P4e10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1877523
                  67
BLAST score
                  3.0e-29
E value
                  127
Match length
                  90
% identity
                  Arabidopsis thaliana BAC T7I23, complete sequence
NCBI Description
                  [Arabidopsis thaliana]
                  172124
Seq. No.
Seq. ID
                  jC-atXLIB327402P4e12b1
                  BLASTN
Method
NCBI GI
                  g1877523
BLAST score
                  125
                  1.0e-63
E value
                  342
Match length
                  78
% identity
                  Arabidopsis thaliana BAC T7I23, complete sequence
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  172125
                  jC-atXLIB327402P4f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4220645
                  242
BLAST score
                  1.0e-133
E value
                  333
Match length
% identity
                   94
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
                   172126
Seq. No.
Seq. ID
                  jC-atXLIB327402P4f02b1
Method
                  BLASTN
                   g4220645
NCBI GI
                   254
BLAST score
                   1.0e-141
E value
                   334
Match length
% identity
                   94
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
                   172127
Seq. No.
                   jC-atXLIB327402P4f10a1
Seq. ID
Method
                   BLASTN
```

Method BLASTN
NCBI GI g2618602
BLAST score 35
E value 4.0e-10
Match length 75
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MSJ1, complete sequence [Arabidopsis thaliana]

172128 Seq. No. Seq. ID jC-atXLIB327402P4g01b1 BLASTN Method g2582640 NCBI GI 50 BLAST score 5.0e-19 E value 54 Match length 98 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172129 Seq. No. Seq. ID jC-atXLIB327402P4h04b1 BLASTN Method g2582640 NCBI GI BLAST score 49 2.0e-18 E value 64 Match length % identity 94 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172130 Seq. No. Seq. ID jC-atXLIB327402P4h08b1 Method BLASTN g4531433 NCBI GI 72 BLAST score 4.0e-32 E value Match length 232 % identity 88 Arabidopsis thaliana chromosome II P1 MFL8 genomic NCBI Description sequence, complete sequence Seq. No. 172131 jC-atXLIB327403P1a04a1 Seq. ID BLASTN Method g2462264 NCBI GI BLAST score 39 2.0e-12 E value Match length 63 92 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172132 Seq. ID jC-atXLIB327403P1c04b1 BLASTN Method NCBI GI g4567237 BLAST score 146 E value 2.0e-76 Match length 254 91 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No. 172133

Seq. ID

Method



```
jC-atXLIB327403P1c05b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2660661
BLAST score
                  61
E value
                  1.0e-25
                  299
Match length
% identity
                  89
                 Arabidopsis thaliana chromosome V BAC T19K24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172134
                  jC-atXLIB327403P1c08b1
Seq. ID
                  BLASTX
Method
                  g3925363
NCBI GI
BLAST score
                  97
E value
                  1.0e-10
                  70
Match length
% identity
                  53
                 (AF067961) homeodomain protein [Malus domestica]
NCBI Description
Seq. No.
                  172135
Seq. ID
                  jC-atXLIB327403P1c11b1
Method
                  BLASTX
NCBI GI
                  q3176676
BLAST score
                  116
                  1.0e-27
E value
Match length
                  95
                  74
% identity
                  (AC003671) Similar to carbonic anhydrase gb L19255 from
NCBI Description
                  Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963
                  and gb_AA597734 come from this gene. [Arabidopsis thaliana]
                  172136
Seq. No.
Seq. ID
                  jC-atXLIB327403P1c12a1
                  BLASTN
Method
                  g3449330
NCBI GI
BLAST score
                  74
                  3.0e-33
E value
                  238
Match length
                  83
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDJ14, complete sequence [Arabidopsis thaliana]
                  172137
Seq. No.
Seq. ID
                  jC-atXLIB327403P1d06b1
                  BLASTX
Method
NCBI GI
                  g2738248
                  295
BLAST score
E value
                  1.0e-43
                  129
Match length
% identity
                  78
                 (U97200) cobalamin-independent methionine synthase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  172138
```

23550

jC-atXLIB327403P1d07b1

BLASTN

BLAST score

Match length

E value

65 2.0e-28

128



```
NCBI GI
                  g4584841
BLAST score
                  37
                  2.0e-11
E value
Match length
                  45
% identity
                  96
                  Genomic sequence for Arabidopsis thaliana BAC T23E23,
NCBI Description
                  complete sequence
                  172139
Seq. No.
                  jC-atXLIB327403P1d09b1
Seq. ID
Method
                  BLASTN
                  g3047100
NCBI GI
BLAST score
                  64
                  2.0e-27
E value
                  174
Match length
% identity
                  91
NCBI Description Arabidopsis thaliana BAC F6N23
Seq. No.
                  172140
                  jC-atXLIB327403P1e02b1
Seq. ID
Method
                  BLASTX
                  q4154281
NCBI GI
                  162
BLAST score
E value
                  1.0e-11
                  39
Match length
                  72
% identity
                 (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
NCBI Description
Seq. No.
                  172141
Seq. ID
                  jC-atXLIB327403P1g05b1
Method
                  BLASTN
NCBI GI
                  q4580744
BLAST score
                  67
                  3.0e-29
E value
Match length
                  210
% identity
                  76
NCBI Description Sequence of BAC F15I1 from Arabidopsis thaliana chromosome
                  1, complete sequence
Seq. No.
                  172142
Seq. ID
                  jC-atXLIB327403P1g08b1
Method
                  BLASTN
NCBI GI
                  q4580386
                  93
BLAST score
                  1.0e-44
E value
Match length
                  372
                  92
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T8018 genomic
                  sequence, complete sequence
Seq. No.
                  172143
Seq. ID
                  jC-atXLIB327403P1g09b1
Method
                  BLASTN
                  g3420042
NCBI GI
```



```
% identity
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172144
                  jC-atXLIB327403P1h02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3176693
BLAST score
                  62
                  3.0e-26
E value
Match length
                  78
                  94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T27I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172145
Seq. ID
                  jC-atXLIB327403P1h12a1
Method
                  BLASTX
NCBI GI
                  q4678939
BLAST score
                  229
E value
                  7.0e-19
Match length
                  75
% identity
                  60
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  172146
Seq. ID
                  jC-atXLIB327403P3a02a1
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score
                  102
                  5.0e-50
E value
Match length
                  204
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172147
Seq. ID
                  jC-atXLIB327403P3a02b1
Method
                  BLASTN
NCBI GI
                  g2618602
                  96
BLAST score
E value
                  2.0e-46
Match length
                  300
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  172148
Seq. No.
                  jC-atXLIB327403P3a09a1
Seq. ID
Method
                  BLASTN
NCBI GI
```

Method BLASTN
NCBI GI g3873174
BLAST score 39
E value 9.0e-13
Match length 47
% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

NCBI GI



```
172149
Seq. No.
                  jC-atXLIB327403P3a11a2
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
                  56
BLAST score
                  1.0e-22
E value
                  56
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172150
Seq. No.
                  jC-atXLIB327403P3a12b2
Seq. ID
                  BLASTX
Method
                  g2440035
NCBI GI
                  156
BLAST score
                  5.0e-66
E value
                  129
Match length
                  98
% identity
NCBI Description (X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]
                  172151
Seq. No.
Seq. ID
                  jC-atXLIB327403P3b02b2
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                  41
                  1.0e-13
E value
                  73
Match length
                  89
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172152
Seq. No.
Seq. ID
                  iC-atXLIB327403P3b08a2
                  BLASTN
Method
                  g2462264
NCBI GI
                  49
BLAST score
                  2.0e-18
E value
                  57
Match length
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172153
Seq. No.
Seq. ID
                   jC-atXLIB327403P3b09a2
                  BLASTN
Method
NCBI GI
                  q3128136
BLAST score
                   133
                  1.0e-68
E value
Match length
                   360
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1F13, complete sequence [Arabidopsis thaliana]
                  172154
Seq. No.
                   jC-atXLIB327403P3b12a1
Seq. ID
Method
                  BLASTN
```

23553

q3449322



BLAST score 49 E value 1.0e-18 Match length 102 % identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC17, complete sequence [Arabidopsis thaliana]

Seq. No. 172155

Seq. ID jC-atXLIB327403P3b12b1

Method BLASTN
NCBI GI g3449322
BLAST score 123
E value 1.0e-62
Match length 371
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC17, complete sequence [Arabidopsis thaliana]

Seq. No. 172156

Seq. ID jC-atXLIB327403P3c08b1

Method BLASTX
NCBI GI g4585876
BLAST score 138
E value 2.0e-13
Match length 111
% identity 44

NCBI Description (AC005850) Putative serine/threonine kinase [Arabidopsis

thaliana]

Seq. No. 172157

Seq. ID jC-atXLIB327403P3c08b2

Method BLASTX
NCBI GI g3941543
BLAST score 293
E value 5.0e-31
Match length 112
% identity 72

NCBI Description (AF069497) pelota [Arabidopsis thaliana]

>gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)

[Arabidopsis thaliana]

Seq. No. 172158

Seq. ID jC-atXLIB327403P3c10b1

Method BLASTN
NCBI GI g3451055
BLAST score 90
E value 7.0e-43
Match length 205
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 172159

Seq. ID jC-atXLIB327403P3d03a2

Method BLASTN NCBI GI g4325352 BLAST score 156



```
3.0e-82
E value
                  388
Match length
                  91
% identity
NCBI Description Arabidopsis thaliana BAC F5K24
                  172160
Seq. No.
                  jC-atXLIB327403P3d04b1
Seq. ID
                  BLASTX
Method
                  g2076884
NCBI GI
BLAST score
                  173
                  2.0e-12
E value
                   41
Match length
                  83
% identity
                   (U90522) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
```

 Seq. No.
 172161

 Seq. ID
 jC-atXLIB327403P3d11b1

 Method
 BLASTN

 NCBI GI
 q3869065

NCBI GI g3869065 BLAST score 114 E value 3.0e-57 Match length 118 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24M7, complete sequence [Arabidopsis thaliana]

Seq. No. 172162
Seq. ID jC-atXLIB327403P3d12a2
Method BLASTN
NCBI GI g2924651
BLAST score 247

BLAST score 247
E value 1.0e-136
Match length 389
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 172163

Seq. ID jC-atXLIB327403P3e03a1

Method BLASTN
NCBI GI g2288979
BLAST score 90
E value 7.0e-43
Match length 212
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T01024 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172164

Seq. ID jC-atXLIB327403P3e03b1

Method BLASTX
NCBI GI g2289010
BLAST score 322
E value 8.0e-30
Match length 71
% identity 90



```
NCBI Description (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No. 172165
Seq. ID jC-atXLIB327403P3e06a1
Method BLASTN
NCBI GI g3860242
```

BLAST score 40 E value 5.0e-13 Match length 56 % identity 93

NCBI Description Arabidopsis thaliana chromosome I BAC T13M11 genomic

sequence, complete sequence

Seq. No. 172166

Seq. ID jC-atXLIB327403P3e08a1

Method BLASTN
NCBI GI g4713943
BLAST score 49
E value 2.0e-18
Match length 79
% identity 90

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,

complete sequence

Seq. No. 172167

Seq. ID jC-atXLIB327403P3e12a2

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 5.0e-19
Match length 50
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172168

Seq. ID jC-atXLIB327403P3f01b2

Method BLASTN
NCBI GI g2564050
BLAST score 35
E value 6.0e-10
Match length 174
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 172169

Seq. ID jC-atXLIB327403P3f07b1

Method BLASTN
NCBI GI g4733952
BLAST score 55
E value 2.0e-22
Match length 91
% identity 94

NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No. Seq. ID



```
Seq. No.
                  172170
                  jC-atXLIB327403P3f12a1
Seq. ID
Method
                  BLASTX
                  q2129533
NCBI GI
BLAST score
                  250
                  1.0e-23
E value
Match length
                  70
                  89
% identity
                  adenine nucleotide translocase - Arabidopsis thaliana
NCBI Description
                  >gi 1051109 emb CAA89201 (Z49227) adenine nucleotide
                  translocase [Arabidopsis thaliana]
Seq. No.
                  172171
                  jC-atXLIB327403P3g04a2
Seq. ID
Method
                  BLASTN
                  g4165340
NCBI GI
                  270
BLAST score
                  1.0e-150
E value
Match length
                  390
                  96
% identity
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172172
                  jC-atXLIB327403P3g09b1
Seq. ID
Method
                  BLASTN
                  g3985933
NCBI GI
BLAST score
                  68
E value
                  9.0e-30
                  144
Match length
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9E15, complete sequence [Arabidopsis thaliana]
                   172173
Seq. No.
                   jC-atXLIB327403P3h01b1
Seq. ID
Method
                   BLASTN
                   g3449334
NCBI GI
                   47
BLAST score
                   3.0e-17
E value
                   58
Match length
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                   172174
Seq. No.
                   jC-atXLIB327403P3h02b1
Seq. ID
Method
                   BLASTX
                   g1335862
NCBI GI
                   203
BLAST score
                   2.0e-16
E value
                   50
Match length
% identity
                   74
NCBI Description
                  (U42608) clathrin heavy chain [Glycine max]
```

23557

jC-atXLIB327403P3h03a2

Seq. ID

Method



```
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  56
                  1.0e-22
E value
                  64
Match length
                  97
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172176
Seq. No.
Seq. ID
                  jC-atXLIB327403P3h03b1
                  BLASTX
Method
                  g1093327
NCBI GI
BLAST score
                  121
                  3.0e-11
E value
                  73
Match length
                  55
% identity
NCBI Description mitotic centromere-associated kinesin [Cricetulus griseus]
Seq. No.
                  172177
                  jC-atXLIB327403P3h07b1
Seq. ID
                  BLASTN
Method
                  g2618603
NCBI GI
BLAST score
                  59
                  8.0e-25
E value
                  89
Match length
                  91
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSL3, complete sequence [Arabidopsis thaliana]
                  172178
Seq. No.
Seq. ID
                  jC-atXLIB327403P3h07b2
                  BLASTX
Method
NCBI GI
                  g3201623
BLAST score
                  799
                  1.0e-85
E value
Match length
                  151
                  99
% identity
                  (AC004669) shaggy-like kinase dzeta [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  172179
                  iC-atXLIB327403P3h09b1
Seq. ID
Method
                  BLASTX
                  q127041
NCBI GI
BLAST score
                  238
                  7.0e-20
E value
Match length
                  44
                  95
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
                  172180
Seq. No.
```

23558

jC-atXLIB327403P4d04a1

BLASTN



NCBI GI g3420043 BLAST score 159 E value 3.0e-84 Match length 255 % identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172181

Seq. ID jC-atXLIB327403P4h07a1

Method BLASTN
NCBI GI g3386593
BLAST score 111
E value 1.0e-55
Match length 213
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172182

Seq. ID jC-atXLIB327404P1b06b1

Method BLASTX
NCBI GI g3228517
BLAST score 189
E value 4.0e-18
Match length 58
% identity 88

NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]

Seq. No. 172183

Seq. ID jC-atXLIB327404P1c01a1

Method BLASTN
NCBI GI g3128136
BLAST score 122
E value 5.0e-62
Match length 269
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 172184

Seq. ID jC-atXLIB327404P1c02a1

Method BLASTN
NCBI GI g2462264
BLAST score 42
E value 3.0e-14
Match length 54
% identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172185

Seq. ID jC-atXLIB327404P1c03a1

Method BLASTN
NCBI GI g4662609
BLAST score 73
E value 7.0e-33
Match length 128

NCBI Description



```
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
                   complete sequence
Seq. No.
                   172186
Seq. ID
                   jC-atXLIB327404P1c04a1
Method
                   BLASTN
NCBI GI
                   g2576360
                   82
BLAST score
E value
                   5.0e-38
Match length
                   102
                   95
% identity
                  Arabidopsis thaliana lysine and histidine specific
NCBI Description
                   transporter mRNA, complete cds
                   172187
Seq. No.
Seq. ID
                   jC-atXLIB327404P1c05a1
Method
                   BLASTN
NCBI GI
                   q3335356
BLAST score
                   52
                   1.0e-20
E value
                   141
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172188
                   jC-atXLIB327404P1c06a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2290120
                   42
BLAST score
                   4.0e-14
E value
Match length
                   65
                   92
% identity
                   HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                   gene, partial cds
                   172189
Seq. No.
Seq. ID
                   jC-atXLIB327404P1c07a1
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   44
                   2.0e-15
E value
Match length
                   52
% identity
                   96
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                   172190
Seq. No.
                   jC-atXLIB327404P1c11a1
Seq. ID
Method
                   BLASTN
                   g3449329
NCBI GI
BLAST score
                   89
E value
                   3.0e-42
Match length
                   179
                   92
% identity
```

MDH9, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
172191
Seq. No.
Seq. ID
                  jC-atXLIB32740,4P1d01a1
                  BLASTN
Method
                  g4510392
NCBI GI
BLAST score
                  61
E value
                  1.0e-25
                  173
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC T17D12 genomic
NCBI Description
                  sequence, complete sequence
                  172192
Seq. No.
Seq. ID
                  jC-atXLIB327404P1d05a1
Method
                  BLASTN
NCBI GI
                  g2462264
                  49
BLAST score
                  2.0e-18
E value
                  53
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172193
Seq. No.
Seq. ID
                   jC-atXLIB327404P1e04a1
                  BLASTN
Method
                  g2462264
NCBI GI
                  56
BLAST score
                  2.0e-22
E value
                   56
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172194
Seq. No.
                   jC-atXLIB327404P1f01a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4757409
BLAST score
                   132
                   6.0e-68
E value
Match length
                   355
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MVC8, complete sequence
Seq. No.
                   172195
Seq. ID
                   jC-atXLIB327404P1f06a1
Method
                   BLASTX
NCBI GI
                   g4678948
BLAST score
                   229
                   8.0e-19
E value
Match length
                   88
                   57
% identity
```

Seq. No. 172196

NCBI Description

Seq. ID jC-atXLIB327404P1f07a1

Method BLASTN NCBI GI g2462264

23561

(AL049711) putative protein [Arabidopsis thaliana]



```
36
BLAST score
                  1.0e-10
E value
                  63
Match length
                  90
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172197
Seq. No.
Seq. ID
                  jC-atXLIB327404P1f10a1
                  BLASTN
Method
NCBI GI
                  g531828
                  36
BLAST score
                  1.0e-10
E value
Match length
                  44
                  95
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172198
Seq. No.
Seq. ID
                  jC-atXLIB327404P1g04a1
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  41
                  1.0e-13
E value
Match length
                  53
                  94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172199
Seq. No.
                  jC-atXLIB327404P1g07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1532270
                  90
BLAST score
                  7.0e-43
E value
                  230
Match length
                  93
% identity
NCBI Description Arabidopsis thaliana mRNA for
                  deltal-pyrroline-5-carboxylate synthase, complete cds
                  172200
Seq. No.
                   jC-atXLIB327404P1g08a1
Seq. ID
Method
                  BLASTN
                  q3341671
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
                  114
Match length
                  88
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F16B22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172201
Seq. ID
                   jC-atXLIB327404P1g09a1
Method
                  BLASTN
NCBI GI
                  g2462264
                  51
BLAST score
                  1.0e-19
E value
                  55
Match length
% identity
                  98
```

23562

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



172202 Seq. No. jC-atXLIB327404P2b12b1 Seq. ID BLASTN Method g4756963 NCBI GI BLAST score 46 E value 7.0e-17 65 Match length 94 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 NCBI Description (ESSA project) 172203 Seq. No. Seq. ID jC-atXLIB327404P2c10b1 Method BLASTN NCBI GI g3985958 BLAST score 190 E value 1.0e-102 Match length 393 % identity 97 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MZN1, complete sequence [Arabidopsis thaliana] 172204 Seq. No. Seq. ID jC-atXLIB327404P2g10b1 BLASTX Method NCBI GI g1346194 277 BLAST score E value 1.0e-72 Match length 147 % identity 92 GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29) NCBI Description >qi 1022797 (U37697) glutathione reductase [Arabidopsis thaliana] 172205 Seq. No. jC-atXLIB327404P2g12b1 Seq. ID BLASTX Method NCBI GI g1711513 BLAST score 616 3.0e-64 E value Match length 129 94 % identity SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54) NCBI Description >gi 515681 (U12127) signal recognition particle 54 kDa subunit [Arabidopsis thaliana] 172206 Seq. No. jC-atXLIB327404P3c11a1 Seq. ID Method BLASTN

NCBI GI g4063735
BLAST score 72
E value 1.0e-32
Match length 102
% identity 95

NCBI Description Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5

cM, complete sequence [Arabidopsis thaliana]



```
172207
Seq. No.
Seq. ID
                  jC-atXLIB327404P3d06a1
                  BLASTN.
Method
                  g2462264
NCBI GI
BLAST score
                  52
                  4.0e-20
E value
                  52
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172208
Seq. No.
Seq. ID
                  jC-atXLIB327404P3d08a1
                  BLASTX
Method
                  g3395440
NCBI GI
                  397
BLAST score
                  2.0e-38
E value
                  154
Match length
                  47
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                  172209
Seq. No.
Seq. ID
                  jC-atXLIB327404P3e05a1
                  BLASTX
Method
NCBI GI
                  g4056433
                  238
BLAST score
                  1.0e-19
E value
                  120
Match length
                  43
% identity
                   (AC005990) Similar to anter-specific proline-rich protein
NCBI Description
                   (CEX) gb X60376 from Brassica napus. [Arabidopsis thaliana]
                  172210
Seq. No.
Seq. ID
                  jC-atXLIB327404P3e08a1
Method
                  BLASTN
                  q3080430
NCBI GI
                  347
BLAST score
                  0.0e + 00
E value
                  362
Match length
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
NCBI Description
                   (ESSAII project)
                  172211
Seq. No.
                   jC-atXLIB327404P3g06a1
Seq. ID
Method
                  BLASTN
                  q2462264
NCBI GI
BLAST score
                   55
                   5.0e-22
E value
                   59
Match length
% identity
                   98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
```

Seq. No. 172212

Seq. ID jC-atXLIB327404P3g08a1

Method BLASTN NCBI GI q3281847



```
BLAST score
                  137
                  4.0e-71
E value
Match length
                  185
                  94
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20
NCBI Description
                  (ESSAII project)
                  172213
Seq. No.
                  jC-atXLIB327404P3g10a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
                  39
BLAST score
                  2.0e-12
E value
                  39
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172214
Seq. No.
Seq. ID
                  jC-atXLIB327404P3h03a1
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  50
                  7.0e-19
E value
                  61
Match length
                  97
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172215
Seq. No.
Seq. ID
                  jC-atXLIB327404P3h10a1
Method
                  BLASTX
                  q4588001
NCBI GI
                  206
BLAST score
                  5.0e-16
E value
                  76
Match length
                  52
% identity
                  (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   172216
Seq. ID
                   jC-atXLIB327404P3h11a1
                  BLASTX
Method
NCBI GI
                  q4467159
BLAST score
                   340
                   1.0e-31
E value
                  88
Match length
% identity
                   76
NCBI Description (AL035540) hypothetical protein [Arabidopsis thaliana]
                   172217
Seq. No.
Seq. ID
                   jC-atXLIB327404P4a03b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI 94585882
BLAST score 348
E value 1.0e-32
Match length 141
% identity 57

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein



[Arabidopsis thaliana]

Seq. No. 172218 jC-atXLIB327404P4a08b1 Seq. ID BLASTX Method NCBI GI q2598227 BLAST score 414 1.0e-40 E value 103 Match length 82 % identity (AJ222585) AT-hook protein 1 [Arabidopsis thaliana] NCBI Description Seq. No. 172219 Seq. ID jC-atXLIB327404P4b02b1 BLASTN Method g2582640 NCBI GI 46 BLAST score 2.0e-16 E value Match length 53 % identity 98 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172220 Seq. No. Seq. ID jC-atXLIB327404P4b03b1 BLASTN Method NCBI GI g2582640 BLAST score 46 1.0e-16 E value Match length 54 96 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 Seq. No. 172221 Seq. ID jC-atXLIB327404P4b12a1 BLASTN Method NCBI GI g2760165 BLAST score 110 E value 6.0e-55 Match length 271 % identity 87 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MAC9, complete sequence [Arabidopsis thaliana] 172222 Seq. No. jC-atXLIB327404P4c02a1 Seq. ID BLASTN Method NCBI GI g2924733 BLAST score 124 4.0e-63 E value Match length 241 88 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Seq. No. 172223

MUF9, complete sequence [Arabidopsis thaliana]



jC-atXLIB327404P4c08a1 Seq. ID BLASTN Method NCBI GI g540252 BLAST score 41 7.0e-14E value Match length 49 96 % identity NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds Seq. No. 172224 Seq. ID jC-atXLIB327404P4c11a1 BLASTN Method NCBI GI g2462264 BLAST score 44 2.0e-15 E value 48 Match length 98 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172225 Seq. ID jC-atXLIB327404P4d07b1 BLASTN Method g2582640 NCBI GI BLAST score 59 3.0e-24 E value 71 Match length 96 % identity NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40 Seq. No. 172226 Seq. ID jC-atXLIB327404P4d09a1 Method BLASTX g3617741 NCBI GI BLAST score 173 3.0e-12E value 55 Match length % identity NCBI Description (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana] Seq. No. 172227 Seq. ID jC-atXLIB327404P4d12a1 Method BLASTN NCBI GI q2351061 BLAST score 103 E value 1.0e-50 Match length 243 % identity 88 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No. 172228

Seq. ID jC-atXLIB327404P4e02a1

Method BLASTN NCBI GI g540252 BLAST score 44

NCBI Description



```
2.0e-15
E value
                  48
Match length
                  98
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  172229
Seq. No.
Seq. ID
                  jC-atXLIB327404P4e03a1
Method
                  BLASTN
                  g540252
NCBI GI
BLAST score
                  42
                  4.0e-14
E value
                  46
Match length
                  98
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  172230
Seq. No.
Seq. ID
                  jC-atXLIB327404P4e08a1
Method
                  BLASTN
                  g3757512
NCBI GI
BLAST score
                  167
E value
                  5.0e-89
Match length
                  269
                  92
% identity
                  Arabidopsis thaliana chromosome II BAC F12A24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  172231
Seq. No.
Seq. ID
                  jC-atXLIB327404P4e10a1
Method
                  BLASTX
                  g99743
NCBI GI
BLAST score
                  375
E value
                  7.0e-36
Match length
                  94
% identity
NCBI Description
                  2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2
                  - Arabidopsis thaliana
                  172232
Seq. No.
Seq. ID
                  jC-atXLIB327404P4e12a1
Method
                  BLASTN
NCBI GI
                  q2290120
BLAST score
                  48
                  9.0e-18
E value
Match length
                  48
                  100
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  172233
Seq. ID
                  jC-atXLIB327404P4e12b1
Method
                  BLASTX
NCBI GI
                  g4539601
BLAST score
                  155
                  3.0e-10
E value
Match length
                  52
% identity
                  54
```

(AL049522) serine/threonine-protein kinase 23568

Seq. ID

Method

BLASTN



[Schizosaccharomyces pombe]

```
172234
Seq. No.
                  jC-atXLIB327404P4f02a1
Seq. ID
                  BLASTN
Method
                  g2290120
NCBI GI
                  34
BLAST score
                  1.0e-09
E value
                  42
Match length
                  95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172235
Seq. No.
Seq. ID
                  jC-atXLIB327404P4f06a1
                  BLASTN
Method
                  g600854
NCBI GI
BLAST score
                  58
                  6.0e-24
E value
                  114
Match length
% identity
                  94
NCBI Description Arabidopsis thaliana bZIP protein mRNA, complete cds
                  172236
Seq. No.
Seq. ID
                  jC-atXLIB327404P4f07a1
                  BLASTN
Method
                  g531828
NCBI GI
BLAST score
                  41
                  8.0e-14
E value
Match length
                  45
% identity
                  98
NCBI Description Cloning vector pSport1, complete cds
                  172237
Seq. No.
Seq. ID
                  jC-atXLIB327404P4f08b1
Method
                  BLASTX
                  g2651310
NCBI GI
                  309
BLAST score
                  3.0e-28
E value
Match length
                  129
% identity
                  44
NCBI Description
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
                  thaliana]
                  172238
Seq. No.
Seq. ID
                  iC-atXLIB327404P4f09a1
                  BLASTN
Method
NCBI GI
                  g531828
BLAST score
                  53
                  1.0e-20
E value
                  53
Match length
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172239
Seq. No.
                   jC-atXLIB327404P4f10a1
```



```
NCBI GI
                  g540252
BLAST score
                  48
                  1.0e-17
E value
Match length
                  48
% identity
                  100
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  172240
Seq. No.
                  jC-atXLIB327404P4f12a1
Seq. ID
                  BLASTN
Method
                  q540252
NCBI GI
                  50
BLAST score
E value
                  6.0e-19
                  50
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  172241
Seq. ID
                  jC-atXLIB327404P4g04a1
Method
                  BLASTN
                  q3241939
NCBI GI
                  89
BLAST score
                  2.0e-42
E value
Match length
                  268
% identity
                  81
NCBI Description Arabidopsis thaliana chromosome II BAC T26J13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172242
Seq. ID
                   jC-atXLIB327404P4g05a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  51
E value
                   2.0e-19
Match length
                  55
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   172243
                   jC-atXLIB327404P4g06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2462264
                   40
BLAST score
                   4.0e-13
E value
Match length
                   44
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172244
Seq. No.
                   jC-atXLIB327404P4g07b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1184984
                   78
BLAST score
                   1.0e-35
E value
Match length
                   106
                   94
% identity
```

NCBI Description Arabidopsis thaliana GTP-binding protein ATGB3 mRNA,



complete cds

Seq. No. 172245 Seq. ID jC-atXLIB327404P4q10a1 Method BLASTX q1345973 NCBI GI BLAST score 122 E value 8.0e-10 53 Match length 74 % identity OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM NCBI Description >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC

1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 172246

Seq. ID jC-atXLIB327404P4g12a1

Method BLASTN
NCBI GI g16553
BLAST score 104
E value 3.0e-51
Match length 223
% identity 97

NCBI Description A.thaliana mRNA for eukaryotic translation initiation

factor 4A-1

Seq. No. 172247

Seq. ID jC-atXLIB327404P4h05a1

Method BLASTN
NCBI GI g2760168
BLAST score 88

E value 1.0e-41 Match length 183 % identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 172248

Seq. ID jC-atXLIB327404P4h08a1

Method BLASTN
NCBI GI g3510345
BLAST score 64
E value 3.0e-27
Match length 220
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No. 172249

Seq. ID jC-atXLIB327404P4h09a1

Method BLASTN NCBI GI g2290120

E value

Match length

2.0e-48

195



```
BLAST score
                  45
                  6.0e-16
E value
Match length
                  61
                  93
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  172250
Seq. ID
                  jC-atXLIB327404P4h11a1
                  BLASTX
Method
NCBI GI
                  g2632103
BLAST score
                  49
                  2.0e-16
E value
Match length
                  66
                  76
% identity
NCBI Description
                  (Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                  172251
Seq. ID
                  jC-atXLIB327405P1a09a2
Method
                  BLASTN
NCBI GI
                  g3449325
BLAST score
                  70
                  6.0e-31
E value
                  256
Match length
                  88
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K16H17, complete sequence [Arabidopsis thaliana]
                  172252
Seq. No.
Seq. ID
                   jC-atXLIB327405P1b02b2
Method
                  BLASTN
NCBI GI
                  g2924768
BLAST score
                  60
E value
                   6.0e-25
Match length
                  121
% identity
                  Arabidopsis thaliana chromosome II BAC F25I18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172253
                  jC-atXLIB327405P1b03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4539415
BLAST score
                  44
                  9.0e-16
E value
Match length
                  91
                  87
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                  project)
Seq. No.
                  172254
Seq. ID
                  jC-atXLIB327405P1b04a2
Method
                  BLASTN
NCBI GI
                  g4589430
BLAST score
                  99
```



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLD14, complete sequence
                  172255
Seq. No.
Seq. ID
                  jC-atXLIB327405P1b04b2
                  BLASTN
Method
                  g4589430
NCBI GI
                  93
BLAST score
                  1.0e-44
E value
                  297
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLD14, complete sequence
                  172256
Seq. No.
Seq. ID
                  jC-atXLIB327405P1b06a2
                  BLASTN
Method
                  g2290120
NCBI GI
BLAST score
                  47
                  3.0e-17
E value
                  47
Match length
                  100
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172257
Seq. No.
Seq. ID
                  jC-atXLIB327405P1c03a2
                  BLASTN
Method
NCBI GI
                  g2462264
                  54
BLAST score
                  2.0e-21
E value
                  54
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172258
Seq. No.
Seq. ID
                  jC-atXLIB327405P1c05a2
                  BLASTN
Method
NCBI GI
                  q2462264
                  54
BLAST score
E value
                  2.0e-21
                  54
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172259
Seq. No.
Seq. ID
                   jC-atXLIB327405P1c07a2
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  42
                  3.0e-14
E value
Match length
                  45
                   98
% identity
NCBI Description Cloning vector pSport1, complete cds
```

Seq. No. 172260



Seq. ID jC-atXLIB327405P1c10a2 Method BLASTN

NCBI GI g3449317
BLAST score 204
E value 1.0e-111
Match length 428
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKM21, complete sequence [Arabidopsis thaliana]

Seq. No. 172261

Seq. ID jC-atXLIB327405P1c10b1

Method BLASTN
NCBI GI g3449317
BLAST score 57
E value 4.0e-23
Match length 283
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKM21, complete sequence [Arabidopsis thaliana]

Seq. No. 172262

Seq. ID jC-atXLIB327405P1c12a2

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 5.0e-19
Match length 50
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172263

Seq. ID jC-atXLIB327405P1d04a2

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 2.0e-21
Match length 54
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172264

Seq. ID jC-atXLIB327405P1d06a2

Method BLASTN
NCBI GI g3513725
BLAST score 51
E value 1.0e-19
Match length 51
% identity 100

NCBI Description Arabidopsis thaliana BAC F8M12

Seq. No. 172265

Seq. ID jC-atXLIB327405P1d08a2

Method BLASTN
NCBI GI g2351073
BLAST score 35
E value 5.0e-10



```
87
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYJ24, complete sequence [Arabidopsis thaliana]
                  172266
Seq. No.
                  jC-atXLIB327405P1d10a2
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  39
                  1.0e-12
E value
                  54
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172267
Seq. No.
Seq. ID
                  jC-atXLIB327405P1d10b1
                  BLASTN
Method
                  q3128139
NCBI GI
BLAST score
                  59
                   9.0e-25
E value
                  110
Match length
                   90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIK19, complete sequence [Arabidopsis thaliana]
                   172268
Seq. No.
Seq. ID
                   iC-atXLIB327405P1e02a2
                   BLASTN
Method
NCBI GI
                   q2462264
                   52
BLAST score
                   3.0e-20
E value
                   52
Match length
                   100
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                   172269
Seq. No.
                   jC-atXLIB327405P1e03b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2582640
BLAST score
                   54
                   2.0e-21
E value
                   73
Match length
                   93
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172270
Seq. No.
                   jC-atXLIB327405P1e05a2
Seq. ID
                   BLASTN
Method
                   g1255986
NCBI GI
                   85
BLAST score
```

Method BLASIN

NCBI GI g1255986

BLAST score 85

E value 3.0e-40

Match length 161

% identity 88

NCBI Description Arabidopsis thaliana GF14chi isoform (GRF1) gene, complete

cds



```
Seq. No.
                  172271
Seq. ID
                  jC-atXLIB327405P1e10a2
Method
                  BLASTN
NCBI GI
                  g4757389
BLAST score
                  173
                  2.0e-92
E value
Match length
                  404
                  53
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F1505, complete sequence
Seq. No.
                  172272
                  jC-atXLIB327405P1e10b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  40
                  6.0e-13
E value
Match length
                  60
% identity
                  92
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  172273
Seq. No.
                  jC-atXLIB327405P1e12a2
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
Match length
                  48
                  94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172274
Seq. ID
                  jC-atXLIB327405P1e12b2
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  56
E value
                  1.0e-22
Match length
                  68
% identity
                  96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172275
                  jC-atXLIB327405P1f03a2
Seq. ID
                  BLASTX
Method
                  g3122703
                  295
                  1.0e-26
```

NCBI GI BLAST score E value Match length 82 76 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal

protein L23a [Fritillaria agrestis]

172276 Seq. No.

Seq. ID jC-atXLIB327405P1f03b2



BLASTN Method NCBI GI q2582640 34 BLAST score 2.0e-09 E value Match length 64 92 % identity

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

172277 Seq. No.

jC-atXLIB327405P1f06b1 Seq. ID

BLASTN Method NCBI GI g402551 BLAST score 61 1.0e-25 E value Match length 85

% identity NCBI Description A.thaliana gene for acetohydroxy acid isomeroreductase

172278 Seq. No.

Seq. ID jC-atXLIB327405P1f10a2

94

BLASTN Method NCBI GI g2462264 BLAST score 57 E value 3.0e-23 57 Match length 100 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172279

iC-atXLIB327405P1f11b1 Seq. ID

BLASTN Method q2335089 NCBI GI BLAST score 60 E value 2.0e-25 Match length 138 96 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172280

jC-atXLIB327405P1g06a2 Seq. ID

Method BLASTN NCBI GI g2462264 BLAST score 54 2.0e-21 E value 54 Match length 100 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172281

jC-atXLIB327405P1g08b2 Seq. ID

Method BLASTN NCBI GI q3540210 BLAST score 67 4.0e-29 E value 200 Match length



```
% identity
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172282
                  jC-atXLIB327405P1g11a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  54
                  2.0e-21
E value
Match length
                  54
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172283
Seq. ID
                  jC-atXLIB327405P1h01a2
Method
                  BLASTN
NCBI GI
                  g2924654
BLAST score
                  135
                  1.0e-69
E value
Match length
                  266
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172284
Seq. ID
                  jC-atXLIB327405P1h09a2
Method
                  BLASTN
                  g3298610
NCBI GI
BLAST score
                  81
                  2.0e-37
E value
Match length
                  169
                  87
% identity
NCBI Description Arabidopsis thaliana BAC T2H3
                  172285
Seq. No.
                  jC-atXLIB327405P2a05b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829918
BLAST score
                   288
                  1.0e-25
E value
Match length
                   69
                  75
% identity
                  (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                  172286
Seq. No.
                   jC-atXLIB327405P2a06a1
Seq. ID
Method
                  BLASTN
```

NCBI GI q2980787 BLAST score 410 0.0e+00E value Match length 431 % identity 99

Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 NCBI Description

(ESSAII project)

Method

NCBI GI

E value

BLAST score

BLASTN

131

q3250673

2.0e-67



```
Seq. No.
                  172287
Seq. ID
                  jC-atXLIB327405P2a11a1
Method
                  BLASTX
NCBI GI
                  g2809251
BLAST score
                  621
E value
                  9.0e-65
Match length
                  117
% identity
                 (AC002560) F21B7.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  172288
Seq. ID
                  jC-atXLIB327405P2a12b2
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  39
E value
                  2.0e-12
Match length
                  55
                  93
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172289
Seq. ID
                  jC-atXLIB327405P2b01a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  47
E value
                  3.0e-17
Match length
                  55
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172290
Seq. ID
                  jC-atXLIB327405P2b03a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  49
E value
                  2.0e-18
Match length
                  61
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172291
Seq. ID
                  jC-atXLIB327405P2b05a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  52
E value
                  4.0e-20
Match length
                  56
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172292
Seq. ID
                  jC-atXLIB327405P2b07a1
```



Match length 387 % identity 87

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5

(ESSAII project)

Seq. No. 172293

Seq. ID jC-atXLIB327405P2b09a1

Method BLASTX
NCBI GI g1703227
BLAST score 203
E value 9.0e-16
Match length 82
% identity 50

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC

TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)

(ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148 emb CAA81231_ (Z26322) alanine

aminotransferase [Hordeum vulgare]

Seq. No. 172294

Seq. ID jC-atXLIB327405P2b09b2

Method BLASTX
NCBI GI g3694807
BLAST score 361
E value 3.0e-34
Match length 142
% identity 57

NCBI Description (AF055898) alanine aminotransferase [Zea mays]

Seq. No. 172295

Seq. ID jC-atXLIB327405P2b12a1

Method BLASTX
NCBI GI g1076668
BLAST score 207
E value 3.0e-16
Match length 39
% identity 100

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase

[Solanum tuberosum]

Seq. No. 172296

Seq. ID jC-atXLIB327405P2c01a1

Method BLASTN
NCBI GI g2462264
BLAST score 37
E value 3.0e-11
Match length 49
% identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172297

Seq. ID jC-atXLIB327405P2c02a1

Method BLASTX
NCBI GI g1737218
BLAST score 167
E value 1.0e-11



```
Match length
                   67
% identity
                  48
                  (U79959) vacuolar sorting receptor homolog [Arabidopsis
NCBI Description
                  thaliana]
                  172298
Seq. No.
                  jC-atXLIB327405P2c03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4539309
                  374
BLAST score
                  0.0e+00
E value
                  426
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
                  (ESSA project)
Seq. No.
                  172299
Seq. ID
                  jC-atXLIB327405P2c04a1
Method
                  BLASTN
NCBI GI
                  q2462264
                  35
BLAST score
                  5.0e-10
E value
                  43
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172300
Seq. No.
                  jC-atXLIB327405P2c05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264310
BLAST score
                  284
                  1.0e-158
E value
Match length
                  340
                  95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172301
Seq. ID
                  jC-atXLIB327405P2c07b2
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  47
E value
                  3.0e-17
Match length
                  55
% identity
                  96
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172302
Seq. ID
                  jC-atXLIB327405P2c08b2
Method
                  BLASTX
NCBI GI
                  g1762584
                  112
BLAST score
```

4.0e-05 E value Match length 126 % identity 24

(U63373) polygalacturonase isoenzyme 1 beta subunit homolog NCBI Description

NCBI Description



[Arabidopsis thaliana]

```
172303
Seq. No.
                  jC-atXLIB327405P2c09a1
Seq. ID
                  BLASTN
Method
                  g3510347
NCBI GI
                  91
BLAST score
                  2.0e-43
E value
                  361
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  172304
Seq. No.
Seq. ID
                  jC-atXLIB327405P2c09b2
Method
                  BLASTN
                  g3510347
NCBI GI
                  40
BLAST score
                   5.0e-13
E value
                  111
Match length
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  172305
Seq. No.
Seq. ID
                   jC-atXLIB327405P2c10b2
Method
                  BLASTN
                  g3449317
NCBI GI
                   68
BLAST score
                   1.0e-29
E value
                   255
Match length
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKM21, complete sequence [Arabidopsis thaliana]
                   172306
Seq. No.
Seq. ID
                   jC-atXLIB327405P2c11a1
                   BLASTN
Method
                   g2290120
NCBI GI
BLAST score
                   49
E value
                   2.0e-18
                   49
Match length
                   100
% identity
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                   gene, partial cds
Seq. No.
                   172307
Seq. ID
                   jC-atXLIB327405P2d02a1
                   BLASTN
Method
                   g4584531
NCBI GI
BLAST score
                   59
E value
                   2.0e-24
Match length
                   103
                   89
% identity
```

23582

(ESSA project)

Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8

NCBI Description



```
172308
Seq. No.
Seq. ID
                   jC-atXLIB327405P2d03b2
Method
                  BLASTN
NCBI GI
                  g2642152
BLAST score
                   40
                   5.0e-13
E value
                   84
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC T517 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  172309
Seq. No.
Seq. ID
                   jC-atXLIB327405P2d09b2
Method
                  BLASTN
                  g3510347
NCBI GI
BLAST score
                   60
                   6.0e-25
E value
                   103
Match length
                   92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172310
Seq. ID
                   jC-atXLIB327405P2d11a1
                   BLASTX
Method
                   g1465735
NCBI GI
BLAST score
                   396
E value
                   2.0e-38
Match length
                   112
% identity
                   76
                   (U44133) violaxanthin de-epoxidase precursor [Arabidopsis
NCBI Description
                   thaliana] >gi 3063441 (AC003981) F22013.3 [Arabidopsis
                   thaliana]
Seq. No.
                   172311
Seq. ID
                   jC-atXLIB327405P2e05b2
                   BLASTN
Method
                   g2924734
NCBI GI
BLAST score
                   96
E value
                   2.0e-46
Match length
                   343
% identity
                   90
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172312
Seq. ID
                   jC-atXLIB327405P2e12a1
Method
                   BLASTX
NCBI GI
                   g231536
BLAST score
                   364
                   1.0e-34
E value
                   70
Match length
% identity
                   100
```

23583

(EC 3.4.11.1) - Arabidopsis thaliana

CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)

(LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi 99683 pir S22399 leucyl aminopeptidase



>gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative
leucine aminopeptidase [Arabidopsis thaliana]

Seq. No. 172313

Seq. ID jC-atXLIB327405P2f02a1

Method BLASTN
NCBI GI g3688169
BLAST score 43
E value 8.0e-15
Match length 148
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21

(ESSAII project)

Seq. No. 172314

Seq. ID jC-atXLIB327405P2f04a1

Method BLASTN
NCBI GI g540252
BLAST score 41
E value 1.0e-13
Match length 53
% identity 94

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No. 172315

Seq. ID jC-atXLIB327405P2f06a1

Method BLASTN
NCBI GI g2462264
BLAST score 42
E value 3.0e-14
Match length 50
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172316

Seq. ID jC-atXLIB327405P2f06b2

Method BLASTX
NCBI GI g480450
BLAST score 168
E value 1.0e-11
Match length 98
% identity 43

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis

thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 172317

Seq. ID jC-atXLIB327405P2f07a1

Method BLASTN
NCBI GI g2462264
BLAST score 38
E value 8.0e-12
Match length 50
% identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
172318
Seq. No.
                  jC-atXLIB327405P2f08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2290120
BLAST score
                  53
                  9.0e-21
E value
Match length
                  64
% identity
                  97
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172319
Seq. No.
Seq. ID
                  jC-atXLIB327405P2f09a1
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  53
                  9.0e-21
E value
                  53
Match length
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172320
                  jC-atXLIB327405P2g05a1
Seq. ID
Method
                  BLASTN
                  q4589434
NCBI GI
BLAST score
                  215
E value
                  1.0e-117
Match length
                  389
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ7, complete sequence
                  172321
Seq. No.
Seq. ID
                  jC-atXLIB327405P2g08a1
                  BLASTN
Method
                  g2160155
NCBI GI
BLAST score
                  207
                  1.0e-112
E value
                  428
Match length
                  92
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  172322
Seq. No.
Seq. ID
                  jC-atXLIB327405P2h02a1
Method
                  BLASTN
NCBI GI
                  q3282170
                  51
BLAST score
                  1.0e-19
E value
```

123 Match length % identity 93

NCBI Description Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 172323

Seq. ID jC-atXLIB327405P2h04a1

Method BLASTN

E value

Match length % identity



```
g2462264
NCBI GI
                  49
BLAST score
                  2.0e-18
E value
                  53
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172324
Seq. No.
Seq. ID
                  jC-atXLIB327405P2h11a1
Method
                  BLASTN
NCBI GI
                  g3241917
BLAST score
                  60
                  6.0e-25
E value
Match length
                  253
% identity
                  80
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
                  172325
Seq. No.
                  jC-atXLIB327405P2h12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  34
                  2.0e-09
E value
Match length
                  50
% identity
                  92
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172326
Seq. No.
Seq. ID
                  jC-atXLIB327405P3a01a1
                  BLASTN
Method
NCBI GI
                  q531828
BLAST score
                  51
                  1.0e-19
E value
Match length
                  51
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172327
Seq. No.
Seq. ID
                  jC-atXLIB327405P3a10b1
Method
                  BLASTN
                  g2760164
NCBI GI
BLAST score
                  66
E value
                  1.0e-28
                  88
Match length
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
                  172328
Seq. No.
                  jC-atXLIB327405P3a12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2358139
BLAST score
                  139
```

23586

3.0e-72

298



```
Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
NCBI Description
                  sequence [Arabidopsis thaliana]
                  172329
Seq. No.
                  jC-atXLIB327405P3b02b1
Seq. ID
Method
                  BLASTN
                  g2582640
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
Match length
                  72
% identity
                  95
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172330
Seq. No.
                  jC-atXLIB327405P3c06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  40
                  5.0e-13
E value
                  56
Match length
% identity
                  93
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172331
Seq. No.
                  iC-atXLIB327405P3c12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  62
E value
                  4.0e-26
Match length
                  62
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172332
Seq. No.
Seq. ID
                  jC-atXLIB327405P3e06a1
                  BLASTX
Method
                  q480450
NCBI GI
                  89
BLAST score
                  1.0e-15
E value
                  69
Match length
                  69
% identity
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
```

Seq. ID jC-atXLIB327405P3f01b1

Method BLASTN
NCBI GI g3169169
BLAST score 132
E value 6.0e-68
Match length 313
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  172334
Seq. ID
                  jC-atXLIB327405P3f03a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  52
E value
                  4.0e-20
                  56
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172335
Seq. No.
Seq. ID
                  jC-atXLIB327405P3f08a1
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  52
E value
                  4.0e-20
                  56
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172336
Seq. No.
Seq. ID
                  jC-atXLIB327405P3g03a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  38
                  8.0e-12
E value
Match length
                  54
                  94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172337
Seq. No.
Seq. ID
                  jC-atXLIB327405P3g06a1
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  33
                  9.0e-09
E value
Match length
                  41
% identity
                  95
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172338
Seq. ID
                  jC-atXLIB327405P3g08a1
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  56
E value
                  2.0e-22
Match length
                  56
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
```

Seq. ID jC-atXLIB327405P3h04b1

Method BLASTN
NCBI GI g2618599
BLAST score 47
E value 4.0e-17
Match length 186



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBD2, complete sequence [Arabidopsis thaliana]
                  172340
Seq. No.
Seq. ID
                  jC-atXLIB327405P3h05a1
                  {\tt BLASTN}
Method
                  q531828
NCBI GI
                  56
BLAST score
                  2.0e-22
E value
                  60
Match length
                  98
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172341
Seq. No.
                  jC-atXLIB327405P3h05b1
Seq. ID
                  BLASTN
Method
                  g2290179
NCBI GI
                  33
BLAST score
                  8.0e-09
E value
Match length
                  40
% identity
                  98
                  HIV-1 strain H35 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172342
Seq. No.
                  jC-atXLIB327405P3h06a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  53
                  8.0e-21
E value
                  53
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172343
Seq. No.
Seq. ID
                   jC-atXLIB327405P3h09b1
                  BLASTX
Method
NCBI GI
                  g1706772
BLAST score
                   449
                   2.0e-44
E value
Match length
                  129
% identity
                   74
NCBI Description FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE
                   SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE)
                   >gi 1076324 pir S54251 farnesyl-diphosphate
                   farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana
                   >qi 798820 emb CAA60385 (X86692) farnesyl-diphosphate
                   farnesyltransferase [Arabidopsis thaliana]
                   >gi 806325 dbj BAA06103 (D29017) squalene synthase
                   [Arabidopsis thaliana] >gi 2232212 (AF004560) squalene
                   synthase 1 [Arabidopsis thaliana]
                   >qi 3096933 emb CAA18843.1 (AL023094) farnesyl-diphosphate
```

farnesyltransferase [Arabidopsis thaliana] >gi_4098519
(U79159) squalene synthase [Arabidopsis thaliana]



```
jC-atXLIB327405P3h12a1
Seq. ID
Method
                  BLASTX
                  g2583124
NCBI GI
BLAST score
                  307
E value
                  7.0e-28
Match length
                  90
                  72
% identity
                   (AC002387) 5-enolpyruvylshikimate-3-phosphate synthase
NCBI Description
                   (EPSP) [Arabidopsis thaliana]
                  172345
Seq. No.
                  iC-atXLIB327405P4a03a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  55
E value
                  6.0e-22
Match length
                  63
% identity
                  97
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172346
                  jC-atXLIB327405P4b06a1
Seq. ID
Method
                  BLASTN
                  g1223909
NCBI GI
BLAST score
                  74
                  3.0e - 33
E value
Match length
                   315
% identity
                  89
                  Arabidopsis thaliana chaperonin-60 alpha subunit gene,
NCBI Description
                  nuclear gene encoding plastid protein, complete cds
                  172347
Seq. No.
Seq. ID
                   jC-atXLIB327405P4b09a1
                  BLASTN
Method
NCBI GI
                  g3510347
BLAST score
                   55
                  6.0e-22
E value
                   83
Match length
                   92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
                   172348
Seq. No.
Seq. ID
                   jC-atXLIB327405P4b10b1
                   BLASTX
Method
                   q3600035
NCBI GI
                   157
BLAST score
E value
                   1.0e-18
                   87
Match length
% identity
NCBI Description
                  (AF080119) contains similarity to GTP-binding proteins
                   [Arabidopsis thaliana]
```

Seq. ID jC-atXLIB327405P4c03a1

Method BLASTN NCBI GI 92760171

E value Match length



```
56
 BLAST score
                   1.0e-22
 E value
 Match length
                   136
                   86
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
· NCBI Description
                   MPA24, complete sequence [Arabidopsis thaliana]
                   172350
 Seq. No.
 Seq. ID
                   jC-atXLIB327405P4c05a1
 Method
                   BLASTN
 NCBI GI
                   g2529657
 BLAST score
                   110
 E value
                    9.0e-55
 Match length
                   271
                    91
 % identity
                   Arabidopsis thaliana chromosome II BAC T30B22 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                   172351
 Seq. No.
                    jC-atXLIB327405P4c06b1
 Seq. ID
 Method
                   BLASTN
                   g3510339
 NCBI GI
                    107
 BLAST score
                    6.0e-53
 E value
 Match length
                    225
                    95
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K3K7, complete sequence [Arabidopsis thaliana]
                    172352
 Seq. No.
 Seq. ID
                    jC-atXLIB327405P4c07b1
 Method
                    BLASTN
                    g2656031
 NCBI GI
                    48
 BLAST score
                    3.0e-18
 E value
                    126
 Match length
                    93
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MXC20
                    172353
 Seq. No.
 Seq. ID
                    jC-atXLIB327405P4c09a1
 Method
                    BLASTN
 NCBI GI
                    g2462264
                    53
 BLAST score
                    1.0e-20
 E value
                    57
 Match length
 % identity
 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
 Seq. No.
                    172354
 Seq. ID
                    jC-atXLIB327405P4c09b1
                    BLASTN
 Method
 NCBI GI
                    q531828
 BLAST score
                    49
```

23591

2.0e-18



% identity NCBI Description Cloning vector pSport1, complete cds 172355 Seq. No. Seq. ID jC-atXLIB327405P4d02a1 Method BLASTN g2462264 NCBI GI BLAST score 53 E value 8.0e-21 57 Match length % identity 98 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172356 Seq. No. jC-atXLIB327405P4d03b1 Seq. ID Method BLASTN NCBI GI g2582640 BLAST score 42 2.0e-14 E value Match length 64 94 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 Seq. No. 172357 jC-atXLIB327405P4d04a1 Seq. ID Method BLASTN g3132469 NCBI GI 79 BLAST score 3.0e-36 E value 119 Match length % identity 92 Arabidopsis thaliana chromosome II BAC T29F13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 172358 Seq. No. Seq. ID jC-atXLIB327405P4d07a1 BLASTN Method g2462264 NCBI GI BLAST score 37 E value 3.0e-1156 Match length 91 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172359 Seq. No. Seq. ID jC-atXLIB327405P4d08a1 BLASTN Method q2462264 NCBI GI 50 BLAST score 6.0e-19 E value

54 Match length 98 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

172360 Seq. No.

Seq. ID jC-atXLIB327405P4d09a1

Match length



```
BLASTN
Method
                  g2290120
NCBI GI
                  50
BLAST score
                  5.0e-19
E value
Match length
                  66
                  94
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172361
Seq. No.
                   jC-atXLIB327405P4d09b1
Seq. ID
                  BLASTN
Method
                  q531828
NCBI GI
                   40
BLAST score
                   5.0e-13
E value
Match length
                   44
                   98
% identity
NCBI Description Cloning vector pSport1, complete cds
                   172362
Seq. No.
                   jC-atXLIB327405P4e01a1
Seq. ID
Method
                   BLASTN
                   q2749918
NCBI GI
                   86
BLAST score
                   2.0e-40
E value
                   145
Match length
                   90
% identity
                  Arabidopsis thaliana chromosome I BAC F3I6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172363
                   jC-atXLIB327405P4e03a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2462264
BLAST score
                   52
                   4.0e-20
E value
                   52
Match length
                   100
% identity
                   Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                   172364
Seq. No.
Seq. ID
                   jC-atXLIB327405P4e04a1
                   BLASTN
Method
                   q2462264
NCBI GI
                   49
BLAST score
E value
                   2.0e-18
                   53
Match length
                   98
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                   172365
                   jC-atXLIB327405P4e05a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4454022
BLAST score
                   103
                   1.0e-50
E value
```



% identity Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 NCBI Description (ESSAII project) Seq. No. 172366 jC-atXLIB327405P4e05b1 Seq. ID BLASTN Method g4454022 NCBI GI BLAST score 35 5.0e-10 E value Match length 229 % identity 85 Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 NCBI Description (ESSAII project) Seq. No. 172367 jC-atXLIB327405P4e06a1 Seq. ID

Method BLASTN NCBI GI g2462264 BLAST score 38 E value 9.0e-12 Match length 53 % identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

172368 Seq. No.

jC-atXLIB327405P4e10a1 Seq. ID

BLASTN Method g2462264 NCBI GI 53 BLAST score 9.0e-21 E value Match length 53 100 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

172369 Seq. No.

Seq. ID jC-atXLIB327405P4e11b1

BLASTN Method g3319885 NCBI GI 139 BLAST score 3.0e-72 E value 281 Match length 88 % identity

NCBI Description Arabidopsis thaliana mRNA for PRT1 protein

Seq. No. 172370

Seq. ID jC-atXLIB327405P4f01a1

BLASTN Method NCBI GI g531828 BLAST score 44 2.0e-15 E value 52 Match length 96 % identity

NCBI Description Cloning vector pSport1, complete cds

172371 Seq. No.

Seq. ID jC-atXLIB327405P4f02a1



```
BLASTN
Method
                  g2462264
NCBI GI
                  35
BLAST score
                  5.0e-10
E value
                  51
Match length
                  94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172372
Seq. No.
Seq. ID
                  jC-atXLIB327405P4f03a1
                  BLASTN
Method
                  g2462264
NCBI GI
                  50
BLAST score
                  6.0e-19
E value
Match length
                  54
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172373
Seq. No.
Seq. ID
                  jC-atXLIB327405P4f05a1
Method
                  BLASTN
                  g166933
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                  94
Match length
                  90
% identity
                  A.thaliana ubiquitin extension protein (UBQ5) gene,
NCBI Description
                  complete cds
                  172374
Seq. No.
Seq. ID
                  jC-atXLIB327405P4f06a1
                  BLASTN
Method
                  q288062
NCBI GI
BLAST score
                  85
                  7.0e-40
E value
Match length
                  142
                  89
% identity
NCBI Description A.thaliana mRNA for ketol-acid reductoisomerase subunit
                  172375
Seq. No.
Seq. ID
                  jC-atXLIB327405P4f06b1
Method
                  BLASTN
NCBI GI
                  g402551
BLAST score
                  41
                  2.0e-13
E value
Match length
                  57
                  93
% identity
NCBI Description A.thaliana gene for acetohydroxy acid isomeroreductase
                  172376
Seq. No.
```

Seq. ID jC-atXLIB327405P4f07a1

BLASTN Method NCBI GI g2462264 BLAST score 53 E value 1.0e-20 Match length 57 % identity 98



```
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172377
Seq. No.
                  jC-atXLIB327405P4f10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
                  45
BLAST score
                  5.0e-16
E value
                  53
Match length
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172378
Seq. No.
                  jC-atXLIB327405P4g01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  53
                  6.0e-21
E value
                  111
Match length
                  89
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  172379
Seq. No.
                  jC-atXLIB327405P4g02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062153
BLAST score
                  120
                  9.0e-61
E value
Match length
                  61
% identity
                  95
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172380
Seq. ID
                  jC-atXLIB327405P4g03a1
                  BLASTN
Method
NCBI GI
                  g2618599
                  92
BLAST score
                  6.0e-44
E value
                  163
Match length
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBD2, complete sequence [Arabidopsis thaliana]
                  172381
Seq. No.
Seq. ID
                  jC-atXLIB327405P4g04a1
Method
                  BLASTN
NCBI GI
                  g2828187
                  80
BLAST score
                  7.0e-37
E value
                  148
Match length
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

K21C13, complete sequence [Arabidopsis thaliana]

E value Match length



jC-atXLIB327405P4q06a1 Seq. ID BLASTN Method g2226430 NCBI GI 33 BLAST score E value 1.0e-08 37 Match length 97 % identity NCBI Description Mus saxicola haptoglobin mRNA, complete cds 172383 Seq. No. jC-atXLIB327405P4g07a1 Seq. ID Method BLASTN q2290120 NCBI GI BLAST score 50 6.0e-19 E value Match length 61 % identity 95 HIV-1 strain MO2 from USA, envelope glycoprotein (env) NCBI Description gene, partial cds Seq. No. 172384 jC-atXLIB327405P4g07b1 Seq. ID Method BLASTX q2828012 NCBI GI 202 BLAST score 8.0e-18 E value 80 Match length 60 % identity (AF036891) starch synthase I precursor [Zea mays] NCBI Description Seq. No. 172385 Seq. ID jC-atXLIB327405P4g09a1 Method BLASTN NCBI GI q2462264 BLAST score 53 E value 9.0e-21 57 Match length 98 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172386 Seq. No. Seq. ID jC-atXLIB327405P4g10a1 Method BLASTX q2245085 NCBI GI BLAST score 151 E value 9.0e-18 78 Match length % identity NCBI Description (Z97343) lactate dehydrogenase [Arabidopsis thaliana] Seq. No. 172387 Seq. ID jC-atXLIB327405P4g11a1 BLASTN Method NCBI GI q1931636 BLAST score 276

23597

1.0e-154



% identity NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence Seq. No. 172388 jC-atXLIB327405P4g12a1 Seq. ID Method BLASTN q2098816 NCBI GI BLAST score 102 5.0e-50 E value Match length 178 % identity 95 NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence 172389 Seq. No. jC-atXLIB327405P4h10b1 Seq. ID Method BLASTX NCBI GI q4415916 BLAST score 147 3.0e-09 E value 63 Match length 48 % identity NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis thalianal 172390 Seq. No. jC-atXLIB327406P1a01a1 Seq. ID Method BLASTN NCBI GI q2656029 BLAST score 70 6.0e - 31E value Match length 118 % identity 92 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MQB2 172391 Seq. No. Seq. ID jC-atXLIB327406P1a03b1 Method BLASTN g2582640 NCBI GI BLAST score 55 5.0e-22 E value Match length 71 % identity 96 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40

Seq. No. 172392

Seq. ID jC-atXLIB327406P1e10a1

Method BLASTN
NCBI GI g2182286
BLAST score 103
E value 9.0e-51
Match length 233
% identity 90

NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]



```
172393
Seq. No.
Seq. ID
                  jC-atXLIB327406P1f01b1
                  BLASTN
Method
                  g2582640
NCBI GI
                  57
BLAST score
                  3.0e-23
E value
                  77
Match length
                  95
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172394
Seq. No.
Seq. ID
                  jC-atXLIB327406P1f04b1
                  BLASTN
Method
                  g1313925
NCBI GI
                  64
BLAST score
                  2.0e-27
E value
                  160
Match length
                  85
% identity
NCBI Description B.oleracea mRNA for IFA binding protein (sp7)
                  172395
Seq. No.
Seq. ID
                  jC-atXLIB327406P1f05a1
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
                  51
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172396
Seq. No.
                   jC-atXLIB327406P1f09a1
Seq. ID
                  BLASTN
Method
                  g166787
NCBI GI
BLAST score
                  115
                   8.0e-58
E value
                  255
Match length
                   92
% identity
NCBI Description A.thaliana chloroplast ATP synthase gamma subunit (atpC2)
                   gene, complete cds
                   172397
Seq. No.
                   jC-atXLIB327406P1g02a1
Seq. ID
                   BLASTN
Method
                   q2462264
NCBI GI
                   40
BLAST score
                   5.0e-13
E value
                   52
Match length
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172398
Seq. No.
                   jC-atXLIB327406P1h09b1
```

Seq. ID

Method BLASTN NCBI GI g2582640 42

BLAST score



E value 3.0e-14
Match length 72
% identity 92

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172399

Seq. ID jC-atXLIB327406P1h11b1

Method BLASTX
NCBI GI g2738248
BLAST score 166
E value 2.0e-11
Match length 122
% identity 25

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 172400

Seq. ID jC-atXLIB327406P1h12b1

Method BLASTN
NCBI GI 94490291
BLAST score 294
E value 1.0e-164
Match length 350
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5

(ESSA project)

Seq. No. 172401

Seq. ID jC-atXLIB327406P2a01b1

Method BLASTN
NCBI GI g531832
BLAST score 37
E value 2.0e-11
Match length 53
% identity 94

NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 172402

Seq. ID jC-atXLIB327406P2a06a1

Method BLASTN
NCBI GI g2462264
BLAST score 53
E value 5.0e-21
Match length 57
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172403

Seq. ID jC-atXLIB327406P2a09b1

Method BLASTN
NCBI GI g2582640
BLAST score 50
E value 6.0e-19
Match length 65
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

Seq. ID



factor, RSp40

```
172404
Seq. No.
                  jC-atXLIB327406P2a10a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                  54
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172405
Seq. No.
                   jC-atXLIB327406P2a10b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
                  68
BLAST score
                   7.0e-30
E value
                   76
Match length
                   99
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   172406
                   jC-atXLIB327406P2b04a1
Seq. ID
                   BLASTX
Method
                   g2160692
NCBI GI
                   267
BLAST score
                   3.0e-23
E value
                   68
Match length
                   78
% identity
                  (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   172407
Seq. No.
                   jC-atXLIB327406P2b05a1
Seq. ID
                   BLASTX
Method
                   q4115381
NCBI GI
BLAST score
                   184
                   1.0e-13
E value
                   46
Match length
                   76
% identity
NCBI Description (AC005967) putative limonene cyclase [Arabidopsis thaliana]
                   172408
Seq. No.
                   jC-atXLIB327406P2b06b1
Seq. ID
Method
                   BLASTN
                   g2582640
NCBI GI
BLAST score
                   57
                   4.0e-23
E value
                   75
Match length
                   95
 % identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
                   172409
 Seq. No.
```

jC-atXLIB327406P2b07a1

E value

Match length % identity

1.0e-09

95



```
Method
                  BLASTX
NCBI GI
                  q1432056
BLAST score
                  64
                  3.0e-21
E value
                  73
Match length
% identity
                  62
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
                  172410
Seq. No.
Seq. ID
                  jC-atXLIB327406P2b08a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  54
                  2.0e-21
E value
                  54
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172411
Seq. No.
                  jC-atXLIB327406P2b09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3550981
BLAST score
                  55
                  6.0e-22
E value
Match length
                  338
% identity
NCBI Description Arabidopsis thaliana mutM homologue gene, complete cds
                  172412
Seq. No.
                  jC-atXLIB327406P2c01a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  56
E value
                  2.0e-22
                  56
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172413
Seq. No.
                  jC-atXLIB327406P2c01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3800746
BLAST score
                  42
                  3.0e-14
E value
Match length
                  46
                  98
% identity
NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                  complete cds
                  172414
Seq. No.
Seq. ID
                  jC-atXLIB327406P2c12a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  34
```



```
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172415
Seq. No.
                  jC-atXLIB327406P2d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914667
                  195
BLAST score
                  9.0e-15
E value
Match length
                  61
% identity
                  62
                  50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 2459427 (AC002332) putative chloroplast 50S ribosomal
                  protein L28 [Arabidopsis thaliana]
                  172416
Seq. No.
Seq. ID
                  jC-atXLIB327406P2d05a1
Method
                  BLASTN
NCBI GI
                  g1022806
BLAST score
                  80
E value
                  7.0e - 37
Match length
                  92
% identity
                  97
NCBI Description Arabidopsis thaliana cellulase (OR16pep) mRNA, complete cds
Seq. No.
                  172417
                  jC-atXLIB327406P2d09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  33
                  8.0e-09
E value
Match length
                  33
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172418
Seq. No.
Seq. ID
                  jC-atXLIB327406P2d09b1
Method
                  BLASTN
                  g2582640
NCBI GI
                  43
BLAST score
                  9.0e-15
E value
                  67
Match length
% identity
                  91
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172419
Seq. No.
```

Seq. ID jC-atXLIB327406P2e01a1

Method BLASTN
NCBI GI g2673901
BLAST score 171
E value 4.0e-91
Match length 261
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172420



```
jC-atXLIB327406P2e05a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  54
E value
                  3.0e-21
                  54
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172421
Seq. No.
                  jC-atXLIB327406P2e11b1
Seq. ID
                  BLASTN
Method
                  q2582640
NCBI GI
BLAST score
                  60
E value
                  6.0e-25
Match length
                  68
% identity
                  99
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172422
Seq. ID
                  jC-atXLIB327406P2f05a1
Method
                  BLASTN
NCBI GI
                  g4510360
BLAST score
                  203
                  1.0e-110
E value
Match length
                   267
% identity
                   59
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                  172423
                   jC-atXLIB327406P2f08a1
Seq. ID
                   BLASTX
Method
                  g3402487
NCBI GI
BLAST score
                   434
                  8.0e-43
E value
                   92
Match length
                   95
% identity
                  (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   172424
Seq. No.
Seq. ID
                   jC-atXLIB327406P2g02a1
Method
                   BLASTN
NCBI GI
                   g3449321
BLAST score
                   440
```

0.0e + 00E value Match length 472 98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 172425

Seq. ID jC-atXLIB327406P2g06a1

BLASTN Method NCBI GI g2462264



98

% identity

```
53
BLAST score
                  5.0e-21
E value
                  57
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172426
                  jC-atXLIB327406P2g06b1
Seq. ID
                  BLASTX
Method
                  g2454184
NCBI GI
                  456
BLAST score
                  2.0e-45
E value
                  137
Match length
                  70
% identity
                  (U80186) pyruvate dehydrogenase E1 beta subunit
NCBI Description
                   [Arabidopsis thaliana]
                  172427
Seq. No.
                   jC-atXLIB327406P2h02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2290120
                   49
BLAST score
                   3.0e-18
E value
                   65
Match length
                   94
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                   gene, partial cds
                   172428
Seq. No.
                   jC-atXLIB327406P2h03a1
Seq. ID
Method
                   BLASTN
                   q2462264
NCBI GI
                   52
BLAST score
                   4.0e-20
E value
                   56
Match length
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172429
Seq. No.
Seq. ID
                   jC-atXLIB327406P2h06a1
                   BLASTN
Method
NCBI GI
                   q2462264
                   54
BLAST score
                   2.0e-21
E value
                   54
Match length
% identity
                   100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172430
Seq. No.
                   jC-atXLIB327406P2h07a1
Seq. ID
Method
                   BLASTN
                   g2462264
NCBI GI
BLAST score
                   53
                   9.0e-21
E value
                   57
Match length
```

23605

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
172431
Seq. No.
                  jC-atXLIB327406P3a03b2
Seq. ID
                  BLASTX
Method
                  q3641837
NCBI GI
BLAST score
                  373
                  9.0e-36
E value
                  96
Match length
                  80
% identity
NCBI Description
                  (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
                  172432
Seq. No.
                  jC-atXLIB327406P3a05a2
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  56
E value
                  5.0e-23
Match length
                  60
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172433
                  jC-atXLIB327406P3a08b2
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
                  37
BLAST score
E value
                  1.0e-11
Match length
                  45
                   96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172434
                   jC-atXLIB327406P3b01a2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2462264
BLAST score
                   49
                   1.0e-18
E value
Match length
                   53
% identity
                   98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172435
Seq. No.
Seq. ID
                   jC-atXLIB327406P3b03b2
Method
                   BLASTN
                   g3941523
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
                   46
Match length
                   93
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
```

23606

172436

BLASTN

jC-atXLIB327406P3b08b2

Seq. No. Seq. ID

Method

E value Match length

% identity



```
g531832
NCBI GI
                  51
BLAST score
                  1.0e-19
E value
                  58
Match length
                  98
% identity
NCBI Description Cloning vector pSport2, complete sequence
                  172437
Seq. No.
Seq. ID
                   jC-atXLIB327406P3c02b2
                  BLASTN
Method
                  g3941523
NCBI GI
                   48
BLAST score
                   6.0e-18
E value
                   52
Match length
                   98
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                   172438
Seq. No.
Seq. ID
                   jC-atXLIB327406P3c07b2
Method
                   BLASTX
                   g2244977
NCBI GI
                   723
BLAST score
                   1.0e-76
E value
                   147
Match length
                   92
% identity
                  (Z97340) cysteine proteinase [Arabidopsis thaliana]
NCBI Description
                   172439
Seq. No.
Seq. ID
                   jC-atXLIB327406P3d01a2
Method
                   BLASTN
                   g2462264
NCBI GI
                   38
BLAST score
                   3.0e-12
E value
Match length
                   50
                   94
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172440
Seq. No.
Seq. ID
                   jC-atXLIB327406P3d05a2
                   BLASTX
Method
NCBI GI
                   g2244905
BLAST score
                   364
                   5.0e-46
E value
Match length
                   125
% identity
                   70
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   172441
                   jC-atXLIB327406P3d08a2
Seq. ID
Method
                   BLASTN
                   g2290120
NCBI GI
                   52
BLAST score
```

23607

5.0e-20



```
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  172442
Seq. No.
                  jC-atXLIB327406P3d09a2
Seq. ID
Method 4.
                  BLASTN
NCBI GI
                  q166643
BLAST score
                  94
                  4.0e-45
E value
Match length
                  203
% identity
                  89
                  Arabidopsis thaliana chlorophyll A/B-binding protein gene,
NCBI Description
                  complete cds
                  172443
Seq. No.
Seq. ID
                  jC-atXLIB327406P3d10a2
Method
                  BLASTN
                  g643089
NCBI GI
                  73
BLAST score
                  1.0e-32
E value
Match length
                  154
% identity
                  88
                  A.thaliana mRNA for NADH: ubiquinone oxidoreductase (complex
NCBI Description
                  I)
                  172444
Seq. No.
                  jC-atXLIB327406P3d10b2
Seq. ID
                  BLASTN
Method
                  g1234869
NCBI GI
                  46
BLAST score
                  1.0e-16
E value
Match length
                  140
                  90
% identity
NCBI Description A.thaliana PSST gene
                  172445
Seq. No.
Seq. ID
                   jC-atXLIB327406P3d11a2
                  BLASTN
Method
NCBI GI
                  q3859590
BLAST score
                  153
                   2.0e-80
E value
Match length
                  269
                   92
% identity
NCBI Description Arabidopsis thaliana BAC T15B16
                   172446
Seq. No.
Seq. ID
                   jC-atXLIB327406P3d11b2
                   BLASTX
Method
                   g3859606
NCBI GI
BLAST score
                   169
E value
                   8.0e-12
Match length
                   81
% identity
                   53
```

NCBI Description

23608

PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

(AF104919) contains similarity to cysteine proteases (Pfam:

Seq. ID

Method NCBI GI



```
jC-atXLIB327406P3d12b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3617742
BLAST score
                  271
E value
                  9.0e-24
Match length
                  87
                  64
% identity
                  (AC005687) RAP2.6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  172448
Seq. ID
                  jC-atXLIB327406P3e06b2
Method
                  BLASTN
NCBI GI
                  g3386593
BLAST score
                  40
E value
                  5.0e-13
Match length
                  92
% identity
                  86
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172449
Seq. ID
                  jC-atXLIB327406P3e09a2
Method
                  BLASTN
NCBI GI
                  q3643588
BLAST score
                  315
E value
                  1.0e-177
Match length
                  424
% identity
                  95
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172450
Seq. ID
                  jC-atXLIB327406P3e10b2
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                  49
                  2.0e-18
E value
                  69
Match length
                  94
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                   172451
Seq. ID
                   jC-atXLIB327406P3e11b2
                  BLASTN
Method
NCBI GI
                  g4757392
BLAST score
                   303
                  1.0e-170
E value
Match length
                   410
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
Seq. No.
                   172452
```

23609

jC-atXLIB327406P3f01b2

BLASTX

g2828267



```
BLAST score
                  642
E value
                  3.0e-67
Match length
                  142
                  87
% identity
                  (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
NCBI Description
                  172453
Seq. No.
                  jC-atXLIB327406P3f12b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2149639
BLAST score
                  200
E value
                  1.0e-108
                  356
Match length
% identity
                  Arabidopsis thaliana Argonaute protein (AGO1) mRNA,
NCBI Description
                  complete cds
                  172454
Seq. No.
                  jC-atXLIB327406P3g04b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16306
BLAST score
                  63
E value
                  1.0e-26
Match length
                  316
                  86
% identity
NCBI Description A.thaliana genes encoding glycine-rich proteins
                  172455
Seq. No.
                  jC-atXLIB327406P3g09b2
Seq. ID
                  BLASTN
Method
                  g3643588
NCBI GI
                   39
BLAST score
                   2.0e-12
E value
                   101
Match length
                   91
% identity
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   172456
Seq. No.
Seq. ID
                   jC-atXLIB327406P3g10a2
                   BLASTN
Method
                   g3789706
NCBI GI
BLAST score
                   224
                   1.0e-123
E value
                   366
Match length
% identity
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   172457
Seq. No.
Seq. ID
                   jC-atXLIB327406P3g11b2
                   BLASTN
Method
                   g3046856
NCBI GI
BLAST score
                   71
E value
                   2.0e-31
```

278

87

Match length % identity



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 172458

Seq. ID jC-atXLIB327406P3h01b2

Method BLASTN
NCBI GI g2582640
BLAST score 62

E value 3.0e-26 Match length 86 % identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172459

Seq. ID jC-atXLIB327406P3h06a2

Method BLASTN
NCBI GI g531828
BLAST score 54
E value 2.0e-21
Match length 62
% identity 97

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172460

Seq. ID jC-atXLIB327406P3h12a2

Method BLASTN
NCBI GI g2149639
BLAST score 134
E value 5.0e-69
Match length 365
% identity 88

NCBI Description Arabidopsis thaliana Argonaute protein (AGO1) mRNA,

complete cds

Seq. No. 172461

Seq. ID jC-atXLIB327406P4a04b2

Method BLASTX
NCBI GI g3831451
BLAST score 117
E value 5.0e-09
Match length 70
% identity 57

NCBI Description (AC005700) putative O-GlcNAc transferase [Arabidopsis

thaliana]

Seq. No. 172462

Seq. ID jC-atXLIB327406P4a06b2

Method BLASTN
NCBI GI g2582640
BLAST score 55
E value 5.0e-22
Match length 63
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40



172463 Seq. No. jC-atXLIB327406P4a08b2 Seq. ID BLASTN Method g2582640 NCBI GI BLAST score 42 3.0e-14E value Match length 66 92 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172464 Seq. No. jC-atXLIB327406P4c08a2 Seq. ID BLASTN Method g1483219 NCBI GI BLAST score 94 3.0e-45E value Match length 126 94 % identity NCBI Description A.thaliana mRNA for peroxidase ATPla, clone EST 103m21t7 Seq. No. 172465 jC-atXLIB327406P4d01b2 Seq. ID BLASTN Method g2191126 NCBI GI BLAST score 36 E value 4.0e-11 Match length 122 87 % identity NCBI Description Arabidopsis thaliana BAC IG002N01 Seq. No. 172466 jC-atXLIB327406P4d02b2 Seq. ID BLASTN Method g507219 NCBI GI 296 BLAST score 1.0e-166 E value 421 Match length 93 % identity Arabidopsis thaliana homeodomain protein (PRHA) mRNA, NCBI Description complete cds Seq. No. 172467 jC-atXLIB327406P4d07a2 Seq. ID BLASTN Method NCBI GI g4165340 BLAST score 150 1.0e-78 E value 307 Match length 91 % identity Arabidopsis thaliana chromosome I BAC F11M15 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172468

Seq. ID jC-atXLIB327406P4d07b2

Method BLASTN NCBI GI g4165340



```
BLAST score
                  2.0e-09
E value
Match length
                  166
                  91
% identity
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  172469
Seq. No.
                   jC-atXLIB327406P4e09a2
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1532162
                  59
BLAST score
                  2.0e-24
E value
                  142
Match length
                  89
% identity
                  Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
NCBI Description
                  AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                   genes, partial cds, AT.I.24-7, ascorbate peroxidase
                   (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
Seq. No.
                   172470
                   jC-atXLIB327406P4e09b2
Seq. ID
Method
                   BLASTN
                   g1532162
NCBI GI
                   79
BLAST score
                   3.0e-36
E value
Match length
                   283
% identity
                   89
                  Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
NCBI Description
                   AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                   genes, partial cds, AT.I.24-7, ascorbate peroxidase
                   (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
Seq. No.
                   172471
                   jC-atXLIB327406P4f01b2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3046854
                   48
BLAST score
                   8.0e-18
E value
                   234
Match length
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRG7, complete sequence [Arabidopsis thaliana]
                   172472
Seq. No.
Seq. ID
                   jC-atXLIB327406P4f04a2
Method
                   BLASTN
NCBI GI
                   q4159712
                   173
BLAST score
                   2.0e-92
E value
Match length
                   275
                   74
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MWI23, complete sequence
```

23613

172473

jC-atXLIB327406P4g07a2

Seq. No.

Seq. ID



Method BLASTX
NCBI GI g4581113
BLAST score 313
E value 1.0e-28
Match length 67
% identity 93

NCBI Description (AC005825) putative actin depolymerizing factor

[Arabidopsis thaliana]

Seq. No. 172474

Seq. ID jC-atXLIB327406P4h06a2

Method BLASTN
NCBI GI g2462264
BLAST score 51
E value 2.0e-19
Match length 51
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172475

Seq. ID jC-atXLIB327406P4h07b2

Method BLASTX
NCBI GI g4699942
BLAST score 434
E value 7.0e-43
Match length 150
% identity 63

NCBI Description (AC007166) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 172476

Seq. ID jC-atXLIB327407P1a04a1

Method BLASTX
NCBI GI g1351987
BLAST score 201
E value 1.0e-15
Match length 44
% identity 86

NCBI Description ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)

(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_507946 (L29083) glutamine-dependent asparagine synthetase

[Arabidopsis thaliana]

Seq. No. 172477

Seq. ID jC-atXLIB327407P1a06b2

Method BLASTN
NCBI GI 94753195
BLAST score 81
E value 1.0e-37
Match length 97
% identity 96

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 172478

Seq. ID jC-atXLIB327407P1a07a2

Method BLASTN

NCBI GI BLAST score



```
q4589445
NCBI GI
BLAST score
                  89
                  3.0e-42
E value
                  214
Match length
                  50
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWL2, complete sequence
                   172479
Seq. No.
                   jC-atXLIB327407Pla08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2252639
                  82
BLAST score
                   5.0e-38
E value
                   130
Match length
% identity
                  Genomic sequence of Arabidopsis BAC F8A5, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                   172480
Seq. No.
                   jC-atXLIB327407P1a11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3414927
                   190
BLAST score
                   1.0e-102
E value
                   218
Match length
                   97
% identity
                  Arabidopsis thaliana PsbY precursor (psbY) mRNA, nuclear
NCBI Description
                   gene encoding chloroplast protein, complete cds
                   172481
Seq. No.
                   jC-atXLIB327407P1b02a1
Seq. ID
                   BLASTN
Method
                   g3510247
NCBI GI
                   86
BLAST score
                   2.0e-40
E value
                   98
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC F19D11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   172482
Seq. No.
Seq. ID
                   jC-atXLIB327407P1b02b1
Method
                   BLASTN
                   g3941523
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
                   100
% identity
                   Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                   mRNA, complete cds
                   172483
Seq. No.
Seq. ID
                   jC-atXLIB327407P1b03b1
                   BLASTN
Method
```

g2582640



E value 1.0e-19 Match length 55 % identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172484

Seq. ID jC-atXLIB327407P1b05a1

Method BLASTN
NCBI GI g3176695
BLAST score 83
E value 9.0e-39
Match length 87
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic

sequence contains phyA marker, complete sequence

[Arabidopsis thaliana]

Seq. No. 172485

Seq. ID jC-atXLIB327407P1b06a1

Method BLASTN
NCBI GI g4406752
BLAST score 95
E value 8.0e-46
Match length 103
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F19B11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172486

Seq. ID jC-atXLIB327407P1b08a1

Method BLASTN
NCBI GI g4309719
BLAST score 50
E value 5.0e-19
Match length 50
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172487

Seq. ID jC-atXLIB327407P1b09a1

Method BLASTN
NCBI GI g3668073
BLAST score 34
E value 2.0e-09
Match length 45
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T4C15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172488

Seq. ID jC-atXLIB327407P1b11a1

Method BLASTN
NCBI GI g3399678
BLAST score 148
E value 2.0e-77



Match length 220 % identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 172489

Seq. ID jC-atXLIB327407P1b12a1

Method BLASTN
NCBI GI g2337888
BLAST score 105
E value 8.0e-52
Match length 125
% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 172490

Seq. ID jC-atXLIB327407P1c01a1

Method BLASTN
NCBI GI g4263774
BLAST score 69
E value 2.0e-30
Match length 97
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T20F21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172491

Seq. ID jC-atXLIB327407P1c02b1

Method BLASTN
NCBI GI g2582640
BLAST score 43
E value 8.0e-15
Match length 71
% identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172492

Seq. ID jC-atXLIB327407P1c03a1

Method BLASTN
NCBI GI g3985952
BLAST score 154
E value 4.0e-81
Match length 218
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 172493

Seq. ID jC-atXLIB327407P1c03b1

Method BLASTN
NCBI GI g3985952
BLAST score 101
E value 1.0e-49
Match length 137
% identity 96



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 172494

Seq. ID jC-atXLIB327407P1c04a1

Method BLASTX
NCBI GI g1871192
BLAST score 239
E value 3.0e-20
Match length 53
% identity 75

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 172495

Seq. ID jC-atXLIB327407P1c05a1

Method BLASTN
NCBI GI g4539309
BLAST score 65
E value 6.0e-28
Match length 77
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22

(ESSA project)

Seq. No. 172496

Seq. ID jC-atXLIB327407P1c05a2

Method BLASTN
NCBI GI 94539309
BLAST score 68
E value 1.0e-29
Match length 217

Match length 217 % identity 82

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22

(ESSA project)

Seq. No. 172497

Seq. ID jC-atXLIB327407P1c12a1

Method BLASTN
NCBI GI g2252639
BLAST score 55
E value 2.0e-22
Match length 91
% identity 90

NCBI Description Genomic sequence of Arabidopsis BAC F8A5, complete sequence

[Arabidopsis thaliana]

Seq. No. 172498

Seq. ID jC-atXLIB327407P1d02a2

Method BLASTN
NCBI GI g531828
BLAST score 36
E value 1.0e-10
Match length 67
% identity 90

NCBI Description Cloning vector pSport1, complete cds

Seq. No.

Seq. ID



```
172499
Seq. No.
Seq. ID
                  jC-atXLIB327407P1d02b2
                  BLASTN
Method
                  g2582640
NCBI GI
                  45
BLAST score
                  5.0e-16
E value
                  72
Match length
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                   172500
Seq. No.
Seq. ID
                   jC-atXLIB327407P1d03a2
                   BLASTN
Method
                  g2290120
NCBI GI
                   56
BLAST score
                   1.0e-22
E value
                   68
Match length
                   96
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                   gene, partial cds
                   172501
Seq. No.
                   jC-atXLIB327407P1d05a1
Seq. ID
                   BLASTN
Method
                   g3128136
NCBI GI
                   111
BLAST score
                   2.0e-55
E value
                   114
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K1F13, complete sequence [Arabidopsis thaliana]
                   172502
Seq. No.
                   jC-atXLIB327407P1d07a1
Seq. ID
                   BLASTN
Method
                   g2564049
NCBI GI
                   42
BLAST score
                   3.0e-14
E value
Match length
                   42
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172503
                   jC-atXLIB327407P1d07a2
Seq. ID
                   BLASTN
Method
                   g2564049
NCBI GI
BLAST score
                   61
E value
                   1.0e-25
Match length
                   133
                   87
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MLE2, complete sequence [Arabidopsis thaliana]
                   172504
```

jC-atXLIB327407P1d09a1

NCBI GI



```
BLASTN
  Method
                    g3046847
  NCBI GI
                    141
  BLAST score
                    3.0e-73
  E value
                    145

    Match length

                    99
  % identity
                    Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
  NCBI Description
                    K11J9, complete sequence [Arabidopsis thaliana]
                    172505
  Seq. No.
                     jC-atXLIB327407P1d12b1
  Seq. ID
                    BLASTN
  Method
                    q3941523
  NCBI GI
                     47
  BLAST score
                     3.0e-17
  E value
  Match length
                     47
                     100
  % identity
                    Arabidopsis thaliana putative transcription factor (MYB92)
  NCBI Description
                     mRNA, complete cds
  Seq. No.
                     172506
                     jC-atXLIB327407P1e02b1
  Seq. ID
                     BLASTN
  Method
                     q2582640
  NCBI GI
                     39
  BLAST score
                     2.0e-12
  E value
  Match length
                     53
                     96
  % identity
                    Arabidopsis thaliana mRNA for arginine/serine-rich splicing
  NCBI Description
                     factor, RSp40
                     172507
  Seq. No.
  Seq. ID
                     jC-atXLIB327407P1e05a2
                     BLASTX
  Method
                     q99736
  NCBI GI
  BLAST score
                     203
                     9.0e-16
  E value
                     107
  Match length
                     49
   % identity
                     NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
  NCBI Description
                     Arabidopsis thaliana >gi_16187_emb_CAA46814_ (X66016)
                     NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                     172508
   Seq. No.
                     jC-atXLIB327407P1e05b2
   Seq. ID
                     BLASTN
  Method
  NCBI GI
                     g531832
                     50
   BLAST score
                     2.0e-19
   E value
                     54
   Match length
                     98
   % identity
   NCBI Description Cloning vector pSport2, complete sequence
                     172509
   Seq. No.
   Seq. ID
                     jC-atXLIB327407P1e06b2
                     BLASTX
   Method
```

23620

q3738287



```
127
BLAST score
                  2.0e-14
E value
Match length
                  65
% identity
                  64
                  (AC005309) glutathione s-transferase, GST6 [Arabidopsis
NCBI Description
                  thaliana]
                  172510
Seq. No.
Seq. ID
                  jC-atXLIB327407P1e07a2
                  BLASTN
Method
NCBI GI
                  g4455262
                  50
BLAST score
                  6.0e-19
E value
                  222
Match length
% identity
                  81
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                  (ESSAII project)
                  172511
Seq. No.
                  jC-atXLIB327407P1e10a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832689
                  88
BLAST score
                  1.0e-41
E value
Match length
                  168
% identity
                  89
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21
                  (ESSAII project)
                  172512
Seq. No.
Seq. ID
                  jC-atXLIB327407P1e12b1
                  BLASTN
Method
NCBI GI
                  g3941523
                  40
BLAST score
                  4.0e-13
E value
                  40
Match length
                  100
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  172513
Seq. No.
Seq. ID
                  jC-atXLIB327407P1f02b2
                  BLASTN
Method
                  g4587677
NCBI GI
BLAST score
                  42
                  1.0e-14
E value
Match length
                  54
                  94
% identity
                  Arabidopsis thaliana chromosome II BAC T22C12 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  172514
                  jC-atXLIB327407P1g02a2
```

Seq. ID

Method BLASTN NCBI GI g2290120 BLAST score 39 E value 2.0e-12



55 Match length 93 % identity HIV-1 strain MO2 from USA, envelope glycoprotein (env) NCBI Description gene, partial cds 172515 Seq. No. jC-atXLIB327407P1g03a2 Seq. ID Method BLASTX NCBI GI g3298443 302 BLAST score E value 2.0e-27 Match length 76 78 % identity (AB010880) chloroplast ribosomal protein L17 [Nicotiana NCBI Description tabacum] 172516 Seq. No. jC-atXLIB327407P1h02a2 Seq. ID Method BLASTN g2924505 NCBI GI BLAST score 42 E value 3.0e-14 Match length 281 82 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 NCBI Description (ESSAII project) 172517 Seq. No. jC-atXLIB327407P2a01b1 Seq. ID BLASTN Method g3941523 NCBI GI BLAST score 48 6.0e-18E value 52 Match length 98 % identity Arabidopsis thaliana putative transcription factor (MYB92) NCBI Description mRNA, complete cds 172518 Seq. No. Seq. ID jC-atXLIB327407P2a02b1 BLASTN Method g3868723 NCBI GI BLAST score 47 2.0e-17 E value 96 Match length 96 % identity Arabidopsis thaliana chromosome V map 60.5 cM, complete NCBI Description sequence [Arabidopsis thaliana] 172519 Seq. No. Seq. ID jC-atXLIB327407P2a03b1 BLASTN Method q4756963 NCBI GI

Method BLASTN
NCBI GI g4756963
BLAST score 136
E value 3.0e-70
Match length 143
% identity 99



```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
                  172520
Seq. No.
                  jC-atXLIB327407P2a05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3941523
BLAST score
                  41
E value
                  1.0e-13
Match length
                  48
                  98
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  172521
Seq. No.
                  jC-atXLIB327407P2a06b1
Seq. ID
Method
                  BLASTN
                  g2582640
NCBI GI
BLAST score
                  62
                  4.0e-26
E value
Match length
                  74
% identity
                  97
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172522
Seq. No.
                  jC-atXLIB327407P2a07b1
Seq. ID
                  BLASTN
Method
                  g3337347
NCBI GI
                  127
BLAST score
                   6.0e-65
E value
Match length
                   143
                   69
% identity
                  Arabidopsis thaliana chromosome II BAC F13P17 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   172523
Seq. No.
Seq. ID
                   jC-atXLIB327407P2a09b1
                   BLASTN
Method
                   g2582640
NCBI GI
BLAST score
                   43
                   9.0e-15
E value
Match length
                   54
                   96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172524
Seq. No.
Seq. ID
                   jC-atXLIB327407P2a12b1
                   BLASTN
Method
NCBI GI
                   g2351062
                   129
BLAST score
```

4.0e-66 E value Match length 139 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]



172525

```
Seq. No.
                  jC-atXLIB327407P2b02b1
Seq. ID
                  BLASTN
Method
                  g2244901
NCBI GI
                  46
BLAST score
                  1.0e-16
E value
                  61
Match length
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  172526
Seq. No.
Seq. ID
                   jC-atXLIB327407P2b03b1
Method
                  BLASTN
                  g4589428
NCBI GI
                   99
BLAST score
                   3.0e-48
E value
                   115
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
                   172527
Seq. No.
                   jC-atXLIB327407P2b04b1
Seq. ID
                   BLASTN
Method
                   g4589430
NCBI GI
BLAST score
                   68
                   1.0e-29
E value
                   101
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MLD14, complete sequence
                   172528
Seq. No.
                   jC-atXLIB327407P2b06b1
Seq. ID
                   BLASTN
Method
                   g3941523
NCBI GI
BLAST score
                   41
                   1.0e-13
E value
Match length
                   48
% identity
                   Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                   mRNA, complete cds
                   172529
Seq. No.
                   jC-atXLIB327407P2b11b1
Seq. ID
                   BLASTN
Method
                   g2582640
NCBI GI
                   48
BLAST score
                   8.0e-18
E value
                   75
Match length
                   91
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
```

Seq. No. 172530

Seq. No.

Seq. ID Method 172535

BLASTN

jC-atXLIB327407P2c06b1



jC-atXLIB327407P2c01b1 Seq. ID BLASTN Method NCBI GI g2582640 58 BLAST score 1.0e-23 E value 74 Match length 95 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172531 Seq. No. Seq. ID jC-atXLIB327407P2c02b1 Method BLASTN g3510343 NCBI GI 262 BLAST score 1.0e-145 E value 316 Match length 97 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MJC20, complete sequence [Arabidopsis thaliana] 172532 Seq. No. jC-atXLIB327407P2c03b1 Seq. ID BLASTN Method NCBI GI g3985931 BLAST score 141 3.0e-73 E value 153 Match length 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana] 172533 Seq. No. jC-atXLIB327407P2c04b1 Seq. ID Method BLASTN NCBI GI g4049332 BLAST score 48 9.0e-18 E value Match length 48 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project) 172534 Seq. No. Seq. ID jC-atXLIB327407P2c05b1 Method BLASTN q4584519 NCBI GI 43 BLAST score 8.0e-15 E value Match length 80 92 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)

NCBI GI

BLAST score

q2582640

38



```
q2582640
NCBI GI
BLAST score
                  52
E value
                  4.0e-20
                  60
Match length
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172536
                  jC-atXLIB327407P2c07b1
Seq. ID
Method
                  BLASTN
                  g3941523
NCBI GI
BLAST score
                  40
E value
                  5.0e-13
Match length
                  43
                  98
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  172537
Seq. ID
                  jC-atXLIB327407P2c08b1
Method
                  BLASTN
                  q4490291
NCBI GI
BLAST score
                   68
E value
                  1.0e-29
Match length
                   68
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
NCBI Description
                   (ESSA project)
                  172538
Seq. No.
                   jC-atXLIB327407P2c09b1
Seq. ID
                  BLASTN
Method
                  g4512690
NCBI GI
                  79
BLAST score
                   2.0e-36
E value
                   87
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
NCBI Description
                   sequence, complete sequence
                   172539
Seq. No.
Seq. ID
                   jC-atXLIB327407P2c11b1
                   BLASTN
Method
                   q4519193
NCBI GI
BLAST score
                   57
                   4.0e-23
E value
                   142
Match length
% identity
                   44
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MDC11, complete sequence
Seq. No.
                   172540
Seq. ID
                   jC-atXLIB327407P2c12b1
Method
                   BLASTN
```

```
8.0e-12
E value
                  72
Match length
                  91
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172541
Seq. No.
                  jC-atXLIB327407P2d02b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2435508
BLAST score
                  33
                  7.0e-09
E value
                  33
Match length
                  100
% identity
NCBI Description Mus musculus Rigui mRNA, complete cds
                  172542
Seq. No.
                  jC-atXLIB327407P2d04b1
Seq. ID
                  BLASTN
Method
                  q3941523
NCBI GI
                  48
BLAST score
E value
                  5.0e-18
Match length
                   52
% identity
                   98
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   172543
                   jC-atXLIB327407P2d05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   43
                   9.0e-15
E value
                   70
Match length
                   90
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
```

Seq. No. 172544

Seq. ID jC-atXLIB327407P2d07b1

Method BLASTN
NCBI GI g531828
BLAST score 52
E value 4.0e-20
Match length 60
% identity 97

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172545

Seq. ID jC-atXLIB327407P2d08b1

Method BLASTN
NCBI GI g2582640
BLAST score 47
E value 1.0e-17
Match length 59
% identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing



factor, RSp40

```
172546
Seq. No.
                  jC-atXLIB327407P2d09b1
Seq. ID
Method
                  BLASTN
                  g3800746
NCBI GI
BLAST score
                  42
                  1.0e-14
E value
Match length
                  46
% identity
                  98
                  Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
NCBI Description
                  complete cds
                  172547
Seq. No.
                  jC-atXLIB327407P2d10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  48
                  7.0e-18
E value
Match length
                  71
                  93
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172548
Seq. No.
                  jC-atXLIB327407P2d11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449313
BLAST score
                   77
                   2.0e-35
E value
Match length
                  89
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21P3, complete sequence [Arabidopsis thaliana]
                  172549
Seq. No.
Seq. ID
                   jC-atXLIB327407P2d12b1
                  BLASTN
Method
                  g2245073
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
Match length
                   44
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   172550
Seq. No.
Seq. ID
                   jC-atXLIB327407P2e01b1
                   BLASTN
Method
NCBI GI
                   g4760411
BLAST score
                   47
E value
                   3.0e-17
Match length
                   59
                   93
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
```

complete sequence



```
172551
Seq. No.
                  jC-atXLIB327407P2e03b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  42
                  3.0e-14
E value
Match length
                  46
% identity
                  98
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172552
Seq. No.
                  jC-atXLIB327407P2e04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  38
                  8.0e-12
E value
Match length
                  45
% identity
                  96
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172553
                  jC-atXLIB327407P2e05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  68
                  1.0e-29
E value
Match length
                  76
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172554
Seq. No.
Seq. ID
                   jC-atXLIB327407P2e06b1
                  BLASTN
Method
                  q2582640
NCBI GI
BLAST score
                   48
E value
                  7.0e-18
                   52
Match length
                   98
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                   172555
Seq. No.
Seq. ID
                   jC-atXLIB327407P2e07b1
Method
                   BLASTN
NCBI GI
                  q2582640
```

Method BLASTN
NCBI GI g2582640
BLAST score 51
E value 1.0e-19
Match length 71
% identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172556

Seq. ID jC-atXLIB327407P2e09b1



Method BLASTN NCBI GI q2582640 BLAST score 49 2.0e-18 E value Match length 53

% identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

Seq. No. 172557

Seq. ID jC-atXLIB327407P2e11b1

98

Method BLASTN NCBI GI q2582640 BLAST score 45 E value 6.0e-16 45 Match length 100

% identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

172558 Seq. No.

Seq. ID jC-atXLIB327407P2f01b1

Method BLASTN q3985934 NCBI GI 133 BLAST score 2.0e-68 E value 137 Match length % identity 99

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 172559

Seq. ID jC-atXLIB327407P2f02b1

Method BLASTN q2582640 NCBI GI BLAST score 38 5.0e-12E value 42 Match length 98 % identity

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

172560 Seq. No.

Seq. ID jC-atXLIB327407P2f03b1

BLASTN Method g2582640 NCBI GI BLAST score 35 3.0e-10 E value 46 Match length 93 % identity

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

172561 Seq. No.

Seq. ID jC-atXLIB327407P2f05b1

BLASTN Method NCBI GI q3941523



BLAST score 36 E value 1.0e-10 Match length 48 % identity 94

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 172562

Seq. ID jC-atXLIB327407P2f07b1

Method BLASTN
NCBI GI g2582640
BLAST score 45
E value 4.0e-16
Match length 75
% identity 91

% identity 91 NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172563

Seq. ID jC-atXLIB327407P2f08b1

Method BLASTN
NCBI GI g3212846
BLAST score 66
E value 1.0e-28
Match length 66
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172564

Seq. ID jC-atXLIB327407P2f09b1

Method BLASTN
NCBI GI g2582640
BLAST score 44
E value 2.0e-15
Match length 48
% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172565

Seq. ID jC-atXLIB327407P2f11b1

Method BLASTN
NCBI GI g2582640
BLAST score 44
E value 2.0e-15
Match length 51
% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172566

Seq. ID jC-atXLIB327407P2f12b1

Method BLASTN
NCBI GI g4376087
BLAST score 33
E value 7.0e-09



```
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
Seq. No.
                  172567
Seq. ID
                  jC-atXLIB327407P2g03b1
Method
                  BLASTN
NCBI GI
                  g2288979
BLAST score
                  34
E value
                  2.0e-09
Match length
                  58
                  86
% identity
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172568
                  jC-atXLIB327407P2g04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241920
BLAST score
                  65
E value
                   6.0e-28
Match length
                  88
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172569
Seq. ID
                   jC-atXLIB327407P2g05b1
Method
                  BLASTN
                  g3779020
NCBI GI
BLAST score
                   45
                   5.0e-16
E value
Match length
                   45
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T4E14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  172570
Seq. No.
Seq. ID
                   jC-atXLIB327407P2g07b1
Method
                   BLASTN
                   g2828278
NCBI GI
BLAST score
                   60
                   5.0e-25
E value
                   64
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
NCBI Description
                   (ESSAII project)
                   172571
Seq. No.
Seq. ID
                   jC-atXLIB327407P2g08b1
```

Seq. ID jC-atXL1B327407E
Method BLASTN
NCBI GI g4454447
BLAST score 63
E value 9.0e-27

67

99

Match length % identity



Arabidopsis thaliana chromosome II BAC F5H14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. Seq. ID jC-atXLIB327407P2g09b1 Method BLASTN NCBI GI g2582640 BLAST score 42 3.0e-14E value Match length 53 % identity 94 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172573 Seq. No. Seq. ID jC-atXLIB327407P2g10b1 Method BLASTN NCBI GI g3449320 BLAST score 230 1.0e-126 E value Match length 305 % identity 95 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRB17, complete sequence [Arabidopsis thaliana] Seq. No. 172574 Seq. ID jC-atXLIB327407P2g12b1 Method BLASTN g2582640 NCBI GI BLAST score 61 2.0e-25 E value Match length 72 96 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172575 Seq. No. Seq. ID jC-atXLIB327407P2h02b1 BLASTN Method g2582640 NCBI GI BLAST score 62 4.0e-26 E value

Match length 73 96 % identity

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

172576 Seq. No.

Seq. ID jC-atXLIB327407P2h03b1 BLASTN

Method NCBI GI q16306 76 BLAST score 2.0e-34 E value Match length 83 % identity 98

NCBI Description A.thaliana genes encoding glycine-rich proteins



```
172577
Seq. No.
                   jC-atXLIB327407P2h04b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
                   42
BLAST score
E value
                   3.0e-14
                   49
Match length
                   98
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                   172578
                   jC-atXLIB327407P2h07b1
Seq. ID
Method
                   BLASTN
                   q2582640
NCBI GI
                   57
BLAST score
E value
                   4.0e-23
Match length
                   72
                   96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   172579
                   jC-atXLIB327407P2h08b1
Seq. ID
                   BLASTN
Method
                   q2582640
NCBI GI
                   50
BLAST score
E value
                   5.0e-19
                   50
Match length
                   100
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172580
Seq. No.
                   jC-atXLIB327407P2h09b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g166739
BLAST score
                   49
                   1.0e-18
E value
                   57
Match length
                   98
% identity
NCBI Description A.thaliana histone H4 gene, complete cds
                   172581
Seq. No.
                   jC-atXLIB327407P2h11b1
Seq. ID
Method
                   BLASTN
                   g2760164
NCBI GI
BLAST score
                   105
                   8.0e-52
E value
                   130
Match length
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18P6, complete sequence [Arabidopsis thaliana]
```

Seq. No. 172582

Seq. ID jC-atXLIB327407P2h12b1

Method BLASTN

% identity

93



```
g2582640
NCBI GI
                  50
BLAST score
                  6.0e-19
E value
                  72
Match length
                  93
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172583
Seq. No.
                  jC-atXLIB327407P3a01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  43
                  9.0e-15
E value
                  51
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172584
Seq. No.
                   jC-atXLIB327407P3a02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
                  55
BLAST score
                  2.0e-22
E value
                   67
Match length
                   96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172585
Seq. No.
                   jC-atXLIB327407P3a05a1
Seq. ID
Method
                   BLASTN
                   g2462264
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
                   40
Match length
                   95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172586
Seq. No.
                   jC-atXLIB327407P3a06a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2462264
BLAST score
                   51
                   1.0e-19
E value
                   51
Match length
                   100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172587
Seq. No.
Seq. ID
                   jC-atXLIB327407P3a08a1
                   BLASTN
Method
                   q2462264
NCBI GI
BLAST score
                   38
E value
                   8.0e-12
                   54
Match length
```



NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172588

Seq. ID jC-atXLIB327407P3a08b1

Method BLASTN
NCBI GI g1419389
BLAST score 187
E value 1.0e-100
Match length 390
% identity 88

NCBI Description A.thaliana mRNA for thylakoid-bound ascorbate peroxidase

Seq. No. 172589

Seq. ID jC-atXLIB327407P3a10b1

Method BLASTN
NCBI GI g4580365
BLAST score 76
E value 2.0e-34
Match length 98
% identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F3F20 genomic

sequence, complete sequence

Seq. No. 172590

Seq. ID jC-atXLIB327407P3b03a1

Method BLASTN
NCBI GI g2462264
BLAST score 51
E value 1.0e-19
Match length 51
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172591

Seq. ID jC-atXLIB327407P3b04a1

Method BLASTN
NCBI GI g2828184
BLAST score 190
E value 1.0e-102
Match length 293
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSN9, complete sequence [Arabidopsis thaliana]

Seq. No. 172592

Seq. ID jC-atXLIB327407P3b10a1

Method BLASTN
NCBI GI g2462264
BLAST score 34
E value 2.0e-09
Match length 38
% identity 97

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172593

Seq. ID jC-atXLIB327407P3b11a1

Method BLASTN



```
NCBI GI g3757512
BLAST score 190
E value 1.0e-102
Match length 258
% identity 94
```

NCBI Description Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172594

Seq. ID jC-atXLIB327407P3c03b1

Method BLASTN
NCBI GI g4757401
BLAST score 132
E value 7.0e-68
Match length 147
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 172595

Seq. ID jC-atXLIB327407P3c05a1

Method BLASTN
NCBI GI g531828
BLAST score 39
E value 2.0e-12
Match length 54
% identity 95

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172596

Seq. ID jC-atXLIB327407P3c05b1

Method BLASTN
NCBI GI g4539378
BLAST score 114
E value 4.0e-57
Match length 118
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 172597

Seq. ID jC-atXLIB327407P3c08a1

Method BLASTN
NCBI GI g2462264
BLAST score 39
E value 2.0e-12
Match length 51
% identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172598

Seq. ID jC-atXLIB327407P3c09a1

Method BLASTN
NCBI GI g2264302
BLAST score 75
E value 7.0e-34
Match length 99



95

% identity

NCBI Description

```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC12, complete sequence [Arabidopsis thaliana]
                  172599
Seq. No.
                  jC-atXLIB327407P3c09b1
Seq. ID
                  BLASTN
Method
                  g2264302
NCBI GI
BLAST score
                  106
                  2.0e-52
E value
Match length
                  137
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172600
                  jC-atXLIB327407P3c10b1
Seq. ID
                  BLASTN
Method
                  g3449327
NCBI GI
BLAST score
                  81
E value
                  2.0e-37
Match length
                  146
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCA23, complete sequence [Arabidopsis thaliana]
                  172601
Seq. No.
                  jC-atXLIB327407P3c11b1
Seq. ID
                  BLASTN
Method
                  g2828183
NCBI GI
                  87
BLAST score
E value
                   5.0e-41
                  104
Match length
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPL12, complete sequence [Arabidopsis thaliana]
                   172602
Seq. No.
Seq. ID
                   jC-atXLIB327407P3d06a1
                   BLASTN
Method
NCBI GI
                   q3869065
BLAST score
                   212
                   1.0e-115
E value
                   264
Match length
                   95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K24M7, complete sequence [Arabidopsis thaliana]
                   172603
Seq. No.
                   jC-atXLIB327407P3d06b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3869065
BLAST score
                   51
                   1.0e-19
E value
Match length
                   62
```

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



K24M7, complete sequence [Arabidopsis thaliana]

```
172604
Seq. No.
                  jC-atXLIB327407P3d08b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
                  51
BLAST score
                  2.0e-19
E value
                  71
Match length
                  93
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172605
Seq. No.
                   jC-atXLIB327407P3d09a1
Seq. ID
Method
                  BLASTN
                  g540252
NCBI GI
                  39
BLAST score
                   2.0e-12
E value
                  39
Match length
% identity
                  100
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                   172606
Seq. No.
                   jC-atXLIB327407P3d10b1
Seq. ID
                   BLASTN
Method
                   g2582640
NCBI GI
                   54
BLAST score
                   2.0e-21
E value
                   70
Match length
                   94
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172607
Seq. No.
                   jC-atXLIB327407P3d12a1
Seq. ID
                   BLASTN
Method
                   q2462264
NCBI GI
                   44
BLAST score
                   2.0e-15
E value
                   44
Match length
                   100
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                   172608
Seq. ID
                   jC-atXLIB327407P3d12b1
                   BLASTN
Method
                   g2582640
NCBI GI
                   66
BLAST score
                   1.0e-28
E value
Match length
                   74
                   97
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   172609
                   jC-atXLIB327407P3e01a1
Seq. ID
```



Method BLASTN
NCBI GI g540252
BLAST score 39
E value 1.0e-12

Match length 43 % identity 98

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No. 172610

Seq. ID jC-atXLIB327407P3e03a1

Method BLASTN
NCBI GI g1877523
BLAST score 260
E value 1.0e-144
Match length 329

% identity 98
NCBI Description Arabidopsis thaliana BAC T7I23, complete sequence

[Arabidopsis thaliana]

Seq. No. 172611

Seq. ID jC-atXLIB327407P3e03b1

Method BLASTN
NCBI GI g2582640
BLAST score 40

E value 2.0e-13 Match length 44 % identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172612

Seq. ID jC-atXLIB327407P3e04b1

Method BLASTN
NCBI GI g217828
BLAST score 34
E value 2.0e-09
Match length 41
% identity 95

NCBI Description Arabidopsis thaliana APK1 gene for protein

tyrosine-serine-threonine kinase

Seq. No. 172613

Seq. ID jC-atXLIB327407P3e07b1

Method BLASTN
NCBI GI g4028969
BLAST score 146
E value 2.0e-76
Match length 206
% identity 98

NCBI Description Arabidopsis thaliana pollenless3 (178) gene, complete cds;

beta-9 tubulin (TUB9) gene, partial cds; and unknown gene

Seq. No. 172614

Seq. ID jC-atXLIB327407P3e10a1

Method BLASTN
NCBI GI g2290120
BLAST score 55

Match length

% identity

113



```
6.0e-22
E value
                  62
Match length
                  97
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172615
Seq. No.
                   jC-atXLIB327407P3e10b1
Seq. ID
Method
                  BLASTN
                  g2582640
NCBI GI
                  59
BLAST score
                  2.0e-24
E value
                  70
Match length
                   97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172616
Seq. No.
                   jC-atXLIB327407P3f01b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2582640
BLAST score
                   33
                   3.0e-09
E value
Match length
                   41
                   95
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172617
Seq. No.
Seq. ID
                   jC-atXLIB327407P3f02b1
Method
                   BLASTX
                   q1762584
NCBI GI
                   155
BLAST score
E value
                   4.0e-10
                   43
Match length
                   77
% identity
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   172618
Seq. ID
                   jC-atXLIB327407P3f06a1
                   BLASTN
Method
NCBI GI
                   q2462264
                   35
BLAST score
                   5.0e-10
E value
Match length
                   47
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172619
Seq. No.
Seq. ID
                   jC-atXLIB327407P3f07a1
                   BLASTN
Method
NCBI GI
                   g2880038
BLAST score
                   89
E value
                   3.0e-42
```



```
Arabidopsis thaliana chromosome II BAC T11J7 genomic
   NCBI Description
                      sequence, complete sequence [Arabidopsis thaliana]
ر ۽ کو ڪون
                      172620
   Seq. No.
                      jC-atXLIB327407P3f08b1
   Seq. ID
                      BLASTN
   Method
                      g2341023
   NCBI GI
                      76
   BLAST score
                      5.0e - 35
   E value
                      76
   Match length
   % identity
                      100
                      Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
   NCBI Description
                      1, complete sequence [Arabidopsis thaliana]
                      172621
   Seq. No.
                      jC-atXLIB327407P3f09b1
   Seq. ID
                      BLASTN
   Method
                      g2582640
   NCBI GI
                      45
   BLAST score
                      5.0e-16
   E value
                      77
   Match length
    % identity
                      91
                      Arabidopsis thaliana mRNA for arginine/serine-rich splicing
   NCBI Description
                      factor, RSp40
                      172622
   Seq. No.
   Seq. ID
                      jC-atXLIB327407P3g01b1
                      BLASTX
   Method
                      g320558
   NCBI GI
   BLAST score
                      184
   E value
                      9.0e-14
                      62
   Match length
                      66
    % identity
                      DNA-binding protein - Arabidopsis thaliana >gi 601843
   NCBI Description
                       (M25268) DNA-binding protein [Arabidopsis thaliana]
                      172623
    Seq. No.
    Seq. ID
                      jC-atXLIB327407P3g02a1
                      BLASTN
    Method
    NCBI GI
                      g4468801
                      155
    BLAST score
                      1.0e-81
    E value
                      208
    Match length
    % identity
                      Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
    NCBI Description
                       (ESSA project)
                       172624
    Seq. No.
    Seq. ID
                       jC-atXLIB327407P3g05a1
                       BLASTN
    Method
    NCBI GI
                      g531828
    BLAST score
                       47
                       3.0e-17
    E value
    Match length
                       47
    % identity
                      100
```

NCBI Description Cloning vector pSport1, complete cds

NCBI GI



```
172625
Seq. No.
Seq. ID
                  jC-atXLIB327407P3g08a1
Method
                  BLASTN
                  g4581084
NCBI GI
                  55
BLAST score
                  6.0e-22
E value
                  63
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                  sequence, complete sequence
                  172626
Seq. No.
                  jC-atXLIB327407P3g09a1
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
                  37
BLAST score
                  3.0e-11
E value
                  45
Match length
                  96
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172627
Seq. No.
                  jC-atXLIB327407P3g09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
                  37
BLAST score
                  2.0e-11
E value
                  49
Match length
                   96
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
                   172628
Seq. No.
                   jC-atXLIB327407P3g10a1
Seq. ID
Method
                   BLASTN
                   q2827513
NCBI GI
BLAST score
                   127
                   6.0e-65
E value
Match length
                   131
% identity
                   99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
NCBI Description
                   (ESSAII project)
                   172629
Seq. No.
                   jC-atXLIB327407P3g11a1
Seq. ID
Method
                   BLASTN
                   g531828
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   44
                   95
% identity
NCBI Description Cloning vector pSport1, complete cds
                   172630
Seq. No.
                   jC-atXLIB327407P3g12b1
Seq. ID
Method
                   BLASTX
```

23643

g1620898



```
183
BLAST score
                  2.0e-13
E value
                  44
Match length
                  84
% identity
                  (D87957) protein involved in sexual development [Homo
NCBI Description
                  sapiens]
                  172631
Seq. No.
                  jC-atXLIB327407P3h02a1
Seq. ID
                  BLASTN
Method
                  q4519190
NCBI GI
                  59
BLAST score
                  2.0e-24
E value
                  225
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K6A12, complete sequence
                  172632
Seq. No.
Seq. ID
                  jC-atXLIB327407P3h04a1
Method
                  BLASTN
                  g16302
NCBI GI
                  58
BLAST score
                  9.0e-24
E value
                  135
Match length
                  18
% identity
                  A.thaliana mRNA encoding glycine rich protein
NCBI Description
                  172633
Seq. No.
Seq. ID
                  jC-atXLIB327407P3h04b1
Method
                  BLASTN
                  g16302
NCBI GI
                  76
BLAST score
                  2.0e-34
E value
Match length
                  84
                   99
% identity
                  A.thaliana mRNA encoding glycine rich protein
NCBI Description
                  172634
Seq. No.
Seq. ID
                   jC-atXLIB327407P3h06a1
                  BLASTN
Method
NCBI GI
                  q2264321
                   183
BLAST score
                   2.0e-98
E value
                   294
Match length
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172635
                   jC-atXLIB327407P3h09b1
Seq. ID
```

Method BLASTN g2582640 NCBI GI 66 BLAST score 1.0e-28 E value Match length 74 97 % identity



Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172636 Seq. No. jC-atXLIB327407P3h10b1 Seq. ID Method BLASTN NCBI GI g3941523 BLAST score 40 E value 4.0e-13 Match length 44 % identity 98 Arabidopsis thaliana putative transcription factor (MYB92) NCBI Description mRNA, complete cds 172637 Seq. No. jC-atXLIB327407P3h11b1 Seq. ID Method BLASTX NCBI GI g3851636 47 BLAST score 2.0e-13 E value 67 Match length % identity 60 (AF098519) unknown [Avicennia marina] >gi_4128206 NCBI Description (AF056316) 40S ribosome protein S7 [Avicennia marina] 172638 Seq. No. jC-atXLIB327407P4a01a1 Seq. ID Method BLASTN g2462264 NCBI GI BLAST score 37 3.0e-11 E value Match length 41 98 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172639 Seq. No. Seq. ID jC-atXLIB327407P4a05a1 BLASTN Method g2462264 NCBI GI 37 BLAST score 3.0e-11 E value 41 Match length 98 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172640 Seq. No.

iC-atXLIB327407P4a05b1 Seq. ID

Method BLASTN g166689 NCBI GI 95 BLAST score 8.0e-46 E value 95 Match length 100 % identity

A.thaliana 3-deoxy-D-arabino-heptulosonate 7-phosphate NCBI Description

synthase (DHS2) mRNA, complete cds

Seq. No. 172641



```
iC-atXLIB327407P4a06b1
Seq. ID
                  BLASTN
Method
                  q2582640
NCBI GI
                  58
BLAST score
                  9.0e-24
E value
Match length
                  70
                  96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172642
Seq. No.
Seq. ID
                  jC-atXLIB327407P4a09a1
                  BLASTN
Method
                  q4521999
NCBI GI
                  237
BLAST score
                  1.0e-130
E value
Match length
                  282
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC F2G1 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  172643
Seq. ID
                   jC-atXLIB327407P4a09b1
Method
                  BLASTN
                  q4160668
NCBI GI
                  38
BLAST score
                  8.0e-12
E value
Match length
                  45
                  96
% identity
NCBI Description Arabidopsis thaliana mRNA for AtRer1B, complete cds
                   172644
Seq. No.
Seq. ID
                   jC-atXLIB327407P4a10b1
Method
                   BLASTX
NCBI GI
                   g2842424
BLAST score
                   215
                   4.0e-17
E value
Match length
                   62
% identity
                   66
NCBI Description (AJ223948) RNA helicase [Homo sapiens]
                   172645
Seq. No.
                   jC-atXLIB327407P4b01a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4159704
                   92
BLAST score
                   4.0e-44
E value
Match length
                   183
                   87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
```

Seq. No. 172646

Seq. ID jC-atXLIB327407P4b06b1

Method BLASTN NCBI GI g2582640

BLAST score 52



```
4.0e-20
E value
                  71
Match length
                  96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172647
Seq. No.
                  jC-atXLIB327407P4b09a1
Seq. ID
Method
                  BLASTN
                  g531828
NCBI GI
                  37
BLAST score
                  3.0e-11
E value
Match length
                  41
                  98
% identity
                  Cloning vector pSport1, complete cds
NCBI Description
                  172648
Seq. No.
                  jC-atXLIB327407P4b09b1
Seq. ID
                  BLASTN
Method
                  g633027
NCBI GI
BLAST score
                  102
E value
                  4.0e-50
Match length
                  112
                  97
% identity
NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C
                  172649
Seq. No.
                   jC-atXLIB327407P4b10a1
Seq. ID
                  BLASTN
Method
                  g4580516
NCBI GI
                   283
BLAST score
                   1.0e-158
E value
                   342
Match length
                   96
% identity
                  Arabidopsis thaliana scarecrow-like 5 (SCL5) mRNA, partial
NCBI Description
                   cds
                   172650
Seq. No.
                   jC-atXLIB327407P4b12a1
Seq. ID
                   BLASTN
Method
                   g2462264
NCBI GI
BLAST score
                   37
E value
                   3.0e-11
Match length
                   41
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172651
Seq. No.
Seq. ID
                   jC-atXLIB327407P4b12b1
                   BLASTN
Method
NCBI GI
                   q4263753
BLAST score
                   101
                   2.0e-49
E value
Match length
                   101
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,
```

complete sequence [Arabidopsis thaliana]



```
172652
Seq. No.
Seq. ID
                  jC-atXLIB327407P4c01b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  43
                  8.0e-15
E value
                  55
Match length
% identity
                  95
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172653
Seq. No.
Seq. ID
                  jC-atXLIB327407P4c02a1
Method
                  BLASTN
                  g2290120
NCBI GI
                  38
BLAST score
                  8.0e-12
E value
Match length
                  64
                  92
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172654
Seq. No.
Seq. ID
                  jC-atXLIB327407P4c05a1
                  BLASTN
Method
NCBI GI
                  g2832611
BLAST score
                  78
                  1.0e-35
E value
                  86
Match length
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
NCBI Description
                   (ESSAII project)
                  172655
Seq. No.
Seq. ID
                   jC-atXLIB327407P4c06b1
Method
                  BLASTN
NCBI GI
                  g2582640
                  36
BLAST score
E value
                  1.0e-10
Match length
                   66
% identity
                   93
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172656
Seq. ID
                   jC-atXLIB327407P4c07a1
                  BLASTN
Method
```

Method BLASTN
NCBI GI g2462264
BLAST score 41
E value 1.0e-13
Match length 49
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172657

Seq. ID jC-atXLIB327407P4c09a1

BLAST score

E value

295

1.0e-165



```
BLASTN
Method
                  g2462264
NCBI GI
                  49
BLAST score
                  2.0e-18
E value
                  53
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172658
Seq. No.
                  jC-atXLIB327407P4c10b1
Seq. ID
                  BLASTN
Method
                  g3046856
NCBI GI
                  45
BLAST score
                  5.0e-16
E value
                  49
Match length
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI22, complete sequence [Arabidopsis thaliana]
                  172659
Seq. No.
                  jC-atXLIB327407P4c11a1
Seq. ID
Method
                  BLASTN
                  q1871502
NCBI GI
                  60
BLAST score
                  6.0e-25
E value
                  64
Match length
                  98
% identity
NCBI Description A.thaliana bfruct4 gene
                  172660
Seq. No.
Seq. ID
                   jC-atXLIB327407P4c12b1
Method
                  BLASTX
                   g3983125
NCBI GI
                   336
BLAST score
                   2.0e-31
E value
                   82
Match length
                   77
% identity
                  (AF097648) phosphate/triose-phosphate transloc. r
NCBI Description
                  precursor [Arabidopsis thaliana]
                   172661
Seq. No.
Seq. ID
                   jC-atXLIB327407P4d01b1
Method
                   BLASTN
                   q2582640
NCBI GI
                   46
BLAST score
E value
                   1.0e-16
Match length
                   69
                   91
% identity
NCBI Description Arabidopsis thaliana mRN arginine/serine-rich splicing
                   factor, RSp40
                   172662
Seq. No.
                   jC-atXLIB327407P4d .1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4732168
```



```
397
 Match length
                    99
 % identity
                   Arabidopsis thaliana BAC T1J24
 NCBI Description
                    172663
 Seq. No.
                    jC-atXLIB327407P4d05b1
 Seq. ID
                    BLASTN
Method
 NCBI GI
                    g2582640
                    50
 BLAST score
                    6.0e-19
 E value
 Match length
                    70
                    94
 % identity
                    Arabidopsis thaliana mRNA for arginine/serine-rich splicing
 NCBI Description
                    factor, RSp40
 Seq. No.
                    172664
                    jC-atXLIB327407P4d08a1
 Seq. ID
                    BLASTN
 Method
                    g531828
 NCBI GI
                    45
 BLAST score
 E value
                    5.0e-16
                    59
 Match length
                    95
 % identity
 NCBI Description Cloning vector pSport1, complete cds
                    172665
 Seq. No.
                    jC-atXLIB327407P4d08b1
 Seq. ID
                    BLASTN
 Method
                    g2582640
 NCBI GI
 BLAST score
                    51
                    2.0e-19
 E value
                    71
 Match length
                    93
 % identity
                    Arabidopsis thaliana mRNA for arginine/serine-rich splicing
 NCBI Description
                    factor, RSp40
                    172666
 Seq. No.
                    jC-atXLIB327407P4d10a1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g3228389
                    210
 BLAST score
 E value
                    1.0e-114
                    262
 Match length
                    94
 % identity
                    Genomic sequence for Arabidopsis thaliana BAC F17L21,
 NCBI Description
                    complete sequence [Arabidopsis thaliana]
                    172667
 Seq. No.
 Seq. ID
                    jC-atXLIB327407P4d12a1
                    BLASTN
 Method
 NCBI GI
                    q4589434
```

Method BLASTN
NCBI GI g458943
BLAST score 185
E value 1.0e-99
Match length 216
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ7, complete sequence



```
172668
Seq. No.
                 jC-atXLIB327407P4e02a1
Seq. ID
                  BLASTN
Method
                  g14342
NCBI GI
BLAST score
                  77
                  4.0e-35
E value
                  117
Match length
                  92
% identity
NCBI Description A.thaliana mRNA for carbonic anhydrase
Seq. No.
                  172669
                  jC-atXLIB327407P4e05b1
Seq. ID
                  BLASTN
Method
                  q2582640
NCBI GI
                  49
BLAST score
E value
                  2.0e-18
                  76
Match length
                   91
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                   172670
                   jC-atXLIB327407P4e06b1
Seq. ID
                   BLASTN
Method
                   g2351064
NCBI GI
                   32
BLAST score
E value
                   3.0e-08
                   63
Match length
                   44
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172671
                   jC-atXLIB327407P4e07b1
Seq. ID
                   BLASTX
Method
                   q266829
NCBI GI
BLAST score
                   289
                   9.0e-26
E value
                   67
Match length
                   87
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1
NCBI Description
                   >gi_81655_pir__S20882 phosphoprotein phosphatase (EC
                   3.1.3.16) 1 catalytic chain (clone TOPP1) - Arabidopsis
                   thaliana >gi 16431 emb CAA45611_ (X64328) protein
                   phosphatase-1 [Arabidopsis thaliana] >gi_166572 (M93408)
                   phosphoprotein phosphatase 1 [Arabidopsis thaliana]
                   >qi 3980395 (AC004561) phosphoprotein phosphatase-type 1
                   catalytic subunit [Arabidopsis thaliana]
                   172672
Seq. No.
Seq. ID
                   jC-atXLIB327407P4e09b1
                   BLASTN
Method
                   g4678705
NCBI GI
BLAST score
                   36
```

23651

1.0e-10

43

E value

Match length



```
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                  (ESSA project)
Seq. No.
                  172673
                  jC-atXLIB327407P4f03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q531828
                  37
BLAST score
E value
                  4.0e-11
Match length
                  61
% identity
                  90
NCBI Description Cloning vector pSport1, complete cds
                  172674
Seq. No.
                  jC-atXLIB327407P4f07b1
Seq. ID
Method
                  BLASTX
                  q3582335
NCBI GI
                  436
BLAST score
                  3.0e-43
E value
                  156
Match length
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  172675
Seq. No.
                  jC-atXLIB327407P4f08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4741961
BLAST score
                  141
                  3.0e-73
E value
                  175
Match length
% identity
                  94
NCBI Description Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds
                  172676
Seq. No.
Seq. ID
                  jC-atXLIB327407P4f11a1
                  BLASTN
Method
                  g4584841
NCBI GI
                  85
BLAST score
                  7.0e-40
E value
                  97
Match length
                   97
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T23E23,
NCBI Description
                  complete sequence
                  172677
Seq. No.
Seq. ID
                   jC-atXLIB327407P4g01b1
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                   63
E value
                  1.0e-26
                  71
Match length
                   97
% identity
```

Seq. No. 172678

factor, RSp40

23652

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing



Seq. ID jC-atXLIB327407P4g03b1

Method BLASTN
NCBI GI g2582640
BLAST score 33
E value 7.0e-09
Match length 40
% identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172679

Seq. ID jC-atXLIB327407P4g04a1

Method BLASTN
NCBI GI g2462264
BLAST score 37
E value 2.0e-11
Match length 52
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172680

Seq. ID jC-atXLIB327407P4g05a1

Method BLASTN
NCBI GI g2244991
BLAST score 286
E value 1.0e-160
Match length 424
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 172681

Seq. ID jC-atXLIB327407P4g09a1

Method BLASTN
NCBI GI g2462264
BLAST score 33
E value 8.0e-09
Match length 45
% identity 93

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172682

Seq. ID jC-atXLIB327407P4g09b1

Method BLASTN
NCBI GI g2582640
BLAST score 53
E value 7.0e-21
Match length 73
% identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172683

Seq. ID jC-atXLIB327407P4g11a1

Method BLASTN NCBI GI g2290120

BLAST score 35



```
4.0e-10
E value
                  43
Match length
                  95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  172684
                  jC-atXLIB327407P4g12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4678705
BLAST score
                  89
E value
                  3.0e-42
                  101
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                  172685
Seq. No.
                  jC-atXLIB327407P4h06a1
Seq. ID
Method
                  BLASTX
                   g135860
NCBI GI
BLAST score
                   313
E value
                   1.0e-28
                   82
Match length
                   73
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                   protein gamma - Arabidopsis thaliana
                   >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                   protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                   (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                   >gi 445129 prf__1908432B tonoplast intrinsic protein gamma
                   [Arabidopsis thaliana]
                   172686
Seq. No.
                   jC-atXLIB327407P4h08b1
Seq. ID
                   BLASTN
Method
                   g3068702
NCBI GI
                   189
BLAST score
                   1.0e-102
E value
                   265
Match length
                   92
% identity
                   Arabidopsis thaliana putative transmembrane protein G1p
NCBI Description
                   (AtG1), putative nuclear DNA-binding protein G2p (AtG2),
                   Em1 protein (ATEM1), putative chlorophyll synthetase
                   (AtG4), putative transmembrane protein G5p (AtG5), put
                   172687
Seq. No.
Seq. ID
                   jC-atXLIB327407P4h11b1
                   BLASTN
Method
                   g4539415
NCBI GI
BLAST score
                   108
                   1.0e-53
E value
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

206

project)

76

Match length

% identity



```
172688
Seq. No.
                  jC-atXLIB327407P4h12a1
Seq. ID
                  BLASTN
Method
                  g540252
NCBI GI
                  33
BLAST score
                  7.0e-09
E value
                  33
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  172689
Seq. No.
                  jC-atXLIB327408P1a05a1
Seq. ID
                  BLASTN
Method
                  g3269280
NCBI GI
                  156
BLAST score
                  3.0e-82
E value
                   408
Match length
                   91
% identity
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
NCBI Description
                   (ESSAII project)
                   172690
Seq. No.
                   jC-atXLIB327408P1a07b1
Seq. ID
                   BLASTX
Method
                   q1076348
NCBI GI
                   349
BLAST score
                   8.0e-33
E value
                   73
Match length
                   99
% identity
                  myosin MYA1, class V - Arabidopsis thaliana
NCBI Description
                   >gi 433663_emb_CAA82234_ (Z28389) myosin [Arabidopsis
                   thaliana]
                   172691
Seq. No.
                   jC-atXLIB327408P1b01b1
Seq. ID
                   BLASTX
Method
                   g3075382
NCBI GI
                   708
BLAST score
                   6.0e-75
E value
                   168
Match length
% identity
                   (AC002505) putative peroxisome assembly protein PER8
NCBI Description
                   [Arabidopsis thaliana] >gi_3075384 (AC004484) putative
                   peroxisome assembly protein PER8 [Arabidopsis thaliana]
                   172692
Seq. No.
                   jC-atXLIB327408P1b10b1
Seq. ID
                   BLASTX
Method
                   q4262180
NCBI GI
BLAST score
                   779
                   3.0e-83
E value
Match length
                   149
% identity
                   99
                  (AC005508) 29621 [Arabidopsis thaliana]
NCBI Description
```

172693

Seq. No.



```
jC-atXLIB327408P1d05a1
 Seq. ID
                   BLASTN
Method
NCBI GI
                   g2462264
 BLAST score
                   36
                   1.0e-10
E value
                   51
Match length
                   96
 % identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172694
 Seq. No.
                   jC-atXLIB327408P1d08b1
 Seq. ID
                   BLASTX
Method
                   g543815
 NCBI GI
 BLAST score
                   741
                   8.0e-79
 E value
                   148
 Match length
                   99
 % identity
                   FLORAL HOMEOTIC PROTEIN APETALA3 >gi 282855 pir A42095
 NCBI Description
                   homeotic protein AP3 - Arabidopsis thaliana >gi 166608
                   (M86357) APETELA3 [Arabidopsis thaliana]
                   172695
 Seq. No.
                   jC-atXLIB327408P1d10a1
 Seq. ID
                   BLASTX
 Method
                   g2245029
 NCBI GI
                   477
 BLAST score
                   7.0e-48
 E value
                   90
Match length
                   98
 % identity
 NCBI Description (Z97341) limonene cyclase homolog [Arabidopsis thaliana]
                   172696
 Seq. No.
 Seq. ID
                   jC-atXLIB327408P1d11a1
                   BLASTN
 Method
 NCBI GI
                   q2290120
                   42
 BLAST score
                   3.0e-14
 E value
 Match length
                   64
                   94
 % identity
 NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                   gene, partial cds
                   172697
 Seq. No.
                    jC-atXLIB327408P1d11b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g1944132
 BLAST score
                    663
                    1.0e-69
 E value
 Match length
                   126
                    98
 % identity
                   (AB002560) CUC2 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    172698
                    jC-atXLIB327408P1d12b1
 Seq. ID
                    BLASTN
 Method
                    q2582640
 NCBI GI
```

60

BLAST score

BLAST score

E value Match length 464 2.0e-46

118



6.0e-25 E value 75 Match length 96 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172699 Seq. No. jC-atXLIB327408P1e01b1 Seq. ID Method BLASTX g3859536 NCBI GI BLAST score 791 1.0e-84 E value 146 Match length 99 % identity (AF095453) asparagine synthetase [Arabidopsis thaliana] NCBI Description Seq. No. 172700 jC-atXLIB327408P1e02b1 Seq. ID Method BLASTN g2582640 NCBI GI 63 BLAST score E value 1.0e-26 Match length 71 97 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 172701 Seq. No. jC-atXLIB327408P1e06b1 Seq. ID Method BLASTX g130184 NCBI GI BLAST score 786 4.0e-84 E value Match length 154 99 % identity PHYTOCHROME A >gi 65878 pir FKMUA phytochrome A -NCBI Description Arabidopsis thaliana >gi 16421 emb CAA35221 (X17341) phyA photoreceptor [Arabidopsis thaliana] 172702 Seq. No. Seq. ID jC-atXLIB327408P1f06a1 BLASTN Method NCBI GI g2182285 320 BLAST score 1.0e-180 E value 365 Match length 97 % identity Sequence of BAC F5I14 from Arabidopsis thaliana chromosome NCBI Description 1, complete sequence [Arabidopsis thaliana] Seq. No. 172703 Seq. ID jC-atXLIB327408P1f12b1 BLASTX Method NCBI GI q3335365

% identity (AC003028) high affinity calcium antiporter [Arabidopsis NCBI Description thaliana] 172704 Seq. No. Seq. ID jC-atXLIB327408P1g12b1 BLASTN Method g3366536 NCBI GI BLAST score 76 2.0e-34 E value 268 Match length 87 % identity Genomic sequence for Arabidopsis thaliana BAC T25N2O, NCBI Description complete sequence [Arabidopsis thaliana] 172705 Seq. No. Seq. ID jC-atXLIB327408P1h01a1 BLASTN Method g2290120 NCBI GI BLAST score 53 9.0e-21 E value 60 Match length 98 % identity

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 172706

Seq. ID jC-atXLIB327408P1h03b1

Method BLASTN
NCBI GI g2244991
BLAST score 291
E value 1.0e-163
Match length 457
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 172707

Seq. ID jC-atXLIB327408P1h06b1

Method BLASTX
NCBI GI g1905876
BLAST score 750
E value 7.0e-80
Match length 149
% identity 99

NCBI Description (U90879) biotin carboxylase subunit [Arabidopsis thaliana]

>gi 1916300 (U91414) heteromeric acetyl-CoA carboxylase

biotin carboxylase subunit [Arabidopsis thaliana] >gi_3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana]

Seq. No. 172708

Seq. ID jC-atXLIB327408P2b01a1

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 2.0e-21



% identity

NCBI Description

```
54
Match length
                  100
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  172709
Seq. No.
Seq. ID
                  jC-atXLIB327408P2b09a1
                  BLASTN
Method
NCBI GI
                  g2462264
                  41
BLAST score
                  1.0e-13
E value
                  53
Match length
                  94
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  172710
Seq. No.
                  jC-atXLIB327408P2c05a1
Seq. ID
                  BLASTN
Method
                  g3128136
NCBI GI
                  59
BLAST score
                  2.0e-24
E value
Match length
                  137
% identity
                   91
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1F13, complete sequence [Arabidopsis thaliana]
                   172711
Seq. No.
                   jC-atXLIB327408P2f05b1
Seq. ID
                   BLASTN
Method
                   g2582640
NCBI GI
BLAST score
                   68
E value
                   1.0e-29
                   76
Match length
                   97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172712
Seq. No.
                   jC-atXLIB327408P3a02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2760164
                   303
BLAST score
E value
                   1.0e-169
                   477
Match length
                   93
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18P6, complete sequence [Arabidopsis thaliana]
                   172713
Seq. No.
                   jC-atXLIB327408P3a06b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3687221
BLAST score
                   92
E value
                   5.0e-44
                   251
Match length
```

23659

Arabidopsis thaliana chromosome II BAC F6F22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Method NCBI GI



```
172714
Seq. No.
                  jC-atXLIB327408P3a07b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
                  50
BLAST score
                  9.0e-19
E value
Match length
                  65
% identity
                  95
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  172715
Seq. No.
                  jC-atXLIB327408P3a08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g531828
BLAST score
                  53
                  1.0e-20
E value
Match length
                  65
                  95
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172716
Seq. No.
                  jC-atXLIB327408P3a09a1
Seq. ID
                  BLASTN
Method
                  q2462264
NCBI GI
BLAST score
                  45
                  1.0e-15
E value
                  57
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172717
Seq. No.
Seq. ID
                  jC-atXLIB327408P3a11a1
                  BLASTN
Method
NCBI GI
                  g2462264
                  45
BLAST score
                  8.0e-16
E value
                  57
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172718
Seq. No.
                   jC-atXLIB327408P3b01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2959734
                  240
BLAST score
                   6.0e-20
E value
                  136
Match length
% identity
NCBI Description
                  (Y13650) homologous to GATA-binding transcription factors
                   [Arabidopsis thaliana]
Seq. No.
                  172719
Seq. ID
                   iC-atXLIB327408P3b03a1
```

23660

BLASTN

q4589420



```
264
BLAST score
                  1.0e-146
E value
Match length
                  444
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3G17, complete sequence
                  172720
Seq. No.
Seq. ID
                  jC-atXLIB327408P3b06a1
                  BLASTN
Method
                  g3367500
NCBI GI
                  597
BLAST score
                  0.0e + 00
E value
Match length
                  627
                  99
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
                  172721
Seq. No.
Seq. ID
                  jC-atXLIB327408P3b07a1
Method
                  BLASTN
                  g2462264
NCBI GI
                  47
BLAST score
                  6.0e-17
E value
                  59
Match length
                  95
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  172722
Seq. No.
Seq. ID
                   jC-atXLIB327408P3c07a1
Method
                  BLASTN
NCBI GI
                  q4539353
                  77
BLAST score
                   5.0e - 35
E value
Match length
                   342
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F25I24
NCBI Description
                   (ESSA project)
Seq. No.
                   172723
                   jC-atXLIB327408P3c07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3513727
BLAST score
                   127
                   7.0e-36
E value
Match length
                   125
                   76
% identity
                  (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                   TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                   kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                   thaliana] >gi 4539358 emb CAB40052.1 (AL049525) putative
                   protein [Arabidopsis thaliana]
```

172724

BLASTN

q2462264

iC-atXLIB327408P3c08a1

Seq. No.

Seq. ID Method

NCBI GI



```
48
BLAST score
                  1.0e-17
E value
                  56
Match length
                  96
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  172725
Seq. No.
                  jC-atXLIB327408P3c09a1
Seq. ID
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  53
                  1.0e-20
E value
                  65
Match length
                  95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172726
Seq. No.
                  jC-atXLIB327408P3d05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3367531
BLAST score
                  710
                  6.0e-75
E value
                  154
Match length
                  93
% identity
                   (AC004392) Strong similarity to gi 2160138 F19K23.6 gene
NCBI Description
                  product from A. thaliana BAC gb_ACO00375. [Arabidopsis
                  thaliana]
                  172727
Seq. No.
Seq. ID
                   jC-atXLIB327408P3e06a1
                   BLASTN
Method
                  q3860243
NCBI GI
                   137
BLAST score
E value
                   8.0e-71
                   294
Match length
                   89
% identity
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   172728
Seq. No.
Seq. ID
                   iC-atXLIB327408P3f03a1
                   BLASTX
Method
                   q3169173
NCBI GI
BLAST score
                   68
E value
                   2.0e-54
                   117
Match length
                   91
% identity
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana] >gi 3445215 (AC004786) putative serine
                   carboxypeptidase I [Arabidopsis thaliana]
Seq. No.
                   172729
```

jC-atXLIB327408P3f05a1 Seq. ID

BLASTN Method NCBI GI q531828 BLAST score 54



3.0e-21 E value 65 Match length 97 % identity NCBI Description Cloning vector pSport1, complete cds

172730 Seq. No.

jC-atXLIB327408P3f07a1 Seq. ID

Method BLASTX g2829893 NCBI GI 283 BLAST score E value 4.0e-25 99 Match length % identity 56

NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No. 172731

jC-atXLIB327408P3f10a1 Seq. ID

Method BLASTX NCBI GI g3334123 52 BLAST score E value 6.0e-52 Match length 183 78 % identity

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787

(ACO02334) mitochondrial F1-ATPase, gamma subunit

[Arabidopsis thaliana]

172732 Seq. No.

Seq. ID jC-atXLIB327408P3g08a1

Method BLASTX g2570342 NCBI GI 370 BLAST score 5.0e-35 E value Match length 133 60 % identity

(U90929) glyoxalase II cytoplasmic isozyme [Arabidopsis NCBI Description

thaliana]

172733 Seq. No.

Seq. ID jC-atXLIB327408P3g12a1

Method BLASTN NCBI GI g531828 58 BLAST score 2.0e-23 E value Match length 66 97 % identity

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172734

jC-atXLIB327408P3h08a1 Seq. ID

BLASTN Method NCBI GI q531828 BLAST score 46 1.0e-16 E value Match length 66



```
% identity
NCBI Description Cloning vector pSport1, complete cds
                  172735
Seq. No.
                  jC-atXLIB327408P3h09a1
Seq. ID
                  BLASTN
Method
                  g2290120
NCBI GI
BLAST score
                  48
E value
                  1.0e-17
Match length
                  64
% identity
                  94
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  172736
Seq. ID
                  jC-atXLIB327408P3h12a1
Method
                  BLASTN
NCBI GI
                  g4056429
BLAST score
                  71
                  3.0e - 31
E value
Match length
                  261
% identity
                  84
                  Arabidopsis thaliana chromosome 1 BAC F508 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  172737
Seq. No.
                   jC-atXLIB327408P4a04b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                   63
                  1.0e-26
E value
Match length
                  75
                   97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                   172738
Seq. No.
Seq. ID
                   jC-atXLIB327408P4a06a1
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                   36
                  1.0e-10
E value
Match length
                   40
% identity
                   97
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172739
Seq. No.
Seq. ID
                   iC-atXLIB327408P4a06b1
                   BLASTX
Method
NCBI GI
                   g2499441
BLAST score
                   170
                   8.0e-12
E value
                   80
Match length
```

% identity NCBI Description PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA)

49

>qi 408232 bbs 136255 (S64617) PCNA=proliferating cell nuclear antigen [Brassica napus=oilseed rape, cv. Westar,





apical meristem, Peptide, 263 aa] [Brassica napus]

```
172740
Seq. No.
Seq. ID
                  jC-atXLIB327408P4a08a1
                  BLASTN
Method
                  g2462264
NCBI GI
                  42
BLAST score
                  2.0e-14
E value
Match length
                  57
                  97
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  172741
Seq. No.
                  jC-atXLIB327408P4a08b1
Seq. ID
                  BLASTX
Method
                  g3075395
NCBI GI
                  469
BLAST score
                  6.0e-47
E value
                  93
Match length
                  98
% identity
                  (AC004484) nodulin-35 homologue [Arabidopsis thaliana]
NCBI Description
                  172742
Seq. No.
Seq. ID
                   jC-atXLIB327408P4a09b1
                  BLASTX
Method
NCBI GI
                  g320558
                   335
BLAST score
                   3.0e-31
E value
                  99
Match length
                  72
% identity
                  DNA-binding protein - Arabidopsis thaliana >gi_601843
NCBI Description
                   (M25268) DNA-binding protein [Arabidopsis thaliana]
                   172743
Seq. No.
                   jC-atXLIB327408P4a12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g81615
                   677
BLAST score
                   3.0e-71
E value
                   156
Match length
                   87
% identity
                  G-box-binding factor 1 - Arabidopsis thaliana
NCBI Description
                   >gi 16286 emb CAA45356 (X63894) G-box binding factor 1
                   [Arabidopsis thaliana]
                   172744
Seq. No.
                   jC-atXLIB327408P4b04b1
Seq. ID
                   BLASTX
Method
                   g2924510
NCBI GI
                   748
BLAST score
E value
                   1.0e-79
                   155
Match length
                   90
% identity
                  (AL022023) MYB-like protein [Arabidopsis thaliana]
NCBI Description
                   172745
Seq. No.
Seq. ID
                   jC-atXLIB327408P4b05b1
```



Method BLASTX q3582339 NCBI GI 779 BLAST score 3.0e-83 E value 145 Match length % identity 100 NCBI Description

(AC005496) unknown protein [Arabidopsis thaliana]

172746 Seq. No.

jC-atXLIB327408P4b11a1 Seq. ID

Method BLASTN NCBI GI q16472 BLAST score 208 1.0e-113 E value 252 Match length % identity

NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type

172747 Seq. No.

jC-atXLIB327408P4c03b1 Seq. ID

Method BLASTX NCBI GI q115916 BLAST score 531 4.0e-54 E value 106 Match length % identity 99

NCBI Description CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A

>gi 282863 pir__S23095 protein kinase (EC 2.7.1.37) cdc2 -Arabidopsis thaliana >gi_251888_bbs_109461 p34cdc2 protein kinase [Arabidopsis thaliana, flower, Peptide, 294 aa] >gi 16219_emb_CAA40971 (X57839) p34(cdc2) [Arabidopsis thaliana] >gi_166784 (M59198) protein kinase [Arabidopsis thaliana] >gi_217849_dbj_BAA01623_ (D10850) p32 protein serine/threonine kinase [Arabidopsis thaliana]

>gi 257374 bbs 115411 (S45387) Aracdc2=p34cdc2 protein kinase homolog [Arabidopsis thaliana, ecotype Columbia,

flowers, Peptide, 294 aa] [Arabidopsis thaliana]

172748 Seq. No.

jC-atXLIB327408P4c06b1 Seq. ID

BLASTX Method NCBI GI g2738248 762 BLAST score 3.0e-81 E value 159 Match length % identity 93

(U97200) cobalamin-independent methionine synthase NCBI Description

[Arabidopsis thaliana]

172749 Seq. No.

Seq. ID jC-atXLIB327408P4e02b1

Method BLASTX NCBI GI g2181180 BLAST score 274 5.0e-24 E value Match length 160 36 % identity



```
NCBI Description (Z84377) xylosidase [Aspergillus niger]
                  172750
Seq. No.
                  jC-atXLIB327408P4e05b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
                  63
BLAST score
                  1.0e-26
E value
                  71
Match length
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                   172751
Seq. No.
                   jC-atXLIB327408P4e08b1
Seq. ID
                  BLASTN
Method
                   g2582640
NCBI GI
BLAST score
                   52
                   3.0e-20
E value
                   56
Match length
% identity
                   98
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   172752
Seq. No.
                   jC-atXLIB327408P4f01a1
Seq. ID
                   BLASTN
Method
                   g2462264
NCBI GI
                   47
BLAST score
                   4.0e-17
E value
Match length
                   59
                   95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   172753
Seq. No.
Seq. ID
                   jC-atXLIB327408P4f04b1
                   BLASTN
Method
                   g2842474
NCBI GI
BLAST score
                   453
                   0.0e + 00
E value
                   477
Match length
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
Seq. No.
                   172754
Seq. ID
                   jC-atXLIB327408P4f05b1
                   BLASTX
Method
                   g2435519
NCBI GI
BLAST score
                   309
                   4.0e-28
E value
Match length
                   142
                   73
% identity
                   (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                   cerevisiae vacuolar sorting protein 35 (SW; P34110)
```

[Arabidopsis thaliana]



172755 Seq. No. Seq. ID jC-atXLIB327408P4f06a1 Method BLASTN g2262097 NCBI GI 124 BLAST score 4.0e-63 E value 182 Match length 91 % identity Arabidopsis thaliana chromosome IV BAC T19F6 genomic NCBI Description sequence, complete sequence 172756 Seq. No. Seq. ID jC-atXLIB327408P4f06b1 BLASTN Method g2262097 NCBI GI BLAST score 224 1.0e-123 E value 224 Match length 100 % identity Arabidopsis thaliana chromosome IV BAC T19F6 genomic NCBI Description sequence, complete sequence 172757 Seq. No. Seq. ID jC-atXLIB327408P4f07b1 BLASTX Method q3335365 NCBI GI 526 BLAST score 1.0e-53 E value 145 Match length 76 % identity (AC003028) high affinity calcium antiporter [Arabidopsis NCBI Description thaliana] 172758 Seq. No. Seq. ID jC-atXLIB327408P4f12b1 Method BLASTN g3510337 NCBI GI 235 BLAST score 1.0e-129 E value 446 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K19E20, complete sequence [Arabidopsis thaliana] Seq. No. 172759 Seq. ID jC-atXLIB327408P4g01a1 BLASTN Method NCBI GI g2462264 BLAST score 64 3.0e-27 E value Match length 64 % identity 100 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172760

Seq. ID jC-atXLIB327408P4g03a1

Method BLASTN



NCBI GI g2290120 BLAST score 46 E value 1.0e-16 Match length 65 % identity 95

NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 172761

Seq. ID jC-atXLIB327408P4g03b1

Method BLASTX
NCBI GI g3421072
BLAST score 790
E value 2.0e-84
Match length 157
% identity 98

NCBI Description (AF043519) 20S proteasome subunit PAA2 [Arabidopsis

thaliana] >gi 4006819 (AC005970) 20S proteasome subunit

PAA2 [Arabidopsis thaliana]

Seq. No. 172762

Seq. ID jC-atXLIB327408P4g04b1

Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 1.0e-26
Match length 71
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172763

Seq. ID jC-atXLIB327408P4g10b1

Method BLASTN
NCBI GI g4512646
BLAST score 78
E value 1.0e-35
Match length 384
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F23N11 genomic

sequence, complete sequence

Seq. No. 172764

Seq. ID jC-atXLIB327408P4h04b1

Method BLASTX
NCBI GI g2529681
BLAST score 673
E value 8.0e-71
Match length 151
% identity 86

NCBI Description (AC002535) putative MYB-related transcription factor

(protein P) [Arabidopsis thaliana]

Seq. No. 172765

Seq. ID jC-atXLIB327409Pla06a1

Method BLASTN NCBI GI g2290120

BLAST score

Match length

% identity

E value

49

61

95

2.0e-18



```
43
BLAST score
                  3.0e-15
E value
Match length
                  47
% identity
                  98
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  172766
Seq. No.
Seq. ID
                  jC-atXLIB327409P1a10a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  53
                  1.0e-20
E value
                  53
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172767
Seq. No.
                  jC-atXLIB327409P1a12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  67
                  4.0e-29
E value
Match length
                  75
                  97
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  172768
Seq. No.
                  jC-atXLIB327409P1b02a1
Seq. ID
                  BLASTN
Method
                  g540252
NCBI GI
                  55
BLAST score
                  6.0e-22
E value
                  59
Match length
                  98
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  172769
Seq. No.
Seq. ID
                  jC-atXLIB327409P1b03a1
Method
                  BLASTN
NCBI GI
                  g2262097
BLAST score
                  103
E value
                  1.0e-50
                  331
Match length
                  87
% identity
NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                  sequence, complete sequence
                  172770
Seq. No.
Seq. ID
                  jC-atXLIB327409P1b03b1
                  BLASTN
Method
                  g2582640
NCBI GI
```



NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 172771

Seq. ID jC-atXLIB327409P1b09a1

Method BLASTN NCBI GI g2462264 BLAST score 34

E value 4.0e-09 Match length 53 % identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172772

Seq. ID jC-atXLIB327409P1b10a1

Method BLASTN NCBI GI q4589410 BLAST score 149 E value 5.0e-78 Match length 446 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 172773

% identity

% identity

Seq. ID jC-atXLIB327409P1b11a1

Method BLASTN NCBI GI q2288979 BLAST score 227 E value 1.0e-124 Match length 503 % identity 86

Arabidopsis thaliana chromosome II BAC T01024 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172774

Seq. ID jC-atXLIB327409P1b12a1

Method BLASTN NCBI GI g2462264 BLAST score 43 E value 1.0e-14Match length 59 93

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172775

jC-atXLIB327409P1c05a1 Seq. ID

Method BLASTN NCBI GI g2462264 BLAST score 52 E value 3.0e-20 52 Match length 100 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172776

Seq. ID jC-atXLIB327409P1c07a1



Method BLASTN
NCBI GI g531828
BLAST score 56
E value 2.0e-22
Match length 64
% identity 97
NCBI Description Cloning

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 172777

Seq. ID jC-atXLIB327409P1c08a1

Method BLASTX
NCBI GI g1353266
BLAST score 319
E value 4.0e-29
Match length 65
% identity 98

NCBI Description (U27590) Fe(II) transport protein [Arabidopsis thaliana]

>gi_3250678_emb_CAA19686.1_ (AL024486) Fe(II) transport
protein [Arabidopsis thaliana] >gi 1589711_prf__2211425A Zn

transporter [Saccharomyces cerevisiae]

Seq. No. 172778

Seq. ID jC-atXLIB327409P1c08b1

Method BLASTX
NCBI GI g1353266
BLAST score 91
E value 4.0e-86

Match length 194 % identity 92

NCBI Description (U27590) Fe(II) transport protein [Arabidopsis thaliana] >gi 3250678 emb CAA19686.1 (AL024486) Fe(II) transport

protein [Arabidopsis thaliana] >gi 1589711 prf 2211425A Zn

transporter [Saccharomyces cerevisiae]

Seq. No. 172779

Seq. ID jC-atXLIB327409P1c10a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 8.0e-19
Match length 54
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172780

Seq. ID jC-atXLIB327409P1c12a1

Method BLASTX
NCBI GI g2809238
BLAST score 213
E value 7.0e-17
Match length 103
% identity 50

NCBI Description (AC002560) F21B7.7 [Arabidopsis thaliana]

Seq. No. 172781

Seq. ID jC-atXLIB327409P1d07a1

Method BLASTN



NCBI GI g2288979 BLAST score 495 E value 0.0e+00 Match length 550 % identity 69

NCBI Description Arabidopsis thaliana chromosome II BAC T01024 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172782

Seq. ID jC-atXLIB327409Pld10a1

Method BLASTX
NCBI GI g2811026
BLAST score 405
E value 3.0e-39
Match length 80
% identity 100

NCBI Description TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi 1946 U93215)

TCP1-chaperonin cofactor A isolog [Arabidopsis haliana] >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog

[Arabidopsis thaliana]

Seq. No. 172783

Seq. ID jC-atXLIB327409Pld11a1

Method BLASTX
NCBI GI g464662
BLAST score 112
E value 5.0e-05
Match length 98
% identity 35

NCBI Description CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING

PROTEIN RNP-T) (RNA-BINDING PROTEIN 1)

>gi_282884_pir__S28057 RNA-binding protein RNP-T Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255)
RNA-binding protein [Arabidopsis thaliana] >gi_387569
(M94554) 31 kDa RNA binding protein [Arabidopsis thaliana]
>gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding

protein RNP-T precursor [Arabidopsis thaliana]

>gi_737169_prf__1921382A RNA-binding protein [Arabidopsis

thaliana]

Seq. No. 172784

Seq. ID jC-atXLIB327409Pld12a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 7.0e-19
Match length 54
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172785

Seq. ID jC-atXLIB327409P1e06b1

Method BLASTN
NCBI GI g3128143
BLAST score 48
E value 1.0e-17



Match length 220 % identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No. 172786

Seq. ID jC-atXLIB327409P1e08a1

Method BLASTN
NCBI GI g2462264
BLAST score 49
E value 4.0e-18
Match length 53
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172787

Seq. ID jC-atXLIB327409P1f10a1

Method BLASTN
NCBI GI g2462264
BLAST score 39
E value 3.0e-12
Match length 54
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172788

Seq. ID jC-atXLIB327409P1f12a1

Method BLASTX
NCBI GI g2924781
BLAST score 216
E value 5.0e-19
Match length 84
% identity 51

NCBI Description (AC002334) putative cellulose synthase [Arabidopsis

thaliana]

Seq. No. 172789

Seq. ID jC-atXLIB327409P1q02b1

Method BLASTX
NCBI GI g114330
BLAST score 804
E value 1.0e-105
Match length 214
% identity 93

NCBI Description PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)

>gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
type 1, plasma membrane - Arabidopsis thaliana >gi_166746
(M24107) plasma membrane proton pump H+ ATPase [Arabidopsis

thaliana]

Seq. No. 172790

Seq. ID jC-atXLIB327409P1g03a1

Method BLASTN
NCBI GI g619938
BLAST score 107
E value 5.0e-53
Match length 286

% identity NCBI Description Arabidopsis thaliana starch branching enzyme class II (sbe2-1) mRNA, partial cds 172791 Seq. No. Seq. ID jC-atXLIB327409P1g06a1 Method BLASTN NCBI GI g2462264 BLAST score 39 1.0e-12 E value 55 Match length 93 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 172792 Seq. No. Seq. ID jC-atXLIB327409P1g12b1 Method BLASTX NCBI GI g114335 BLAST score 1159 E value 1.0e-127 237 Match length 97 % identity PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) NCBI Description >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >qi 166629 (J05570) H+-ATPase [Arabidopsis thaliana] Seq. No. 172793 Seq. ID jC-atXLIB327409P1h09a1 Method BLASTN NCBI GI g2462264 BLAST score 45 6.0e-16 E value 53 Match length % identity 96 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172794 Seq. ID jC-atXLIB327409P1h09b1

Method BLASTN NCBI GI g2582640 BLAST score 53 E value 9.0e-21 Match length 72 % identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172795

Seq. ID jC-atXLIB327409P1h11b1

Method BLASTX NCBI GI g2832631 BLAST score 1099 E value 1.0e-120 Match length 222 % identity 98

NCBI Description (AL021711) nodulin-26 - like protein [Arabidopsis thaliana]



```
Seq. No.
                   172796
Seq. ID
                   jC-atXLIB327409P1h12a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                   41
E value
                  1.0e-13
Match length
                  41
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172797
```

Seq. No. 172797
Seq. ID jC-atXLIB327409P2a02a1
Method BLASTN
NCBI GI g4263694
BLAST score 255

BLAST score 255
E value 1.0e-141
Match length 509
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 172798

 Seq. ID
 jC-atXLIB327409P2a04a1

 Method
 BLASTN

 NCBI GI
 g3927822

 BLAST score
 111

 E value
 4.0e-55

BLAST score 111 E value 4.0e-55 Match length 166 % identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172799

Seq. ID jC-atXLIB327409P2a04b1

Method BLASTN
NCBI GI g3927822
BLAST score 292
E value 1.0e-163
Match length 296
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 172800

Seq. ID jC-atXLIB327409P2a05a1

Method BLASTN
NCBI GI g2462264
BLAST score 42
E value 4.0e-14
Match length 54
% identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172801

Seq. ID jC-atXLIB327409P2a07b1

Method BLASTN



NCBI GI g166628
BLAST score 79
E value 2.0e-36
Match length 79
% identity 100

NCBI Description A.thaliana plasma membrane H+-ATPase gene, complete cds

Seq. No. 172802

Seq. ID jC-atXLIB327409P2b03a1

Method BLASTX
NCBI GI g1667582
BLAST score 209
E value 2.0e-16
Match length 90
% identity 51

NCBI Description (U76607) splicing factor At-SRp40 [Arabidopsis thaliana]

Seq. No. 172803

Seq. ID jC-atXLIB327409P2b05b1

Method BLASTN
NCBI GI 94468976
BLAST score 395
E value 0.0e+00
Match length 415
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18

(ESSA project)

Seq. No. 172804

Seq. ID jC-atXLIB327409P2b07a1

Method BLASTX
NCBI GI g2129759
BLAST score 192
E value 4.0e-14
Match length 154
% identity 29

NCBI Description UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana

>gi 1143392_emb_CAA90941_ (Z54214) uridine diphosphate

glucose epimerase [Arabidopsis thaliana]

Seq. No. 172805

Seq. ID jC-atXLIB327409P2b10a1

Method BLASTN
NCBI GI g2462264
BLAST score 56
E value 2.0e-22
Match length 60
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172806

Seq. ID jC-atXLIB327409P2c01a1

Method BLASTN
NCBI GI g2462264
BLAST score 48
E value 9.0e-18
Match length 52

```
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   172807
Seq. ID
                   jC-atXLIB327409P2c02a1
Method
                   BLASTN
NCBI GI
                  g3402695
BLAST score
                  188
E value
                   1.0e-101
Match length
                  272
% identity
                  62
NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172808
Seq. ID
                  jC-atXLIB327409P2c05a1
Method
                  BLASTN
NCBI GI
                  g4713943
BLAST score
                  611
E value
                  0.0e + 00
```

Match length 665 % identity 99 NCBI Description Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,

complete sequence

Seq. No. 172809 Seq. ID jC-atXLIB327409P2c06a1 Method BLASTN NCBI GI g2264304 BLAST score 215 E value 1.0e-117 Match length 235 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 172810

Seq. ID jC-atXLIB327409P2c06b1

Method BLASTX NCBI GI g2501188 BLAST score 730 E value 2.0e-77 Match length 145 % identity 99

NCBI Description THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir S71191 TH14 protein homolog - Arabidopsis thaliana $>\overline{gi}_1\overline{113783}$ (U17589)

Thil protein [Arabidopsis thaliana]

Seq. No. 172811

Seq. ID jC-atXLIB327409P2c07a1

Method BLASTN NCBI GI g3241916 BLAST score 281 E value 1.0e-157 Match length 306 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



K15N18, complete sequence [Arabidopsis thaliana]

Seq. No. 172812 Seq. ID jC-atXLIB327409P2c08a1 Method BLASTN NCBI GI g2462264 BLAST score 54 E value 3.0e-21 Match length 54 % identity 100 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172813 Seq. ID jC-atXLIB327409P2c09a1 Method BLASTN NCBI GI q4760411 BLAST score 577 E value 0.0e + 00Match length 641 % identity 98 NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence Seq. No. 172814 Seq. ID jC-atXLIB327409P2d01a1 Method BLASTN NCBI GI q4589436 BLAST score 144 E value 5.0e-75 Match length 350 % identity 87 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MPA22, complete sequence Seq. No. 172815 Seq. ID jC-atXLIB327409P2d05b1 Method BLASTN NCBI GI g2262097 BLAST score 319 E value 1.0e-179 Match length 402 97 % identity NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence Seq. No. 172816 Seq. ID jC-atXLIB327409P2d07b1 Method BLASTN NCBI GI g2582640 BLAST score 61 E value 2.0e-25 72 Match length

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 172817

97

% identity



```
Seq. ID
                   jC-atXLIB327409P2e06a1
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   53
E value
                   2.0e-20
Match length
                   57
% identity
                   98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   172818
Seq. ID
                   jC-atXLIB327409P2e08b1
Method
                   BLASTN
NCBI GI
                  g4220643
BLAST score
                   171
E value
                   3.0e-91
Match length
                   432
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172819
Seq. ID
                   jC-atXLIB327409P2e09a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  56
E value
                  2.0e-22
Match length
                  60
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172820
Seq. ID
                  jC-atXLIB327409P2f09a1
Method
                  BLASTN
NCBI GI
                  q166657
BLAST score
                  154
E value
                   6.0e - 81
Match length
                  415
% identity
                  85
NCBI Description Arabidopsis thaliana Ccr1 mRNA, complete cds
Seq. No.
                  172821
Seq. ID
                  jC-atXLIB327409P2h02a1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  43
E value
                  7.0e-15
Match length
                  67
% identity
                  91
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
```

Seq. No. 172822

Seq. ID jC-atXLIB327409P2h06a1

Method BLASTN
NCBI GI g2462264
BLAST score 56
E value 2.0e-22



```
Match length
                   56
% identity
                  100
NCBI Description
                 Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172823
Seq. ID
                  jC-atXLIB327409P2h09b1
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  43
E value
                  8.0e-15
Match length
                  57
% identity
                  93
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172824
Seq. ID
                  jC-atXLIB327409P3a01b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  44
E value
                  2.0e-15
Match length
                  72
% identity
                  90
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  172825
Seq. ID
                  jC-atXLIB327409P3a06a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  44
E value
                  2.0e-15
Match length
                  56
% identity
                  95
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172826
Seq. ID
                  jC-atXLIB327409P3a08b1
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  175
E value
                  2.0e-93
Match length
                  412
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172827
Seq. ID
                  jC-atXLIB327409P3a09b1
Method
                  BLASTX
NCBI GI
                  q282994
```

NCBI GI g282994
BLAST score 280
E value 9.0e-25
Match length 93
% identity 54

NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No.

Seq. ID

172833

jC-atXLIB327409P3d09a1



```
Seq. No.
                   172828
Seq. ID
                   jC-atXLIB327409P3b03b1
Method
                   BLASTX
NCBI GI
                   g2191128
BLAST score
                   556
E value
                   4.0e-57
Match length
                   131
% identity
                   81
NCBI Description
                  (AF007269) belongs to the L5P family of ribosomal proteins
                   [Arabidopsis thaliana]
Seq. No.
                   172829
Seq. ID
                   jC-atXLIB327409P3b04a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                   50
E value
                   9.0e-19
Match length
                  54
% identity
                  98
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172830
Seq. ID
                  jC-atXLIB327409P3c01b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  59
E value
                  3.0e-24
Match length
                  70
% identity
                  97
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172831
Seq. ID
                  jC-atXLIB327409P3c02b1
Method
                  BLASTX
NCBI GI
                  g3046703
BLAST score
                  648
E value
                  7.0e-68
Match length
                  135
% identity
                  94
                  (AL021749) protein kinase ADK1-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  172832
Seq. ID
                  jC-atXLIB327409P3c10a1
Method
                  BLASTX
NCBI GI
                  g4056433
BLAST score
                  364
E value
                  2.0e-34
Match length
                  151
% identity
                  49
                  (AC005990) Similar to anter-specific proline-rich protein
NCBI Description
```

23682

(CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Match length

% identity

64 95



```
Method
                   BLASTN
NCBI GI
                  g2462264
BLAST score
                   50
E value
                   6.0e-19
Match length
                   54
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172834
Seq. ID
                   jC-atXLIB327409P3e02a1
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  54
E value
                  2.0e-21
Match length
                   54
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172835
Seq. ID
                  jC-atXLIB327409P3e04a1
Method
                  BLASTX
NCBI GI
                  q3805845
BLAST score
                  318
E value
                  2.0e-36
Match length
                  84
% identity
                  91
NCBI Description
                  (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
                  172836
Seq. ID
                  jC-atXLIB327409P3e08b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  56
E value
                  1.0e-22
Match length
                  75
                  95
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172837
Seq. ID
                  jC-atXLIB327409P3e10a1
Method
                  BLASTX
NCBI GI
                  g2231821
BLAST score
                  204
E value
                  1.0e-15
Match length
                  117
% identity
                  42
NCBI Description
                  (U93028) DNA polymerase I [Bacillus stearothermophilus]
Seq. No.
                  172838
Seq. ID
                  jC-atXLIB327409P3f02a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  53
E value
                  2.0e-20
```

Seq. No.

172844



```
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172839
Seq. ID
                  jC-atXLIB327409P3f03a1
Method
                  BLASTN
                  g2290120
NCBI GI
                  47
BLAST score
E value
                  3.0e-17
Match length
                  66
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  172840
Seq. No.
Seq. ID
                  jC-atXLIB327409P3f05a1
Method
                  BLASTX
NCBI GI
                  g4588376
BLAST score
                  124
E value
                  3.0e-13
Match length
                  68
% identity
                  65
NCBI Description
                  (AF106954) galactinol synthase [Brassica napus]
Seq. No.
                  172841
                  jC-atXLIB327409P3f07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  50
E value
                  9.0e-19
Match length
                  50
                  100
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  172842
Seq. ID
                  jC-atXLIB327409P3g01a1
Method
                  BLASTX
NCBI GI
                  g3033375
BLAST score
                  215
E value
                  5.0e-17
Match length
                  140
% identity
                  30
NCBI Description
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
Seq. No.
                  172843
Seq. ID
                  jC-atXLIB327409P3g05a1
Method
                  BLASTN
NCBI GI
                  g4388714
BLAST score
                  181
E value
                  7.0e-97
Match length
                  288
% identity
                  92
NCBI Description Arabidopsis thaliana chromosome II BAC F5K7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```



Seq. ID jC-atXLIB327409P3g10b1

Method BLASTX
NCBI GI g3420935
BLAST score 779
E value 3.0e-83
Match length 149
% identity 98

NCBI Description (AF082157) beta-glucosidase [Arabidopsis thaliana]

>gi 3421390 (AF082158) beta-glucosidase homolog

[Arabidopsis thaliana]

Seq. No. 172845

Seq. ID jC-atXLIB327409P3h04a1

Method BLASTN
NCBI GI 94680765
BLAST score 73
E value 1.0e-32
Match length 97
% identity 95

NCBI Description Arabidopsis thaliana BAC F14I23 from chromosome V near 69

cM, complete sequence

Seq. No. 172846

Seq. ID jC-atXLIB327409P3h10a1

Mëthod BLASTN
NCBI GI g2462264
BLAST score 54
E value 3.0e-21
Match length 54
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172847

Seq. ID jC-atXLIB327409P4a01a1

Method BLASTN
NCBI GI g2462264
BLAST score 56
E value 2.0e-22
Match length 56
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172848

Seq. ID jC-atXLIB327409P4a06a1

Method BLASTX
NCBI GI g3879811
BLAST score 182
E value 2.0e-13
Match length 67
% identity 49

NCBI Description (Z66524) Homology with Squid retinal-binding protein (PIR

Acc. No. A53057) [Caenorhabditis elegans]

Seq. No. 172849

Seq. ID jC-atXLIB327409P4a07a1

Method BLASTX NCBI GI 93878570



BLAST score 267 E value 3.0e-23 Match length 77

% identity 61

NCBI Description (Z46381) similar to lipoic acid synthase; cDNA EST

yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk476e7.3

CO

Seq. No. 172850

Seq. ID jC-atXLIB327409P4b02a1

Method BLASTN
NCBI GI g2462264
BLAST score 48
E value 9.0e-18
Match length 56

Match length 56 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172851

Seq. ID jC-atXLIB327409P4b02b1

Method BLASTN
NCBI GI g2582640
BLAST score 68
E value 1.0e-29
Match length 75

Match length 75 % identity 99

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172852

Seq. ID jC-atXLIB327409P4b05a1

Method BLASTN
NCBI GI g2462264
BLAST score 47
E value 3.0e-17
Match length 51

Match length 51 % identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172853

Seq. ID jC-atXLIB327409P4b06b1

Method BLASTX
NCBI GI g1523796
BLAST score 540
E value 3.0e-55
Match length 101
% identity 100

NCBI Description (X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 172854

Seq. ID jC-atXLIB327409P4b07b1

Method BLASTX
NCBI GI g1769903
BLAST score 250
E value 2.0e-21



```
Match length 50 % identity 100
```

NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No. 172855

Seq. ID jC-atXLIB327409P4b08a1

Method BLASTN
NCBI GI g2462264
BLAST score 51
E value 1.0e-19
Match length 54

% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172856

Seq. ID jC-atXLIB327409P4b09a1

Method BLASTN
NCBI GI g3702736
BLAST score 286
E value 1.0e-160
Match length 428
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRI1, complete sequence [Arabidopsis thaliana]

Seq. No. 172857

Seq. ID jC-atXLIB327409P4b10b1

Method BLASTN
NCBI GI 94757407
BLAST score 69
E value 2.0e-30

E value 2.0eMatch length 330
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQD19, complete sequence

Seq. No. 172858

Seq. ID jC-atXLIB327409P4b12a1

Method BLASTN
NCBI GI g2828186
BLAST score 81
E value 2.0e-37
Match length 208
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 172859

Seq. ID jC-atXLIB327409P4c01a1

Method BLASTN
NCBI GI g2462264
BLAST score 53
E value 9.0e-21
Match length 57
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
Seq. No.
                   172860
Seq. ID
                   jC-atXLIB327409P4c03a1
Method
                   BLASTN
NCBI GI
                   q4584387
BLAST score
                   64
E value
                   3.0e-27
Match length
                   224
% identity
                   83
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
                   (ESSA project)
Seq. No.
                   172861
Seq. ID
                   jC-atXLIB327409P4c06b1
Method
                   BLASTN
NCBI GI
                   g2505873
BLAST score
                   177
E value
                   9.0e-95
Match length
                   432
% identity
                   98
NCBI Description Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus
Seq. No.
                   172862
Seq. ID
                   jC-atXLIB327409P4c08a1
Method
                   BLASTX
NCBI GI
                   q99713
BLAST score
                   323
E value
                   7.0e-30
Match length
                   63
% identity
                   97
                   homeotic protein agamous - Arabidopsis thaliana
NCBI Description
                   >gi 13455\overline{0}5 emb CAA37642_ (X53579) agamous gene product (AA
                   1-285) [Arabidopsis thaliana] >gi_226968_prf_ 1612343A
                   agamous gene [Arabidopsis sp.]
Seq. No.
                   172863
Seq. ID
                   jC-atXLIB327409P4c09a1
Method
                   BLASTX
NCBI GI
                   g2245093
BLAST score
                   266
E value
                   4.0e-23
Match length
                   84
% identity
                   33
NCBI Description
                  (Z97343) membrane channel protein [Arabidopsis thaliana]
Seq. No.
                  172864
Seq. ID
                   jC-atXLIB327409P4c10a1
Method
                  BLASTX
NCBI GI
                  g4469009
BLAST score
                  282
E value
                  5.0e-25
Match length
                  80
% identity
                  75
```

(AL035602) putative protein [Arabidopsis thaliana]

NCBI Description

Seq. No.

Seq. ID jC-atXLIB327409P4c11a1

172865

Method BLASTN

E value

1.0e-13



```
NCBI GI
                   g2290120
BLAST score
                   55
E value
                   6.0e-22
Match length
                   66
% identity
                   97
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  172866
Seq. ID
                  jC-atXLIB327409P4c11b1
Method
                  BLASTN
NCBI GI
                  g2576362
BLAST score
                  379
                  0.0e+00
E value
Match length
                   434
% identity
                  98
NCBI Description
                  Arabidopsis thaliana amino acid transport protein mRNA,
                  complete cds
Seq. No.
                  172867
Seq. ID
                  jC-atXLIB327409P4c12a1
Method
                  BLASTN
NCBI GI
                  g3128135
BLAST score
                  228
E value
                  1.0e-125
Match length
                  352
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19E1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172868
Seq. ID
                  jC-atXLIB327409P4d01a1
Method
                  BLASTX
NCBI GI
                  g2454184
BLAST score
                  283
E value
                  3.0e-25
Match length
                  81
% identity
                  69
NCBI Description
                  (U80186) pyruvate dehydrogenase E1 beta subunit
                   [Arabidopsis thaliana]
Seq. No.
                  172869
Seq. ID
                  jC-atXLIB327409P4d05a1
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  47
E value
                  3.0e-17
Match length
                  55
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172870
Seq. No.
Seq. ID
                  jC-atXLIB327409P4d11a1
Method
                  BLASTX
NCBI GI
                  g2894378
BLAST score
                  58
```



```
Match length
                   83
% identity
                   45
NCBI Description
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.
                   172871
Seq. ID
                   jC-atXLIB327409P4e01a1
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   56
E value
                   2.0e-22
Match length
                   56
% identity
                   100
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                   172872
Seq. ID
                   jC-atXLIB327409P4e01b1
Method
                   BLASTX
NCBI GI
                   q4263525
BLAST score
                   397
E value
                   2.0e-38
Match length
                   149
% identity
                   59
                  (AC004044) putative photosystem I reaction center subunit
NCBI Description
                   II precursor [Arabidopsis thaliana]
Seq. No.
                   172873
Seq. ID
                   jC-atXLIB327409P4e05a1
Method
                   BLASTN
NCBI GI
                   g4757414
BLAST score
                   101
E value
                   2.0e-49
Match length
                   311
% identity
                   85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
Seq. No.
                   172874
Seq. ID
                   jC-atXLIB327409P4e06b1
Method
                  BLASTX
NCBI GI
                  g1550738
BLAST score
                   434
E value
                  8.0e-43
Match length
                  136
% identity
                   69
NCBI Description
                  (Y08061) endomembrane-associated protein [Arabidopsis
                   thaliana] >gi 2982443 emb CAA18251 (AL022224)
                  endomembrane-associated protein [Arabidopsis thaliana]
Seq. No.
                  172875
Seq. ID
                   jC-atXLIB327409P4e08a1
Method
                  BLASTX
NCBI GI
                  q4587611
```

Method BLASTX
NCBI GI g4587611
BLAST score 367
E value 5.0e-35
Match length 76
% identity 97

NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis



thaliana]

Seq. No. 172876

Seq. ID jC-atXLIB327409P4e08b1

Method BLASTX
NCBI GI g4587611
BLAST score 274
E value 4.0e-24
Match length 111
% identity 59

NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis

thaliana]

Seq. No. 172877

Seq. ID jC-atXLIB327409P4e09a1

Method BLASTN
NCBI GI g2462264
BLAST score 53
E value 9.0e-21

Match length 53 % identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172878

Seq. ID jC-atXLIB327409P4e10a1

Method BLASTX
NCBI GI g2864602
BLAST score 452
E value 6.0e-45
Match length 99
% identity 85

NCBI Description (Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No. 172879

Seq. ID jC-atXLIB327409P4e10b1

Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 1.0e-26
Match length 74

Match length 74 % identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172880

Seq. ID jC-atXLIB327409P4e12a1

Method BLASTN
NCBI GI g4589419
BLAST score 426
E value 0.0e+00
Match length 426
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2I5, complete sequence

Seq. No. 172881

Seq. ID jC-atXLIB327409P4f01a1

Match length

% identity

93

12



```
Method
                   BLASTN
NCBI GI
                   q3985931
BLAST score
                   115
E value
                   1.0e-57
Match length
                   135
% identity
                   96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K21H1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   172882
Seq. ID
                   jC-atXLIB327409P4f02a1
Method
                   BLASTN
NCBI GI
                   g531828
BLAST score
                   54
E value
                   2.0e-21
Match length
                  66
% identity
                   95
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172883
Seq. ID
                  jC-atXLIB327409P4f05a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  54
E value
                  2.0e-21
Match length
                  54
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172884
Seq. ID
                  jC-atXLIB327409P4f06a1
Method
                  BLASTN
NCBI GI
                  q2980640
BLAST score
                  100
E value
                  8.0e-49
Match length
                  321
% identity
                  87
NCBI Description Arabidopsis thaliana mRNA for putative MRP protein
Seq. No.
                  172885
Seq. ID
                  jC-atXLIB327409P4f06b1
Method
                  BLASTX
NCBI GI
                  q2980641
BLAST score
                  688
E value
                  1.0e-72
Match length
                  135
% identity
NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]
Seq. No.
                  172886
Seq. ID
                  jC-atXLIB327409P4q01b1
Method
                  BLASTX
NCBI GI
                  g421929
BLAST score
                  249
E value
                  7.0e-33
```



NCBI Description ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

 Seq. No.
 172887

 Seq. ID
 jC-atXLIB327409P4g03a1

Method BLASTN
NCBI GI g2462264
BLAST score 57
E value 4.0e-23

Match length 61 % identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172888

Seq. ID jC-atXLIB327409P4g07a1

Method BLASTX
NCBI GI g1350680
BLAST score 348
E value 9.0e-33
Match length 98

Match length 98 % identity 73

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 172889

Seq. ID jC-atXLIB327409P4g10a1

Method BLASTN
NCBI GI g4757403
BLAST score 242
E value 1.0e-133
Match length 382

% identity 94 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJL12, complete sequence

Seq. No. 172890

Seq. ID jC-atXLIB327409P4h01a1

Method BLASTN
NCBI GI g2462264
BLAST score 57
E value 4.0e-23
Match length 57
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172891

Seq. ID jC-atXLIB327409P4h01b1

Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 1.0e-26
Match length 74
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172892

Seq. ID jC-atXLIB327409P4h04a1



```
Method
                   BLASTN
NCBI GI
                  q3869075
BLAST score
                   253
E value
                  1.0e-140
Match length
                   414
                   94
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
                  172893
Seq. No.
Seq. ID
                  jC-atXLIB327409P4h05a1
Method
                  BLASTN
NCBI GI
                  q3702731
BLAST score
                  48
                  9.0e-18
E value
                  105
Match length
% identity
                  93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172894
Seq. ID
                  jC-atXLIB327410P1a04a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  54
                  3.0e-21
E value
Match length
                  62
                  97
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172895
Seq. ID
                  jC-atXLIB327410P1a06a1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  57
                  1.0e-23
E value
Match length
                  65
                  97
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
```

Seq. No. 172896

Seq. ID jC-atXLIB327410P1a11b1

Method BLASTX
NCBI GI g3219271
BLAST score 335
E value 6.0e-31
Match length 126
% identity 60

NCBI Description (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No. 172897

Seq. ID jC-atXLIB327410P1a12a1

Method BLASTN
NCBI GI g2462264
BLAST score 56
E value 3.0e-22



96

factor, RSp40

NCBI Description

```
Match length
                   56
                   100
% identity
NCBI Description
                  Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   172898
Seq. ID
                   jC-atXLIB327410P1b04a1
Method
                   BLASTN
NCBI GI
                   g2290120
BLAST score
                   51
E value
                   1.0e-19
Match length
                   59
% identity
                   97
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                   gene, partial cds
Seq. No.
                   172899
Seq. ID
                   jC-atXLIB327410P1b07a1
Method
                   BLASTN
NCBI GI
                   q540252
BLAST score
                   33
E value
                   3.0e-09
Match length
                   33
% identity
                   100
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  172900
Seq. ID
                  jC-atXLIB327410P1b07b1
Method
                  BLASTN
                  g3941523
NCBI GI
BLAST score
                   41
E value
                  2.0e-13
Match length
                   45
                   98
% identity
NCBI Description
                  Arabidopsis thaliana putative transcription factor (MYB92)
                  mRNA, complete cds
Seq. No.
                   172901
Seq. ID
                   jC-atXLIB327410P1b10a1
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  57
E value
                  7.0e-23
Match length
                   65
                  97
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  172902
Seq. ID
                   jC-atXLIB327410P1c03b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  45
E value
                  5.0e-16
Match length
                  53
% identity
```

23695

Arabidopsis thaliana mRNA for arginine/serine-rich splicing



```
Seq. No.
                   172903
Seq. ID
                   jC-atXLIB327410P1c04b1
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   46
E value
                   3.0e-16
Match length
                   58
% identity
                   95
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
Seq. No.
                   172904
                   jC-atXLIB327410P1c07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   49
E value
                   2.0e-18
Match length
                   61
% identity
                   95
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   172905
Seq. ID
                   jC-atXLIB327410P1c08a1
Method
                   BLASTN
NCBI GI
                   q531828
BLAST score
                   40
E value
                   6.0e-13
Match length
                   60
% identity
                   92
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                   172906
Seq. ID
                   jC-atXLIB327410P1c10b1
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                  44
E value
                   4.0e-15
Match length
                  72
% identity
                  90
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172907
Seq. ID
                  jC-atXLIB327410P1d01b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  55
E value
                  5.0e-22
Match length
                  79
% identity
                  92
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
```

Seq. No. 172908

Seq. ID jC-atXLIB327410Pld03b1

factor, RSp40

Method BLASTN



NCBI GI g3941523
BLAST score 33
E value 7.0e-09
Match length 45

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 172909

% identity

Seq. ID jC-atXLIB327410P1d09a1

93

Method BLASTN
NCBI GI g2462264
BLAST score 35
E value 1.0e-09
Match length 63
% identity 89

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172910

Seq. ID jC-atXLIB327410P1d11b1

Method BLASTN
NCBI GI g2582640
BLAST score 33
E value 5.0e-09
Match length 49
% identity 92

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172911

Seq. ID jC-atXLIB327410P1d12b1

Method BLASTN
NCBI GI g2582640
BLAST score 52
E value 2.0e-20
Match length 72
% identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172912

Seq. ID jC-atXLIB327410P1e03b1

Method BLASTN
NCBI GI g2582640
BLAST score 49
E value 3.0e-18
Match length 72
% identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172913

Seq. ID jC-atXLIB327410Ple05a1

Method BLASTN
NCBI GI g2827698
BLAST score 69
E value 2.0e-30



Match length 300 % identity 84

NCBI Description Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11

(ESSAII project)

Seq. No. 172914

Seq. ID jC-atXLIB327410P1e07b1

Method BLASTN
NCBI GI 94469002
BLAST score 86
E value 2.0e-40
Match length 134
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 172915

Seq. ID jC-atXLIB327410Ple08a1

Method BLASTN
NCBI GI g2462264
BLAST score 52
E value 4.0e-20
Match length 52
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172916

Seq. ID jC-atXLIB327410P1e08b1

Method BLASTX
NCBI GI g1345644
BLAST score 412
E value 1.0e-55
Match length 137
% identity 84

NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_

(X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No. 172917

Seq. ID jC-atXLIB327410P1e09a1

Method BLASTN
NCBI GI g2462264
BLAST score 34
E value 3.0e-09
Match length 42
% identity 95

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172918

Seq. ID jC-atXLIB327410Ple10b1

Method BLASTN
NCBI GI g2582640
BLAST score 55
E value 1.0e-21
Match length 78
% identity 92

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Method

NCBI GI BLAST score BLASTN g3219270

84



```
Seq. No.
                  172919
                  jC-atXLIB327410P1f01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3985931
                  200
BLAST score
                  1.0e-108
E value
Match length
                  300
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21H1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172920
                  jC-atXLIB327410P1f02a1
Seq. ID
                  BLASTN
Method
                  q2462264
NCBI GI
BLAST score
                  40
                  9.0e-13
E value
Match length
                  44
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172921
Seq. No.
Seq. ID
                  jC-atXLIB327410P1f04a1
                  BLASTN
Method
NCBI GI
                  g2462264
                  39
BLAST score
                  3.0e-12
E value
Match length
                   43
% identity
                   98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172922
Seq. ID
                  jC-atXLIB327410P1f07a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                   43
                   8.0e-15
E value
Match length
                   51
% identity
                   96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172923
Seq. No.
                   jC-atXLIB327410P1f09b1
Seq. ID
Method
                   BLASTX
                  g2791834
NCBI GI
                   47
BLAST score
                   4.0e-12
E value
                   80
Match length
% identity
                   54
NCBI Description
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  172924
Seq. No.
                   jC-atXLIB327410P1f10b1
Seq. ID
```



E value 5.0e-39 Match length 128 % identity 92

NCBI Description Arabidopsis thaliana ATMKK4 mRNA for MAP kinase kinase 4,

complete cds

Seq. No. 172925

Seq. ID jC-atXLIB327410P1f11a1

Method BLASTN
NCBI GI g2570223
BLAST score 77
E value 8.0e-35

E value 8.0e-35 Match length 444 % identity 84

NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 172926

Seq. ID jC-atXLIB327410P1g08a1

Method BLASTN
NCBI GI g2290120
BLAST score 33

E value 1.0e-08
Match length 33
% identity 100

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 172927

Seq. ID jC-atXLIB327410P1g08b1

Method BLASTN
NCBI GI g2582640
BLAST score 50
E value 5.0e-19

Match length 74 % identity 92

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172928

Seq. ID jC-atXLIB327410P1h01b1

Method BLASTX
NCBI GI g1076422
BLAST score 401
E value 1.0e-38
Match length 139
% identity 65

NCBI Description transcription factor OBF4 - Arabidopsis thaliana

>gi_414613_emb_CAA49524_ (X69899) ocs-element binding

factor 4 [Arabidopsis thaliana]

Seq. No. 172929

Seq. ID jC-atXLIB327410P1h12b1

Method BLASTN
NCBI GI g2582640
BLAST score 46
E value 6.0e-17



Match length 58 % identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172930

Seq. ID jC-atXLIB327410P2a04a1

Method BLASTN
NCBI GI g2462264
BLAST score 41
E value 1.0e-13

Match length 53 % identity 94

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172931

Seq. ID jC-atXLIB327410P2a08b1

Method BLASTX
NCBI GI g1730777
BLAST score 153
E value 7.0e-10
Match length 124
% identity 35

NCBI Description HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC

REGION >gi 1078050 pir S55151 probable membrane protein

YNL132w - yeast (Saccharomyces cerevisiae)

>gi_854505_emb_CAA86893_ (Z46843) orf16 [Saccharomyces
cerevisiae] >gi 1302072 emb CAA96014 (Z71408) ORF YNL132w

[Saccharomyces cerevisiae]

Seq. No. 172932

Seq. ID jC-atXLIB327410P2a10a1

Method BLASTN
NCBI GI g4558674
BLAST score 295
E value 1.0e-165
Match length 418
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F7B19 genomic

sequence, complete sequence

Seq. No. 172933

Seq. ID jC-atXLIB327410P2a11b1

Method BLASTX
NCBI GI g2190548
BLAST score 253
E value 1.0e-21
Match length 54
% identity 80

NCBI Description (AC001229) EST gb ATTS1121 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 172934

Seq. ID jC-atXLIB327410P2a12a1

Method BLASTN NCBI GI g2462264

BLAST score 37



```
E value 3.0e-11
Match length 37
% identity 100
NCBI Description Cucumis
```

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172935

Seq. ID jC-atXLIB327410P2a12b1

Method BLASTN
NCBI GI g2618600
BLAST score 76
E value 2.0e-34
Match length 128
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MDC12, complete sequence [Arabidopsis thaliana]

Seq. No. 172936

Seq. ID jC-atXLIB327410P2b01a1

Method BLASTN
NCBI GI g2462264
BLAST score 34
E value 9.0e-10
Match length 42
% identity 95

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172937

Seq. ID jC-atXLIB327410P2b04a1

Method BLASTN
NCBI GI g2462264
BLAST score 53
E value 9.0e-21
Match length 61

% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172938

Seq. ID jC-atXLIB327410P2b08a1

Method BLASTN
NCBI GI g1785673
BLAST score 413
E value 0.0e+00
Match length 428
% identity 99

NCBI Description A.thaliana mitochondrial genome, part A

Seq. No. 172939

Seq. ID jC-atXLIB327410P2b08b1

Method BLASTX
NCBI GI g1785689
BLAST score 567
E value 2.0e-58
Match length 105
% identity 100

NCBI Description (Y08501) cytochrome c biogenesis orf452 [Arabidopsis

thaliana]



Seq. No. 172940 Seq. ID jC-atXLIB327410P2b10a1 Method BLASTN NCBI GI g2462264 BLAST score 40 5.0e-13 E value Match length 44 % identity 98 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Method BLASTN

NCBI GI g2582640
BLAST score 56
E value 1.0e-22
Match length 68
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172942

Seq. ID jC-atXLIB327410P2b12b1

Method BLASTN
NCBI GI g3800746
BLAST score 35
E value 5.0e-10
Match length 50
% identity 96

NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,

complete cds

Seq. No. 172943

Seq. ID jC-atXLIB327410P2c12a1

Method BLASTN
NCBI GI g540252
BLAST score 42
E value 3.0e-14
Match length 58
% identity 93

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No. 172944

Seq. ID jC-atXLIB327410P2d04b1

Method BLASTX
NCBI GI 94559385
BLAST score 171
E value 5.0e-12
Match length 147
% identity 35

NCBI Description (AC006526) putative cyclic nucleotide-regulated ion channel

protein [Arabidopsis thaliana]

Seq. No. 172945

Seq. ID jC-atXLIB327410P2e01a1

Method BLASTN NCBI GI g2462264



```
BLAST score
E.value
                   2.0e-18
Match length
                   57
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172946
Seq. No.
Seq. ID
                  jC-atXLIB327410P2e01b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  63
E value
                  8.0e-27
Match length
                  71
% identity
                  97
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  172947
Seq. ID
                  jC-atXLIB327410P2e05a1
Method
                  BLASTN
NCBI GI
                  g683503
BLAST score
                  63
E value
                  9.0e-27
Match length
                  83
% identity
                  94
NCBI Description
                  A.thaliana mRNA for 65kDa regulatory subunit of protein
                  phosphatase 2A
Seq. No.
                  172948
Seq. ID
                  jC-atXLIB327410P2e05b1
Method
                  BLASTN
NCBI GI
                  q531832
BLAST score
                  36
E value
                  1.0e-10
Match length
                  44
% identity
                  95
NCBI Description Cloning vector pSport2, complete sequence
Seq. No.
                  172949
Seq. ID
                  jC-atXLIB327410P2f01a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  50
E value
                  5.0e-19
Match length
                  54
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172950
```

Seq. ID jC-atXLIB327410P2f05a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 6.0e-19
Match length 62
% identity 97

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

E value

Match length

NCBI Description

% identity

1.0e-10

65

57



```
Seq. No.
                   172951
Seq. ID
                   jC-atXLIB327410P2f08b1
Method
                  BLASTN
NCBI GI
                  g2264318
BLAST score
                   432
E value
                  0.0e+00
Match length
                   436
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172952
Seq. ID
                  jC-atXLIB327410P2f10a1
Method
                  BLASTX
NCBI GI
                  g2894559
BLAST score
                  170
E value
                  7.0e-12
Match length
                  52
% identity
                  69
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]
Seq. No.
                  172953
Seq. ID
                  jC-atXLIB327410P2f11b1
Method
                  BLASTX
NCBI GI
                  g2654088
BLAST score
                  728
E value
                  2.0e-77
Match length
                  140
% identity
                  100
NCBI Description
                  (AF033118) potassium transporter [Arabidopsis thaliana]
                  >gi 2688979 (AF029876) high-affinity potassium transporter;
                  AtKUPlp [Arabidopsis thaliana] >gi_3150413 (AC004165)
                  high-affinity potassium transporter (AtKUP1) [Arabidopsis
                  thaliana] >gi 3420045 (AC004680) high-affinity potassium
                  transporter (AtKUP1) [Arabidopsis thaliana]
Seq. No.
                  172954
Seq. ID
                  jC-atXLIB327410P2g01a1
Method
                  BLASTN
NCBI GI
                  g3355463
BLAST score
                  77
E value
                  4.0e-35
Match length
                  161
% identity
                  87
NCBI Description Arabidopsis thaliana chromosome II BAC F12L6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  172955
Seq. ID
                  jC-atXLIB327410P2g04a1
Method
                  BLASTX
NCBI GI
                  q4454032
BLAST score
                  160
```

23705

(AL035394) putative protein [Arabidopsis thaliana]

% identity

Seq. No.

97

172961



```
Seq. No.
                  172956
Seq. ID
                  jC-atXLIB327410P2g07a1
Method
                  BLASTX
NCBI GI
                  g2104529
BLAST score
                   406
E value
                  1.0e-39
Match length
                  108
                  76
% identity
NCBI Description (AF001308) putative hexose transporter [Arabidopsis
                  thaliana]
Seq. No.
                  172957
Seq. ID
                  jC-atXLIB327410P2h01a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  54
                  2.0e-21
E value
Match length
                  62
                  97
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172958
Seq. ID
                  jC-atXLIB327410P2h03a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  48
E value
                  9.0e-18
Match length
                  56
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  172959
Seq. No.
Seq. ID
                  jC-atXLIB327410P2h04b1
Method
                  BLASTX
NCBI GI
                  g2499608
BLAST score
                  94
E value
                  4.0e-11
Match length
                  57
% identity
                  65
NCBI Description
                 MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)
                  (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein
                  kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi_457400_dbj BAA04867 (D21840) MAP kinase [Arabidopsis
                  thaliana]
                  172960
Seq. No.
Seq. ID
                  jC-atXLIB327410P2h06a1
Method
                  BLASTN
NCBI GI
                  g2462264
                  36
BLAST score
E value
                  1.0e-10
Match length
                  40
```

23706

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



Seq. ID jC-atXLIB327410P2h07a1 Method BLASTN NCBI GI g2462264 BLAST score 39 E value 2.0e-12 Match length 43 % identity 98 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172962 Seq. ID jC-atXLIB327410P2h08b1 Method BLASTX NCBI GI g2827992 BLAST score 189 E value 4.0e-25 Match length 102 % identity 53 NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum] Seq. No. 172963 jC-atXLIB327410P2h09a1 Seq. ID Method BLASTX NCBI GI g3790581 BLAST score 246 8.0e-21 E value Match length 44 98 % identity NCBI Description (AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana] 172964 Seq. No. Seq. ID jC-atXLIB327410P3a02a1 BLASTN Method NCBI GI g2462264 BLAST score 38 E value 8.0e-12 Match length 42 % identity 98 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 172965 Seq. ID jC-atXLIB327410P3a02b1 Method BLASTN NCBI GI g2582640 BLAST score 48 7.0e-18E value Match length 72 % identity 93 NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

172966 Seq. No.

Seq. ID jC-atXLIB327410P3a03a1

Method BLASTN NCBI GI g2462264 BLAST score 48 E value 9.0e-18

```
Match length
                   60
% identity
                   95
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  172967
Seq. ID
                  jC-atXLIB327410P3a03b1
Method
                  BLASTN
NCBI GI
                  g3047088
BLAST score
                  398
E value
                  0.0e + 00
Match length
                  438
                  98
% identity
NCBI Description Arabidopsis thaliana BAC T26D22
Seq. No.
                  172968
Seq. ID
                  jC-atXLIB327410P3b02a1
Method
                  BLASTN
NCBI GI
                  g1359492
BLAST score
                  102
E value
                  5.0e-50
Match length
                  186
% identity
                  96
NCBI Description A.thaliana mRNA for zinc finger protein DAG1 (BBFa)
                  172969
Seq. No.
Seq. ID
                  jC-atXLIB327410P3b07a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  53
                  9.0e-21
E value
Match length
                  57
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
```

Seq. No. 172970

Seq. ID jC-atXLIB327410P3b12a1

Method BLASTX
NCBI GI g3334323
BLAST score 359
E value 4.0e-34
Match length 70
% identity 97

NCBI Description GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog

[Arabidopsis thaliana] >gi_2104532 gb AAC78700.1

(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis

thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis

thaliana]

Seq. No. 172971

Seq. ID jC-atXLIB327410P3c06b1

Method BLASTX
NCBI GI 94206763
BLAST score 258
E value 3.0e-22
Match length 58
% identity 90

NCBI Description (AF104328) cell_wall-plasma membrane linker protein homolog



[Arabidopsis thaliana]

Seq. No. 172972 Seq. ID

jC-atXLIB327410P3c12a1

Method BLASTN NCBI GI q2462264 BLAST score 42 E value 3.0e-14 Match length 42

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172973

% identity

jC-atXLIB327410P3c12b1 Seq. ID

100

Method BLASTX NCBI GI g2129965 BLAST score 177 1.0e-12 E value Match length 61 % identity 66

NCBI Description Sar1 homolog GTP-binding protein NTGB2 - common tobacco

(fragment) >gi 1184989 (U46928) NTGB2 [Nicotiana tabacum]

Seq. No. 172974

jC-atXLIB327410P3e05a1 Seq. ID

Method BLASTN NCBI GI g2290120 BLAST score 51 E value 1.0e-19 Match length 59 % identity 98

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 172975

Seq. ID jC-atXLIB327410P3e08a1

Method BLASTN NCBI GI g2462264 BLAST score 57 E value 4.0e-23 Match length 57 % identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172976

jC-atXLIB327410P3q09b1 Seq. ID

Method BLASTN NCBI GI g2582640 BLAST score 58 E value 1.0e-23 Match length 70 % identity 96

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

Seq. No. 172977

Seq. ID jC-atXLIB327410P3h07b1



Method BLASTX
NCBI GI g4521249
BLAST score 474
E value 2.0e-47
Match length 126
% identity 75
NCBI Description (AB01391)

NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 172978

Seq. ID jC-atXLIB327410P4a04a1

MethodBLASTNNCBI GIg2462264BLAST score42E value3.0e-14Match length46

% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 172979

Seq. ID jC-atXLIB327410P4a04b1

Method BLASTN
NCBI GI g3941523
BLAST score 44
E-value 2.0e-15

Match length 48 % identity 98

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 172980

Seq. ID jC-atXLIB327410P4a06a1

Method BLASTN
NCBI GI g4757409
BLAST score 69
E value 3.0e-30
Match length 194

Match length 194 % identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVC8, complete sequence

Seq. No. 172981

Seq. ID jC-atXLIB327410P4a07a1

Method BLASTX
NCBI GI g2576361
BLAST score 372
E value 5.0e-39
Match length 108
% identity 81

NCBI Description (U39782) lysine and histidine specific transporter

[Arabidopsis thaliana]

Seq. No. 172982

Seq. ID jC-atXLIB327410P4b02b1

Method BLASTN
NCBI GI g2582640
BLAST score 38
E value 8.0e-12



Match length 54 % identity 94

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172983

Seq. ID jC-atXLIB327410P4b04b1

Method BLASTN NCBI GI g2582640

BLAST score 33 E value 5.0e-09 Match length 45 % identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172984

Seq. ID jC-atXLIB327410P4d10a1

Method BLASTX
NCBI GI g3511153
BLAST score 185
E value 1.0e-13
Match length 59
% identity 56

NCBI Description (AF063015) cell division protein [Homo sapiens]

Seq. No. 172985

Seq. ID jC-atXLIB327410P4e01a1

Method BLASTN
NCBI GI g3869075
BLAST score 355
E value 0.0e+00
Match length 421
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 172986

Seq. ID jC-atXLIB327410P4e04b1

Method BLASTN
NCBI GI g2582640
BLAST score 43
E value 8.0e-15

Match length 74 % identity 91

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 172987

Seq. ID jC-atXLIB327410P4e06a1

Method BLASTN
NCBI GI g2760170
BLAST score 169
E value 5.0e-90
Match length 358
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

NCBI Description



MIO24, complete sequence [Arabidopsis thaliana]

```
172988
Seq. No.
Seq. ID
                   jC-atXLIB327410P4f01b1
Method
                   BLASTX
                  q1083418
NCBI GI
BLAST score
                  195
E value
                  8.0e-15
                  116
Match length
% identity
                   41
                  microtubule-associated serine/threonine protein kinase
NCBI Description
                  MAST205 - mouse >gi 406058 (U02313) protein kinase [Mus
                  musculus]
                  172989
Seq. No.
                   jC-atXLIB327410P4f02b1
Seq. ID
Method
                   BLASTN
                  q3800746
NCBI GI
BLAST score
                   40
                   6.0e-13
E value
                   52
Match length
                   96
% identity
NCBI Description
                  Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                  complete cds
                  172990
Seq. No.
                   jC-atXLIB327410P4f05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                   53
                   9.0e-21
E value
Match length
                   53
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   172991
Seq. ID
                   jC-atXLIB327410P4f11b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                   34
E value
                   2.0e-09
Match length
                   64
                   91
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   172992
Seq. ID
                   jC-atXLIB327410P4g04b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                   37
                   3.0e-11
E value
Match length
                  45
                   96
% identity
```

factor, RSp40

Arabidopsis thaliana mRNA for arginine/serine-rich splicing



```
172993
Seq. No.
Seq. ID
                  jC-atXLIB327410P4g07a1
Method
                  BLASTN
NCBI GI
                  g4678315
BLAST score
                  108
E value
                  1.0e-53
                  418
Match length
% identity
                  96
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15
NCBI Description
                  (ESSA project)
                  172994
Seq. No.
Seq. ID
                  jC-atXLIB327410P4g12a1
Method
                  BLASTN
                  g2290120
NCBI GI
                  56
BLAST score
E value
                  1.0e-22
Match length
                  63
% identity
                  97
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  172995
Seq. No.
                  jC-atXLIB327410P4h02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386548
BLAST score
                  720
                  2.0e-76
E value
Match length
                  141
% identity
                  93
                  (AF079504) H-protein promoter binding factor-2b
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  172996
Seq. ID
                  jC-atXLIB327410P4h03a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  37
E value
                  3.0e-11
Match length
                  53
% identity
                  92
NCBI Description Cloning vector pSport1, complete cds
                  172997
Seq. No.
Seq. ID
                  jC-atXLIB327410P4h03b1
Method
                  BLASTN
NCBI GI
                  g3395421
                  59
BLAST score
E value
                  2.0e-24
Match length
                  127
                  87
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T19C21 genomic
```

Seq. No. 172998

Seq. ID jC-atXLIB327410P4h05a1

Method BLASTN

23713

sequence, complete sequence [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g4220644

289 1.0e-161



```
NCBI GI
                  q531828
BLAST score
                   52
                  3.0e-20
E value
Match length
                  59
% identity
                  97
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  172999
Seq. ID
                  jC-atXLIB327410P4h07b1
Method
                  BLASTX
NCBI GI
                  g1076442
BLAST score
                  507
E value
                  2.0e-51
Match length
                  135
                  70
% identity
NCBI Description
                  beta-glucosidase (EC 3.2.1.21) - rape
                  >gi_757740_emb_CAA57913 (X82577) beta-glucosidase
                   [Brassica napus]
Seq. No.
                  173000
Seq. ID
                  jC-atXLIB327410P4h12a1
Method
                  BLASTX
                  g2290400
NCBI GI
BLAST score
                  336
E value
                  2.0e-31
Match length
                  107
                  63
% identity
NCBI Description (U91339) stearoyl-ACP desaturase [Helianthus annuus]
Seq. No.
                  173001
Seq. ID
                  jC-atXLIB327411P1a01a1
Method
                  BLASTN
NCBI GI
                  q2290120
BLAST score
                  37
E value
                  3.0e-11
Match length
                  60
                  92
% identity
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  173002
Seq. ID
                  jC-atXLIB327411P1a01b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  39
                  2.0e-12
E value
Match length
                  70
% identity
                  89
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  173003
Seq. ID
                  jC-atXLIB327411P1b02b1
Method
                  BLASTN
```



```
Match length
                  474
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXL8, complete sequence [Arabidopsis thaliana]
                  173004
Seq. No.
Seq. ID
                  jC-atXLIB327411P1b07b1
Method
                  BLASTX
NCBI GI
                  g1403138
BLAST score
                  587
                  1.0e-60
E value
Match length
                  113
% identity
                  96
                  (X98190) peroxidase ATP2a [Arabidopsis thaliana]
NCBI Description
                  >gi 4371288 gb AAD18146 (AC006260) putative peroxidase
                  ATP2a [Arabidopsis thaliana]
Seq. No.
                  173005
Seq. ID
                  jC-atXLIB327411P1b11a1
Method
                  BLASTN
NCBI GI
                  q2290120
BLAST score
                  55
E value
                  6.0e-22
Match length
                  62
                  97
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  173006
                  jC-atXLIB327411P1c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  579
                  2.0e-72
E value
                  152
Match length
                  97
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
                  173007
Seq. No.
Seq. ID
                  jC-atXLIB327411P1c12b1
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  636
E value
                  2.0e-66
Match length
                  175
% identity
                  70
```

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 173008

Seq. ID jC-atXLIB327411P1d02a1

Method BLASTN
NCBI GI g2462264
BLAST score 36
E value 1.0e-10



Match length 51 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173009

Seq. ID jC-atXLIB327411P1d03b1

Method BLASTN
NCBI GI g2582640
BLAST score 63
E value 1.0e-26
Match length 71

Match length /1 % identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173010

Seq. ID jC-atXLIB327411P1d06a1

Method BLASTN
NCBI GI g2351062
BLAST score 93
E value 1.0e-44

E value 1.0e
Match length 128
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 173011

Seq. ID jC-atXLIB327411P1d09a1

Method BLASTX
NCBI GI g2459443
BLAST score 127
E value 8.0e-07
Match length 86
% identity 32

NCBI Description (AC002332) putative NAD(P)-dependent cholesterol

dehydrogenase [Arabidopsis thaliana]

Seq. No. 173012

Seq. ID jC-atXLIB327411P1d10b1

Method BLASTN
NCBI GI 94519193
BLAST score 152
E value 5.0e-80
Match length 289
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 173013

Seq. ID jC-atXLIB327411P1d12a1

Method BLASTX
NCBI GI g2369714
BLAST score 239
E value 6.0e-20
Match length 87
% identity 60

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]



```
173014
Seq. No.
Seq. ID
                   jC-atXLIB327411P1d12b1
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                   553
E value
                   9.0e-57
Match length
                  152
% identity
                  70
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                  173015
Seq. No.
Seq. ID
                  jC-atXLIB327411P1e02b1
Method
                  BLASTN
NCBI GI
                  g4490291
BLAST score
                  461
E value
                  0.0e+00
Match length
                  472
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                  (ESSA project)
Seq. No.
                  173016
Seq. ID
                  jC-atXLIB327411P1e07b1
Method
                  BLASTX
NCBI GI
                  g3639089
BLAST score
                  820
E value
                  5.0e-88
Match length
                  157
% identity
                  96
NCBI Description
                  (AF090445) phospholipase D1 [Brassica oleracea]
                  >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1
                  [Brassica oleracea var. capitata]
Seq. No.
                  173017
Seq. ID
                  jC-atXLIB327411P1f09a1
Method
                  BLASTN
NCBI GI
                  g540252
BLAST score
                  33
E value
                  8.0e-09
Match length
                  33
% identity
                  100
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  173018
Seq. ID
                  jC-atXLIB327411P1f10a1
                  BLASTN
                  g2815519
                  177
```

Method NCBI GI BLAST score E value 1.0e-94 Match length 389 % identity 66

NCBI Description Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 173019

Seq. ID jC-atXLIB327411P1f12b1



```
Method
                  BLASTX
NCBI GI
                  g2088654
BLAST score
                  616
E value
                  4.0e-64
                  140
Match length
                  86
% identity
                  (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  173020
Seq. ID
                  jC-atXLIB327411P1g01a1
Method
                  BLASTX
NCBI GI
                  q135860
BLAST score
                  292
E value
                  4.0e-26
Match length
                  59
                  90
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                  (AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic
                  protein gamma - Arabidopsīs thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi 445129 prf _ 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
Seq. No.
                  173021
Seq. ID
                  jC-atXLIB327411P1g06b1
Method
                  BLASTN
                  g2582640
NCBI GI
BLAST score
                  42
                  4.0e-14
E value
Match length
                  54
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
```

Seq. No. 173022

Seq. ID jC-atXLIB327411P1g10a1

Method BLASTN NCBI GI g2290120 BLAST score 56 E value 2.0e-22 Match length 63 % identity 97

NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 173023

Seq. ID jC-atXLIB327411P1h04a1

Method BLASTN NCBI GI g2462264 BLAST score 48 E value 9.0e-18 Match length 48 % identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.

173029



```
Seq. No.
                  173024
Seq. ID
                   jC-atXLIB327411P1h07b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  54
E value
                  3.0e-21
Match length
                  70
                  94
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  173025
Seq. ID
                  jC-atXLIB327411P1h10a1
Method
                  BLASTN
NCBI GI
                  g3928074
BLAST score
                  75
E value
                  7.0e - 34
Match length
                  383
                  83
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T7F6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173026
Seq. ID
                  jC-atXLIB327411P2b01a1
Method
                  BLASTN
NCBI GI
                  g2760165
BLAST score
                  382
                  0.0e+00
E value
Match length
                  414
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173027
Seq. ID
                  jC-atXLIB327411P2b02a1
Method
                  BLASTN
NCBI GI
                  g2290120
                  57
BLAST score
E value
                  4.0e-23
Match length
                  65
                  97
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  173028
Seq. No.
Seq. ID
                  jC-atXLIB327411P2b05a1
Method
                  BLASTN
NCBI GI
                  g4757415
                  77
BLAST score
E value
                  4.0e-35
Match length
                  237
% identity
                  82
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYN21, complete sequence
```



```
Seq. ID
                    jC-atXLIB327411P2b06b1
Method
                    BLASTX
NCBI GI
                   g3461848
BLAST score
                   189
E value
                    4.0e-14
Match length
                   151
                   67
% identity
NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]
                   173030
Seq. No.
Seq. ID
                   jC-atXLIB327411P2b07a1
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   46
E value
                   1.0e-16
Match length
                   54
% identity
                   96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   173031
Seq. ID
                   jC-atXLIB327411P2c07a1
Method
                   BLASTX
NCBI GI
                   q1703108
BLAST score
                   284
E value
                   3.0e-25
Match length
                   54
% identity
                   100
NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
Seq. No.
                   173032
Seq. ID
                   jC-atXLIB327411P2c09a1
Method
                   BLASTX
NCBI GI
                   q2494115
BLAST score
                   297
E value
                   8.0e-27
Match length
                   79
% identity
                   77
NCBI Description
                   (AC002376) Strong similarity to Arabidopsis ATHSAR1
                   (gb_M90418). ESTs gb_T44122,gb_N65276,gb_AA041135 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   173033
Seq. ID
                   jC-atXLIB327411P2c12a1
Method
                   BLASTX
```

NCBI GI g4650842 BLAST score 180 E value 4.0e-13 Match length 67 % identity 54

(AB026185) elongation factor 2 [Lithospermum erythrorhizon] NCBI Description

Seq. No. 173034

Seq. ID jC-atXLIB327411P2e06a1

Seq. ID

Method

NCBI GI



```
Method
                  BLASTX
NCBI GI
                  q4337040
BLAST score
                  236
E value
                   1.0e-19
Match length
                  85
                  53
% identity
                  (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
NCBI Description
                   thaliana] >gi_4337042_gb_AAD18051 (AF124160) molybdopterin
                   synthase sulphurylase [Arabidopsis thaliana]
Seq. No.
                  173035
Seq. ID
                  jC-atXLIB327411P2e07a1
Method
                  BLASTN
NCBI GI
                  q4755185
BLAST score
                  319
E value
                  1.0e-179
Match length
                  389
% identity
                  47
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5G3 genomic
                  sequence, complete sequence
Seq. No.
                  173036
Seq. ID
                  jC-atXLIB327411P2e08a1
Method
                  BLASTX
NCBI GI
                  q3236253
BLAST score
                  599
E value
                  3.0e-62
Match length
                  116
% identity
                  98
NCBI Description
                  (AC004684) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  173037
Seq. ID
                  jC-atXLIB327411P2e10a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  43
E value
                  8.0e-15
Match length
                  65
% identity
                  94
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  173038
Seq. ID
                  jC-atXLIB327411P2e11a1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  53
E value
                  9.0e-21
                  64
Match length
% identity
                  95
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
Seq. No.
                  173039
```

23721

jC-atXLIB327411P2f09a1

BLASTN

g2244788



BLAST score 242 E value 1.0e-133 Match length 340 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 173040

Seq. ID jC-atXLIB327411P2f10a1

Method BLASTN
NCBI GI g1477479
BLAST score 49
E value 2.0e-18
Match length 125

Match length 125 % identity 92

NCBI Description Arabidopsis thaliana carbamoyl phosphate synthetase large

chain (CARB) mRNA, complete cds

Seq. No. 173041

Seq. ID jC-atXLIB327411P2g03a1

Method BLASTN
NCBI GI g2462264
BLAST score 42
E value 3.0e-14

Match length 57 % identity 97

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173042

Seq. ID jC-atXLIB327411P2g05a1

Method BLASTN
NCBI GI g3236234
BLAST score 47
E value 3.0e-17

Match length 158 % identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173043

Seq. ID jC-atXLIB327411P2g07a1

Method BLASTN
NCBI GI g4558656
BLAST score 99
E value 3.0e-48
Match length 188
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T10F5 genomic

sequence, complete sequence

Seq. No. 173044

Seq. ID jC-atXLIB327411P2g08a1

Method BLASTN
NCBI GI g2462264
BLAST score 39
E value 2.0e-12
Match length 54



```
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   173045
Seq. No.
Seq. ID
                   jC-atXLIB327411P2h05a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                   39
E value
                   2.0e-12
Match length
                  54
% identity
                   96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173046
Seq. ID
                   jC-atXLIB327411P3a04a1
Method
                  BLASTX
NCBI GI
                  g3135611
BLAST score
                   387
E value
                  3.0e-37
Match length
                  81
% identity
                  88
                  (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  173047
Seq. ID
                   jC-atXLIB327411P3a04b1
Method
                  BLASTN
                  g3135610
NCBI GI
BLAST score
                  63
E value
                  1.0e-26
Match length
                  99
% identity
                  92
NCBI Description Arabidopsis thaliana cellulose synthase mRNA, partial cds
Seq. No.
                  173048
Seq. ID
                  jC-atXLIB327411P3a07a1
Method
                  BLASTN
NCBI GI
                  g3128137
BLAST score
                  99
E value
                  4.0e-48
Match length
                  221
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173049
Seq. ID
                  jC-atXLIB327411P3a08a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  55
E value
                  6.0e-22
Match length
                  63
% identity
                  97
NCBI Description Cloning vector pSport1, complete cds
```

Seq. No. 173050

Seq. ID jC-atXLIB327411P3a09a1

Method BLASTN

BLAST score

% identity

E value Match length 47 3.0e-17

59

95



```
NCBI GI
                  g2351065
BLAST score
                  371
                  0.0e + 00
E value
Match length
                  411
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHF15, complete sequence [Arabidopsis thaliana]
                  173051
Seq. No.
Seq. ID
                  jC-atXLIB327411P3a10a1
                  BLASTN
Method
                  q531828
NCBI GI
BLAST score
                  56
                  2.0e-22
E value
Match length
                  64
                  97
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  173052
                  jC-atXLIB327411P3a10b1
Seq. ID
Method
                  BLASTN
                  q2582640
NCBI GI
BLAST score
                  50
                  4.0e-19
E value
Match length
                  74
                  93
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  173053
Seq. ID
                  jC-atXLIB327411P3a11a1
                  BLASTN
Method
NCBI GI
                  q2462264
BLAST score
                  36
E value
                  1.0e-10
Match length
                  40
                  97
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173054
Seq. ID
                  jC-atXLIB327411P3b02a1
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  54
E value
                  2.0e-21
Match length
                  54
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173055
Seq. ID
                  jC-atXLIB327411P3b05b1
Method
                  BLASTN
NCBI GI
                  g2582640
```



NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor $_{\rm E}$ RSp40

Seq.-No. 173056

Seq. ID jC-atXLIB327411P3b08b1

Method BLASTX
NCBI GI g1449179
BLAST score 336
E value 2.0e-31
Match length 147
% identity 51

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

Seq. No. 173057

Seq. ID jC-atXLIB327411P3c06a1

Method BLASTN
NCBI GI g2462264
BLAST score 40
E value 5.0e-13
Match length 51

% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173058

Seq. ID jC-atXLIB327411P3c06b1

Method BLASTN
NCBI GI g2062705
BLAST score 42
E value 3.0e-14
Match length 66

% identity 56

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 173059

Seq. ID jC-atXLIB327411P3c12a1

Method BLASTN
NCBI GI g2462264
BLAST score 46
E value 1.0e-16
Match length 50
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173060

Seq. ID jC-atXLIB327411P3d01b1

Method BLASTN
NCBI GI g2582640
BLAST score 38
E value 5.0e-12
Match length 58
% identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173061

Seq. ID jC-atXLIB327411P3d02b1



Method BLASTX
NCBI GI g3395441
BLAST score 190
E value 3.0e-14
Match length 58
% identity 53

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 173062

Seq. ID jC-atXLIB327411P3d07a1

Method BLASTN
NCBI GI g2462264
BLAST score 57
E value 4.0e-23
Match length 57

Match length 57 % identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173063

Seq. ID jC-atXLIB327411P3d07b1

Method BLASTN
NCBI GI g2582640
BLAST score 52
E value 3.0e-20
Match length 60
% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173064

Seq. ID jC-atXLIB327411P3d12a1

Method BLASTN
NCBI GI g3643588
BLAST score 274
E value 1.0e-152
Match length 415
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173065

Seq. ID jC-atXLIB327411P3d12b1

Method BLASTN
NCBI GI g3643588
BLAST score 38
E value 8.0e-12
Match length 53
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173066

Seq. ID jC-atXLIB327411P3e01a1

Method BLASTN
NCBI GI g599624
BLAST score 253
E value 1.0e-140



Match length 413 % identity 91

NCBI Description A.thaliana mRNA for aconitase (ZAPII)

>qi 2300158 emb A45785.1 A45785 Sequence 23 from Patent

WO9520046

Seq. No. 173067

Seq. ID jC-atXLIB327411P3e04b1

Method BLASTX
NCBI GI g2632254
BLAST score 572
E value 5.0e-59
Match length 136
% identity 79

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 173068

Seq. ID jC-atXLIB327411P3e05b1

Method BLASTN
NCBI GI g2656030
BLAST score 54
E value 2.0e-21
Match length 140
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUL8

Seq. No. 173069

Seq. ID jC-atXLIB327411P3e09b1

Method BLASTN
NCBI GI g2281081
BLAST score 56
E value 1.0e-22
Match length 339
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173070

Seq. ID jC-atXLIB327411P3e12a1

Method BLASTN
NCBI GI g3643588
BLAST score 104
E value 3.0e-51
Match length 176
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173071

Seq. ID jC-atXLIB327411P3e12b1

Method BLASTN
NCBI GI g3643588
BLAST score 49
E value 2.0e-18
Match length 192
% identity 83



NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173072

Seq. ID jC-atXLIB327411P3f01a1

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 2.0e-21
Match length 58
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173073

Seq. ID jC-atXLIB327411P3f04a1

Method BLASTN
NCBI GI 94757401
BLAST score 220
E value 1.0e-120
Match length 280
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 173074

Seq. ID jC-atXLIB327411P3f04b1

Method BLASTN
NCBI GI 94757401
BLAST score 38
E value 7.0e-12
Match length 150
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 173075

Seq. ID jC-atXLIB327411P3f05a1

Method BLASTN
NCBI GI g2323343
BLAST score 257
E value 1.0e-142
Match length 407
% identity 91

NCBI Description Arabidopsis thaliana alpha-glucosidase 1 (Aglu1) gene,

complete cds

Seq. No. 173076

Seq. ID jC-atXLIB327411P3f05b1

Method BLASTX
NCBI GI g2323344
BLAST score 177
E value 4.0e-13
Match length 74
% identity 55

NCBI Description (AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]

Seq. No. 173077



Seq. ID jC-atXLIB327411P3f06a1

Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 2.0e-15
Match length 44
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173078

Seq. ID jC-atXLIB327411P3f06b1

Method BLASTN
NCBI GI 94263694
BLAST score 187
E value 1.0e-100
Match length 323
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173079

Seq. ID jC-atXLIB327411P3f07a1

Method BLASTN
NCBI GI g2462264
BLAST score 43
E value 8.0e-15
Match length 43
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173080

Seq. ID jC-atXLIB327411P3f09a1

Method BLASTX
NCBI GI g2498329
BLAST score 287
E value 1.0e-25
Match length 84
% identity 71

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571

pattern-formation protein GNOM - Arabidopsis thaliana
>gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 173081

Seq. ID jC-atXLIB327411P3f10a1

Method BLASTN
NCBI GI g2351067
BLAST score 430
E value 0.0e+00
Match length 430
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MPO12, complete sequence [Arabidopsis thaliana]

Method

NCBI GI

BLASTN

g2462264



```
Seq. No.
                  173082
Seq. ID
                  jC-atXLIB327411P3g03a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  36
E value
                  1.0e-10
Match length
                  44
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173083
Seq. No.
Seq. ID
                  jC-atXLIB327411P3g03b1
                  BLASTX
Method
NCBI GI
                  g4220512
BLAST score
                  292
E value
                  3.0e-26
Match length
                  91
% identity
                  63
                  (AL035356) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                  173084
Seq. No.
Seq. ID
                  jC-atXLIB327411P3g04a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  50
                  6.0e-19
E value
Match length
                  54
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173085
Seq. No.
                  jC-atXLIB327411P3g05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351065
                  289
BLAST score
                  1.0e-161
E value
                  399
Match length
                  93
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHF15, complete sequence [Arabidopsis thaliana]
                  173086
Seq. No.
                  jC-atXLIB327411P3g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122753
BLAST score
                  88
E value
                  3.0e-39
                  102
Match length
                  84
% identity
                  60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb CAB10211.1
NCBI Description
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  173087
                   jC-atXLIB327411P3g09a1
Seq. ID
```



```
BLAST score
                  41
                  1.0e-13
E value
Match length
                  41
% identity
                  100
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                  173088
                  jC-atXLIB327411P3g10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  41
                  1.0e-13
E value
Match length
                  41
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173089
Seq. ID
                  jC-atXLIB327411P3h02a1
Method
                  BLASTN
NCBI GI
                  q4417264
BLAST score
                  190
                  1.0e-102
E value
Match length
                  298
% identity
                  91
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173090
Seq. ID
                  jC-atXLIB327411P3h08b1
Method
                  BLASTX
                  g2341032
NCBI GI
                  325
BLAST score
                  3.0e-30
E value
Match length
                  108
                  58
% identity
                  (AC000104) EST gb_ATTS0956 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                  173091
Seq. No.
                  jC-atXLIB327411P3h09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618601
BLAST score
                  116
                  2.0e-58
E value
                  304
Match length
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173092
                   jC-atXLIB327411P3h12a1
Seq. ID
```

Method BLASTX NCBI GI q1755166 BLAST score 476 9.0e-48 E value Match length 111 82 % identity



```
NCBI Description (U75194) germin-like protein [Arabidopsis thaliana]
                  173093
Seq. No.
Seq. ID
                  jC-atXLIB327412P1a01b1
Method
                  BLASTN
NCBI GI
                  q2582640
                  39
BLAST score
E value
                  2.0e-12
Match length
                  43
% identity
                  98
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  173094
Seq. No.
Seq. ID
                  jC-atXLIB327412P1a04b1
Method
                  BLASTX
NCBI GI
                  g1402916
BLAST score
                  237
E value
                  9.0e-20
                  77
Match length
                  62
% identity
NCBI Description
                  (X98319) peroxidase [Arabidopsis thaliana]
                  >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a
                  [Arabidopsis thaliana]
Seq. No.
                  173095
                  jC-atXLIB327412P1a06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  55
                  6.0e-22
E value
Match length
                  59
                  98
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  173096
Seq. ID
                  jC-atXLIB327412P1a09b1
Method
                  BLASTN
NCBI GI
                  g2435510
BLAST score
                  228
E value
                  1.0e-125
Match length
                  336
% identity
                  92
NCBI Description Arabidopsis thaliana BAC TM017A05
Seq. No.
                  173097
```

Seq. ID jC-atXLIB327412P1a12b1

Method BLASTN NCBI GI g3941523 BLAST score 37 E value 2.0e-11 Match length 45 96 % identity

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds



```
173098
Seq. No.
Seq. ID
                  jC-atXLIB327412P1b01a1
Method
                  BLASTN
NCBI GI
                  q3046852
BLAST score
                  173
                  2.0e-92
E value
                  388
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ16, complete sequence [Arabidopsis thaliana]
                  173099
Seq. No.
Seq. ID
                  jC-atXLIB327412P1b01b1
                  BLASTN
Method
                  q3046852
NCBI GI
BLAST score
                  91
E value
                  2.0e-43
                  319
Match length
% identity
                  90
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ16, complete sequence [Arabidopsis thaliana]
                  173100
Seq. No.
Seq. ID
                  jC-atXLIB327412P1b02a1
                  BLASTN
Method
                  g2290120
NCBI GI
BLAST score
                  48
                  8.0e-18
E value
Match length
                  64
% identity
                  94
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  173101
Seq. ID
                   jC-atXLIB327412P1b03a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  38
E value
                  8.0e-12
Match length
                   42
% identity
                  98
NCBI Description
                  Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173102
Seq. ID
                  jC-atXLIB327412P1b03b1
Method
                  BLASTN
                  g4589438
NCBI GI
BLAST score
                  63
                  1.0e-26
E value
                  87
```

Match length 94 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MQJ2, complete sequence

Seq. No. 173103

jC-atXLIB327412P1b04a1 Seq. ID

Method BLASTN

BLAST score

E value Match length 525 2.0e-53

161



```
NCBI GI
                  g531828
BLAST score -
                  33
                  7.0e-09
E value
Match length
                  33
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
                  173104
Seq. No.
                  iC-atXLIB327412P1b05a1
Seq. ID
Method
                  BLASTN
                  g540252
NCBI GI
                  33
BLAST score
E value
                  6.0e-09
                  33
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  173105
Seq. ID
                  jC-atXLIB327412P1b05b1
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                  53
                  8.0e-21
E value
Match length
                  73
% identity
                  93
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  173106
Seq. ID
                  jC-atXLIB327412P1b06a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  37
E value
                  2.0e-11
Match length
                  41
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173107
                  jC-atXLIB327412P1b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402916
BLAST score
                  182
                  1.0e-13
E value
                  89
Match length
                  54
% identity
                  (X98319) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1429217_emb_CAA67311 (X98775) peroxidase ATP12a
                   [Arabidopsis thaliana]
                  173108
Seq. No.
                  jC-atXLIB327412P1b07b1
Seq. ID
Method
                  BLASTX
                  g3142303
NCBI GI
```



% identity 68

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug

resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 173109

Seq. ID jC-atXLIB327412P1b08b1

Method BLASTX
NCBI GI g115783
BLAST score 439
E value 2.0e-43
Match length 157
% identity 61

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 173110

Seq. ID jC-atXLIB327412P1b11b1

Method BLASTN
NCBI GI g2582640
BLAST score 41
E value 1.0e-13

E value 1.0e Match length 69 % identity 90

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173111

Seq. ID jC-atXLIB327412P1b12a1

Method BLASTN
NCBI GI g2462264
BLAST score 34
E value 2.0e-09
Match length 42
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173112

Seq. ID jC-atXLIB327412P1c02b1

Method BLASTN
NCBI GI g1103321
BLAST score 37
E value 3.0e-11
Match length 49
% identity 94

NCBI Description A.thaliana CKI3 mRNA for casein kinase I

Seq. No. 173113

Seq. ID jC-atXLIB327412P1c07b1

Method BLASTN
NCBI GI g2582640
BLAST score 42
E value 2.0e-14
Match length 50



% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173114

Seq. ID jC-atXLIB327412P1c08b1

Method BLASTN
NCBI GI g2564050
BLAST score 167
E value 9.0e-89
Match length 347
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 173115

Seq. ID jC-atXLIB327412P1c10b1

Method BLASTN
NCBI GI g2582640
BLAST score 56
E value 2.0e-22
Match length 72
% identity 94

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173116

Seq. ID jC-atXLIB327412P1d05a1

Method BLASTN
NCBI GI 94468976
BLAST score 145
E value 1.0e-75
Match length 395
% identity 86

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18

(ESSA project)

Seq. No. 173117

Seq. ID jC-atXLIB327412P1d06a1

Method BLASTN
NCBI GI g4468801
BLAST score 263
E value 1.0e-146
Match length 407
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17

(ESSA project)

Seq. No. 173118

Seq. ID jC-atXLIB327412P1d08a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 5.0e-19
Match length 54
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
173119
Seq. No.
Seq. ID
                  jC-atXLIB327412P1d11b1
                  BLASTN
Method
                  g2582640
NCBI GI
                  38
BLAST score
                  8.0e-12
E value
Match length
                  46
                  96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173120
Seq. No.
Seq. ID
                  jC-atXLIB327412P1d12a1
                  BLASTN
Method
NCBI GI
                  g3702735
BLAST score
                  118
E value
                  1.0e-59
Match length
                  178
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQL5, complete sequence [Arabidopsis thaliana]
                  173121
Seq. No.
Seq. ID
                  jC-atXLIB327412P1d12b1
                  BLASTX
Method
NCBI GI
                  g4586580
                  143
BLAST score
E value
                  2.0e-11
Match length
                  89
% identity
                  55
                  (AB024994) rab-type small GTP-binding protein [Cicer
NCBI Description
                  arietinum]
Seq. No.
                  173122
Seq. ID
                  jC-atXLIB327412P1e09b1
Method
                  BLASTN
NCBI GI
                  q3241922
BLAST score
                  111
E value
                  2.0e-55
Match length
                  398
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173123
                  jC-atXLIB327412P1e11b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  41
E value
                  1.0e-13
                  57
Match length
                  93
% identity
```

Seq. No. 173124

factor, RSp40

NCBI Description

Arabidopsis thaliana mRNA for arginine/serine-rich splicing



jC-atXLIB327412P1f08a1 Seq. ID BLASTX Method g1134882 NCBI GI BLAST score 396 2.0e-38 E value 78 Match length % identity 85 (Z68291) cysteine protease [Pisum sativum] NCBI Description Seq. No. 173125 Seq. ID jC-atXLIB327412P1f09b1

Seq. ID JC-atxLIB3
Method BLASTN
NCBI GI g4490717
BLAST score 243
E value 1.0e-134

E value 1.0e-13
Match length 346
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 173126

Seq. ID jC-atXLIB327412P1f12b1

Method BLASTN
NCBI GI g3702735
BLAST score 44
E value 2.0e-15
Match length 68
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQL5, complete sequence [Arabidopsis thaliana]

Seq. No. 173127

Seq. ID jC-atXLIB327412P1g05b1

Method BLASTN
NCBI GI g2582640
BLAST score 66
E value 8.0e-29
Match length 70
% identity 99

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173128

Seq. ID jC-atXLIB327412P1h09b1

Method BLASTN
NCBI GI g527628
BLAST score 66
E value 1.0e-28
Match length 106
% identity 91

NCBI Description Arabidopsis thaliana clone HAT22 homeobox protein mRNA,

complete cds

Seq. No. 173129

Seq. ID jC-atXLIB327412P1h12b1

Method BLASTN NCBI GI 93941523



BLAST score 33 8.0e-09 E value Match length 45 % identity 93 Arabidopsis thaliana putative transcription factor (MYB92) NCBI Description mRNA, complete cds Seq. No. 173130 jC-atXLIB327412P2b06a1 Seq. ID Method BLASTN NCBI GI g2351071 BLAST score 195 E value 1.0e-105 Match length 263 97 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana] Seq. No. 173131 Seq. ID jC-atXLIB327412P2b07b1 Method BLASTN NCBI GI g2582640 BLAST score 44 E value 2.0e-15 Match length 48 % identity 98 NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40 Seq. No. 173132 jC-atXLIB327412P2b11a1 Seq. ID Method BLASTN g540252 NCBI GI 55 BLAST score 6.0e-22 E value 59 Match length 98 % identity NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds Seq. No. 173133 jC-atXLIB327412P2d01a1 Seq. ID BLASTN Method NCBI GI g2462264 BLAST score 40 5.0e-13 E value 44 Match length 98 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 173134 Seq. No.

Seq. ID jC-atXLIB327412P2d05b1

Method BLASTN
NCBI GI g2582640
BLAST score 66
E value 2.0e-28
Match length 77
% identity 97



NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 173135

Seq. ID jC-atXLIB327412P2d08b1

Method BLASTX
NCBI GI g3193284
BLAST score 169
E value 8.0e-12
Match length 83

% identity 46

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 173136

Seq. ID jC-atXLIB327412P2d10a1

Method BLASTN
NCBI GI g3702737
BLAST score 101
E value 2.0e-49
Match length 310
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSN2, complete sequence [Arabidopsis thaliana]

Seq. No. 173137

Seq. ID jC-atXLIB327412P2e03a1

Method BLASTN
NCBI GI g2462264
BLAST score 39
E value 2.0e-12
Match length 47
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173138

Seq. ID jC-atXLIB327412P2f03a1

Method BLASTN
NCBI GI g398601
BLAST score 251
E value 1.0e-139
Match length 374
% identity 94

NCBI Description A.thaliana ATAF2 mRNA

Seq. No. 173139

Seq. ID jC-atXLIB327412P2f09a1

Method BLASTN
NCBI GI g2462264
BLAST score 37
E value 3.0e-11
Match length 41
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173140

Seq. ID jC-atXLIB327412P2f09b1

Method BLASTN



```
NCBI GI
                  q3800746
BLAST score
                  37
E value
                  3.0e-11
Match length
                  45
% identity
                  96
NCBI Description
                  Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                  complete cds
Seq. No.
                  173141
Seq. ID
                  jC-atXLIB327412P3a03b1
Method
                  BLASTX
NCBI GI
                  g2191153
BLAST score
                   606
                  5.0e-63
E value
Match length
                  136
                  70
% identity
NCBI Description
                  (AF007269) contains similarity to blue copper proteins
                   [Arabidopsis thaliana]
                  173142
Seq. No.
Seq. ID
                  jC-atXLIB327412P3b09a1
Method
                  BLASTN
NCBI GI
                  q3293582
BLAST score
                  81
E value
                  2.0e-37
Match length
                  105
% identity
                  95
NCBI Description Arabidopsis thaliana BAC T15F16
Seq. No.
                  173143
                  jC-atXLIB327412P3c12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2154608
BLAST score
                  53
                  7.0e-21
E value
Match length
                  167
                  91
% identity
NCBI Description Arabidopsis thaliana EXGT-A3 mRNA for endoxyloglucan
                  transferase related protein, complete cds
                  173144
Seq. No.
                  jC-atXLIB327412P3e12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519190
BLAST score
                  251
                  1.0e-139
E value
                  397
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K6A12, complete sequence
Seq. No.
                  173145
                  jC-atXLIB327412P4a02a1
Seq. ID
```

Method BLASTN g414340 NCBI GI BLAST score 76 E value 2.0e-34



```
180
Match length
% identity
                  86
                 A.thaliana rd21A gene for thiol protease, complete cds
NCBI Description
                  173146
Seq. No.
Seq. ID
                  jC-atXLIB327412P4b12a1
                  BLASTX
Method
NCBI GI
                  q4056437
                  209
BLAST score
                  2.0e-16
E value
                  88
Match length
                  52
% identity
                  (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
NCBI Description
                  protein kinase domain. [Arabidopsis thaliana]
                  173147
Seq. No.
Seq. ID
                  jC-atXLIB327412P4d02a1
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
Match length
                  55
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173148
Seq. No.
Seq. ID
                  jC-atXLIB327412P4f04a1
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  51
                  1.0e-19
E value
                  55
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173149
Seq. No.
                  jC-atXLIB327412P4g02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2462264
BLAST score
                   49
                   2.0e-18
E value
Match length
                  57
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   173150
                   jC-atXLIB327412P4h02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1235716
BLAST score
                   95
                   6.0e-46
E value
                  131
Match length
% identity
                   94
NCBI Description Arabidopsis thaliana mRNA for calcium-dependent protein
                  kinase (CDPK), complete cds
```

23742

173151

Seq. No.



```
jC-atXLIB327413P1a02a1
Seq. ID
Method
                  BLASTN
                  q2462264
NCBI GI
BLAST score
                  50
E value
                  2.0e-19
                  54
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173152
Seq. No.
                  jC-atXLIB327413P1a03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1839239
BLAST score
                  108
                  8.0e-54
E value
                  136
Match length
% identity
                  95
NCBI Description Arabidopsis thaliana aVps41p (AVPS41) gene, partial cds
Seq. No.
                  173153
                  jC-atXLIB327413P1a04a1
Seq. ID
                  BLASTN
Method
                  q4455339
NCBI GI
BLAST score
                  75
                  4.0e-34
E value
                  180
Match length
                   93
% identity
                 Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
NCBI Description
                   (ESSAII project)
Seq. No.
                  173154
Seq. ID
                   jC-atXLIB327413P1a06a1
Method
                  BLASTN
NCBI GI
                  q3242970
BLAST score
                  54
                  2.0e-21
E value
Match length
                  114
% identity
                   89
NCBI Description
                  Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM,
                   complete sequence [Arabidopsis thaliana]
                   173155
Seq. No.
                   jC-atXLIB327413P1a07b1
Seq. ID
                  BLASTN
                   q4589434
                   129
BLAST score
                   4.0e-66
E value
Match length
                   148
                   97
```

Method NCBI GI

% identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ7, complete sequence

173156 Seq. No.

Seq. ID jC-atXLIB327413P1a08a1

Method BLASTN g531828 NCBI GI BLAST score 34



```
E value
                  2.0e-09
Match length
                  34
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  173157
Seq. ID
                  jC-atXLIB327413P1a09a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  43
                  8.0e-15
E value
Match length
                  47
% identity
                  98
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  173158
Seq. No.
                  jC-atXLIB327413P1a10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  48
                  9.0e-18
E value
                  75
Match length
                  93
% identity
NCBI Description Cloning vector pSport1, complete cds
                   173159
Seq. No.
Seq. ID
                   jC-atXLIB327413P1a10b1
Method
                   BLASTN
NCBI GI
                   q4662609
BLAST score
                   127
                   6.0e-65
E value
Match length
                   127
% identity
                   100
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
NCBI Description
                   complete sequence
                   173160
Seq. No.
                   jC-atXLIB327413P1b02b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   44
                   2.0e-15
E value
                   74
Match length
                   91
% identity
NCBI Description
                   factor, RSp40
```

Arabidopsis thaliana mRNA for arginine/serine-rich splicing

Seq. No. 173161

jC-atXLIB327413P1b03a1 Seq. ID

BLASTN Method g531828 NCBI GI BLAST score 42 3.0e-14E value Match length 46 98 % identity

NCBI Description Cloning vector pSport1, complete cds



Seq. No. 173162

Seq. ID jC-atXLIB327413P1b04a1

Method BLASTN
NCBI GI g3510336
BLAST score 120
E value 6.0e-61
Match length 233
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 173163

Seq. ID jC-atXLIB327413P1b06b1

Method BLASTN
NCBI GI g2582640
BLAST score 62

E value 4.0e-26 Match length 74 % identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173164

Seq. ID jC-atXLIB327413P1b07b1

Method BLASTN
NCBI GI g2582640
BLAST score 67
E value 4.0e-29
Match length 71
% identity 99

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173165

Seq. ID jC-atXLIB327413P1b08b1

Method BLASTX
NCBI GI g2829903
BLAST score 202
E value 1.0e-15
Match length 54
% identity 78

NCBI Description (AC002311) unknown protein [Arabidopsis thaliana]

Seq. No. 173166

Seq. ID jC-atXLIB327413P1b10a1

Method BLASTN
NCBI GI g531828
BLAST score 52
E value 3.0e-20
Match length 60
% identity 97

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 173167

Seq. ID jC-atXLIB327413P1b12b1

Method BLASTX NCBI GI g4490749



BLAST score 782 1.0e-83 E value Match length 147 % identity 100

(AL035708) 2-dehydro-3-deoxyphosphoheptonate aldolase NCBI Description

[Arabidopsis thaliana]

Seq. No. 173168

jC-atXLIB327413P1c02a1 Seq. ID

Method BLASTN NCBI GI g4753195 BLAST score 69 2.0e-30 E value Match length 214 % identity 90

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 173169

jC-atXLIB327413P1c04a1 Seq. ID

Method BLASTN NCBI GI g2462264 BLAST score 45 4.0e-16 E value

Match length 53 % identity 96

Cucumis sativus mRNA for patatin-like protein, partial NCBI Description

Seq. No. 173170

jC-atXLIB327413P1c05a1 Seq. ID

BLASTN Method g2656027 NCBI GI BLAST score 33 5.0e-09 E value 77 Match length

86 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJH22

173171 Seq. No.

jC-atXLIB327413P1c07a1 Seq. ID

Method BLASTN NCBI GI q4519188 BLAST score 129 E value 4.0e-66 Match length 223 96 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L19, complete sequence

Seq. No. 173172

Seq. ID jC-atXLIB327413P1c12a1

Method BLASTN NCBI GI g2462264 BLAST score 41 E value 1.0e-13 Match length 49



% identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial Seq. No. 173173 jC-atXLIB327413P1d04a1 Seq. ID BLASTX Method NCBI GI g4406808 BLAST score 402 E value 4.0e-39 Match length 94 82 % identity NCBI Description (AC006201) unknown protein [Arabidopsis thaliana] 173174 Seq. No. Seq. ID jC-atXLIB327413P1d07b1 BLASTN Method NCBI GI g3985931 BLAST score 62 1.0e-26 E value 66 Match length % identity 98 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K21H1, complete sequence [Arabidopsis thaliana] 173175 Seq. No. Seq. ID jC-atXLIB327413P1d09a1 Method BLASTN g540252 NCBI GI BLAST score 43 8.0e-15 E value Match length 43 100 % identity NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds Seq. No. 173176 jC-atXLIB327413P1d10a1 Seq. ID Method BLASTN NCBI GI g2462264 BLAST score 49 E value 2.0e-18 Match length 52 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 173177 Seq. No. Seq. ID jC-atXLIB327413P1d11a1 Method BLASTN

NCBI GI g2795802 BLAST score 119 E value 3.0e-60 Match length 238 96 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F17A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173178

jC-atXLIB327413P1d12b1 Seq. ID



BLASTN Method NCBI GI g2582640 40 BLAST score 5.0e-13E value Match length 48 % identity 96

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

173179 Seq. No.

jC-atXLIB327413P1e01b1 Seq. ID

BLASTN Method NCBI GI g2582640 BLAST score 56 1.0e-22 E value Match length 71

% identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

173180 Seq. No.

Seq. ID jC-atXLIB327413P1e02b1

94

Method BLASTN NCBI GI g2582640 BLAST score 60 6.0e-25 E value Match length 76 95 % identity

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

173181 Seq. No.

Seq. ID jC-atXLIB327413P1e05b1

Method BLASTN NCBI GI g4262221 BLAST score 148 E value 2.0e-77 Match length 188 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

173182 Seq. No.

jC-atXLIB327413P1e06a1 Seq. ID

Method BLASTN NCBI GI g2326366 82 BLAST score 4.0e-38 E value Match length 179 91 % identity

NCBI Description Arabidopsis thaliana mRNA for hypothetical protein SEB2,

partial

173183 Seq. No.

Seq. ID jC-atXLIB327413P1e06b1

BLASTN Method NCBI GI g2582640



```
BLAST score
                   38
                   8.0e-12
E value
                   44
Match length
                  95
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173184
Seq. No.
                   jC-atXLIB327413P1e07a1
Seq. ID
                  BLASTN
Method
                   g2462264
NCBI GI
BLAST score
                   48
                  8.0e-18
E value
                  52
Match length
% identity
                  98
NCBI Description
                  Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173185
                   jC-atXLIB327413P1e10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2462264
BLAST score
                   52
E value
                   4.0e-20
                   52
Match length
                   100
% identity
                 Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                  173186
Seq. ID
                   jC-atXLIB327413P1e11a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  51
E value
                   1.0e-19
                  55
Match length
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   173187
                   jC-atXLIB327413P1f04a1
Seq. ID
Method
                   BLASTN
                   g2462264
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   40
                   97
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   173188
                   jC-atXLIB327413P1f07a1
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 2.0e-15
Match length 48
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
173189
Seq. No.
Seq. ID
                  jC-atXLIB327413P1f08a1
                  BLASTN
Method
                  g540252
NCBI GI
                  43
BLAST score
                  8.0e-15
E value
                  43
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  173190
Seq. No.
                  jC-atXLIB327413P1f10a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  39
                  1.0e-12
E value
                  47
Match length
                  96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173191
                  jC-atXLIB327413P1f11b1
Seq. ID
                  BLASTN
Method
                  q2582640
NCBI GI
BLAST score
                  52
E value
                  1.0e-20
                  72
Match length
                  94
% identity
                 Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173192
Seq. No.
Seq. ID
                  jC-atXLIB327413P1f12b1
                  BLASTX
Method
NCBI GI
                  q4558664
                  144
BLAST score
                  8.0e-09
E value
                  104
Match length
% identity
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  173193
                  jC-atXLIB327413P1g06a1
Seq. ID
                  BLASTN
Method
                  q4757392
NCBI GI
BLAST score
                  33
                  2.0e-09
E value
                  49
Match length
                  92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
```

Seq. No. 173194

Seq. ID jC-atXLIB327413P1g07b1

Method BLASTN NCBI GI g18057 BLAST score 224



```
E value
                   1.0e-123
Match length
                   284
                   95
% identity
```

NCBI Description Citrus limon 26S ribosomal RNA gene 3' region

173195 Seq. No.

jC-atXLIB327413P1g11a1 Seq. ID

Method BLASTN NCBI GI q2462264 BLAST score 40 5.0e-13E value Match length 40 % identity 100

Cucumis sativus mRNA for patatin-like protein, partial NCBI Description

173196 Seq. No.

Seq. ID jC-atXLIB327413P1g12a1

BLASTN Method NCBI GI g2832354 49 BLAST score 2.0e-18 E value 149 Match length % identity 88

NCBI Description Arabidopsis thaliana mRNA for HMG gamma protein

173197 Seq. No.

jC-atXLIB327413P1h01b1 Seq. ID

BLASTN Method NCBI GI q2582640 BLAST score 52 E value 4.0e-20 Match length 71 % identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

173198 Seq. No.

jC-atXLIB327413P1h02b1 Seq. ID

Method BLASTN g2582640 NCBI GI BLAST score 71 2.0e-31 E value 75 Match length 99 % identity

Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description

factor, RSp40

173199 Seq. No.

jC-atXLIB327413P1h09b1 Seq. ID

Method BLASTN NCBI GI g4056429 BLAST score 40 E value 5.0e-13Match length 74 97 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC F508 sequence,

complete sequence [Arabidopsis thaliana]



Seq. No. 173200

Seq. ID jC-atXLIB327413P1h10b1

Method BLASTX
NCBI GI 93522961
BLAST score 662
E value 2.0e-69
Match length 124
% identity 99

NCBI Description (AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No. 173201

Seq. ID jC-atXLIB327413P1h12a1

Method BLASTN
NCBI GI g2462264
BLAST score 37
E value 3.0e-11

Match length 45 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173202

Seq. ID jC-atXLIB327413P2a01b1

Method BLASTN
NCBI GI g4159704
BLAST score 189
E value 1.0e-102
Match length 231
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MCB17, complete sequence

Seq. No. 173203

Seq. ID jC-atXLIB327413P2a05b1

Method BLASTX
NCBI GI g2129541
BLAST score 525
E value 3.0e-53
Match length 137
% identity 77

NCBI Description ATPK19 protein - Arabidopsis thaliana >gi 914079 bbs 160872

ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis

thaliana, Peptide, 471 aa] >gi 867995 dbj BAA07661

(D42061) ribosomal-protein S6 kinase homolog [Arabidopsis

thaliana]

Seq. No. 173204

Seq. ID jC-atXLIB327413P2a07b1

Method BLASTN
NCBI GI g2582640
BLAST score 43
E value 7.0e-15
Match length 50
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40



Seq. No. 173205

Seq. ID jC-atXLIB327413P2a08b1

Method BLASTN
NCBI GI g1050427
BLAST score 131
E value 3.0e-67
Match length 263
% identity 88

NCBI Description A.thaliana mRNA for an exon from SNAP25A protein

Seq. No. 173206

Seq. ID jC-atXLIB327413P2a10b1

Method BLASTN
NCBI GI g3859658
BLAST score 121
E value 2.0e-61
Match length 125
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 173207

Seq. ID jC-atXLIB327413P2a11b1

Method BLASTN
NCBI GI g4159710
BLAST score 73
E value 9.0e-33

E value 9.0e-Match length 102 % identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSD23, complete sequence

Seq. No. 173208

Seq. ID jC-atXLIB327413P2b05b1

Method BLASTN
NCBI GI g2842474
BLAST score 75
E value 6.0e-34
Match length 75
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 173209

Seq. ID jC-atXLIB327413P2b06b1

Method BLASTN
NCBI GI g3757512
BLAST score 42
E value 3.0e-14
Match length 42
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F12A24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173210

Seq. ID jC-atXLIB327413P2b07b1

Method BLASTN

NCBI GI

E value

BLAST score

Match length

g4159704 182

9.0e-98

418



```
g2582640
NCBI GI
BLAST score
                  35
                  5.0e-10
E value
Match length
                  43
                  95
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  173211
Seq. No.
Seq. ID
                  jC-atXLIB327413P2b09a1
Method
                  BLASTN
                  q2290120
NCBI GI
BLAST score
                  55
                  6.0e-22
E value
                  62
Match length
                  97
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  173212
Seq. No.
                  jC-atXLIB327413P2b10a1
Seq. ID
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  45
                  5.0e-16
E value
                  45
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173213
                   jC-atXLIB327413P2b10b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2252848
BLAST score
                  83
E value
                   1.0e-38
Match length
                  231
% identity
                   87
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                   173214
Seq. ID
                   jC-atXLIB327413P2b11b1
Method
                   BLASTN
                   g4469002
NCBI GI
                   79
BLAST score
E value
                   3.0e-36
                   83
Match length
                   99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                   (ESSA project)
Seq. No.
                   173215
                   jC-atXLIB327413P2c01a1
Seq. ID
                   BLASTN
Method
```



% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence Seq. No. 173216 jC-atXLIB327413P2c01b1 Seq. ID BLASTN Method g2582640 NCBI GI 49 BLAST score 2.0e-18 E value 57 Match length 96 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 173217 Seq. No. Seq. ID jC-atXLIB327413P2c02a1 BLASTN Method NCBI GI g2462264 54 BLAST score 2.0e-21 E value 54 Match length 100 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 173218 Seq. No. jC-atXLIB327413P2c02b1 Seq. ID BLASTN Method NCBI GI q2582640 BLAST score 41 1.0e-13 E value Match length 52 96 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 173219 Seq. No. Seq. ID jC-atXLIB327413P2c03b1 Method BLASTN NCBI GI g3941523 BLAST score 33 7.0e-09 E value 51 Match length 92 % identity Arabidopsis thaliana putative transcription factor (MYB92) NCBI Description mRNA, complete cds 173220 Seq. No. jC-atXLIB327413P2c05a1 Seq. ID BLASTN Method NCBI GI

Method BLASTN
NCBI GI g2264320
BLAST score 66
E value 2.0e-28
Match length 150
% identity 26

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI10, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  173221
Seq. ID
                  jC-atXLIB327413P2c06b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  36
                  9.0e-11
E value
Match length
                  40
                  97
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  173222
                  jC-atXLIB327413P2c07a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
Match length
                  51
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173223
Seq. No.
Seq. ID
                  jC-atXLIB327413P2c09b1
Method
                  BLASTN
                  g2494106
NCBI GI
BLAST score
                  70 -
                  6.0e-31
E value
Match length
                  84
% identity
                  53
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  173224
Seq. No.
Seq. ID
                  jC-atXLIB327413P2c10b1
Method
                  BLASTN
NCBI GI
                  g4589413
BLAST score
                  67
E value
                  4.0e-29
Match length
                  75
% identity
                  97
                 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K10D11, complete sequence
Seq. No.
                  173225
                  jC-atXLIB327413P2d01b1
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g2582640
BLAST score 41
E value 1.0e-13
Match length 48
% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173226

Seq. ID jC-atXLIB327413P2d02a1



```
Method
                  BLASTN
                  g3510337
NCBI GI
BLAST score
                  250
                  1.0e-138
E value
Match length
                  390
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E20, complete sequence [Arabidopsis thaliana]
                  173227
Seq. No.
Seq. ID
                  jC-atXLIB327413P2d02b1
                  BLASTN
Method
NCBI GI
                  g3510337
BLAST score
                  135
                  1.0e-69
E value
                  135
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E20, complete sequence [Arabidopsis thaliana]
                  173228
Seq. No.
Seq. ID
                  jC-atXLIB327413P2d03b1
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  40
                  5.0e-13
E value
                   47
Match length
                  98
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   173229
Seq. No.
                   jC-atXLIB327413P2d05a1
Seq. ID
Method
                  BLASTX
                  g3377799
NCBI GI
                  89
BLAST score
                   7.0e-11
E value
Match length
                   69
                   67
% identity
                  (AF075597) No definition line found [Arabidopsis thaliana]
NCBI Description
                   173230
Seq. No.
                   jC-atXLIB327413P2d05b1
Seq. ID
Method
                   BLASTX
                   g3377799
NCBI GI
                   225
BLAST score
                   2.0e-18
E value
                   44
Match length
                   52
% identity
NCBI Description (AF075597) No definition line found [Arabidopsis thaliana]
                   173231
Seq. No.
                   jC-atXLIB327413P2d07a1
```

Method BLASTN

g2290120 NCBI GI 55 BLAST score 5.0e-22 E value

Seq. ID

% identity



```
Match length
                  62
                  97
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  173232
Seq. No.
Seq. ID
                  jC-atXLIB327413P2d11b1
Method
                  BLASTN
NCBI GI
                  q4584387
BLAST score
                  143
                  2.0e-74
E value
                  143
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
                  (ESSA project)
                  173233
Seq. No.
Seq. ID
                  jC-atXLIB327413P2e01a1
Method
                  BLASTN
NCBI GI
                  g2459406
                  38
BLAST score
                  7.0e-12
E value
                  78
Match length
                  88
% identity
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  173234
Seq. No.
Seq. ID
                  jC-atXLIB327413P2e04b1
Method
                  BLASTN
NCBI GI
                  q4589410
BLAST score
                  42
                  1.0e-14
E value
Match length
                  57
% identity
                  95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2015, complete sequence
Seq. No.
                  173235
Seq. ID
                   jC-atXLIB327413P2e05a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  33
                  8.0e-09
E value
Match length
                   48
% identity
                   96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   173236
Seq. No.
Seq. ID
                   jC-atXLIB327413P2e06b1
                   BLASTN
Method
NCBI GI
                   g3800746
                   35
BLAST score
                  2.0e-10
E value
                   42
Match length
```

23758

NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,



complete cds

```
Seq. No.
                  173237
Seq. ID
                  jC-atXLIB327413P2e08b1
Method
                  BLASTN
                  g3849811
NCBI GI
                  47
BLAST score
                  3.0e-17
E value
Match length
                  63
                  94
% identity
                  Arabidopsis thaliana chromosome I BAC T2P11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  173238
Seq. No.
Seq. ID
                  jC-atXLIB327413P2e11b1
                  BLASTN
Method
                  g3298610
NCBI GI
BLAST score
                  126
                  2.0e-64
E value
Match length
                  129
                  99
% identity
NCBI Description Arabidopsis thaliana BAC T2H3
                  173239
Seq. No.
Seq. ID
                   jC-atXLIB327413P2f01b1
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                   59
E value
                  8.0e-25
Match length
                   63
                   98
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
Seq. No.
                   173240
                   jC-atXLIB327413P2f04b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4185128
BLAST score
                   68
                   7.0e-30
E value
Match length
                   110
% identity
                   46
                   Arabidopsis thaliana chromosome II P1 MSF3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   173241
Seq. No.
                   jC-atXLIB327413P2f05b1
Seq. ID
                   BLASTN
Method
                   g3046847
NCBI GI
                   85
·BLAST score
                   7.0e-40
E value
                   97
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
                   K11J9, complete sequence [Arabidopsis thaliana]
```

173242

Seq. No.

Match length

% identity

103 97



```
jC-atXLIB327413P2f07b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  47
                  4.0e-17
E value
                  59
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  173243
Seq. No.
Seq. ID
                  jC-atXLIB327413P2f10b1
                  BLASTN
Method
                  q4406790
NCBI GI
                  82
BLAST score
                  4.0e-38
E value
                  94
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T1016 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  173244
Seq. No.
Seq. ID
                  jC-atXLIB327413P2f12b1
                  BLASTX
Method
                  g2495179
NCBI GI
BLAST score
                  269
E value
                  2.0e-23
                  52
Match length
                  98
% identity
NCBI Description PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
                  (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                  SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane
                  synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana
                  >gi 313150 emb CAA51941 (X73535) hydroxymethylbilane
                  synthase [Arabidopsis thaliana] >gi 313838 emb CAA52061
                  (X73839) hydroxymethylbilane synthase [Arabidopsis
                  thaliana]
Seq. No.
                  173245
Seq. ID
                  jC-atXLIB327413P2g09b1
Method
                  BLASTN
NCBI GI
                  q3800746
BLAST score
                  38
E value
                  7.0e-12
Match length
                  49
% identity
                  94
NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                  complete cds
Seq. No.
                  173246
Seq. ID
                  jC-atXLIB327413P2h01b1
Method
                  BLASTN
NCBI GI
                  q3236234
                  88
BLAST score
                  1.0e-41
E value
```



```
Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  173247
Seq. No.
Seq. ID
                  jC-atXLIB327413P2h02b1
                  BLASTN
Method
                  g3800746
NCBI GI
                  38
BLAST score
                  8.0e-12
E value
                  46
Match length
                  96
% identity
                  Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
NCBI Description
                  complete cds
                  173248
Seq. No.
                  jC-atXLIB327413P2h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4098521
BLAST score
                  509
E value
                  1.0e-51
                  105
Match length
                  96
% identity
                  (U79160) HMG-CoA synthase [Arabidopsis thaliana]
NCBI Description
                  >qi 4098523 (U79161) HMG-CoA synthase [Arabidopsis
                   thaliana]
                   173249
Seq. No.
Seq. ID
                   jC-atXLIB327413P2h05a1
                   BLASTN
Method
NCBI GI
                  q2462264
                   56
BLAST score
                   2.0e-22
E value
                   60
Match length
% identity
                   98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   173250
Seq. No.
                   jC-atXLIB327413P2h06b1
Seq. ID
Method
                   BLASTN
                   g3941523
NCBI GI
BLAST score
                   35
                   5.0e-10
E value
                   42
Match length
                   98
% identity
                   Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   173251
                   jC-atXLIB327413P2h07b1
Seq. ID
Method
                   BLASTX
                   g2459417
NCBI GI
                   211
BLAST score
```

E value 7.0e-17

Match length 47 % identity 87

NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19

[Arabidopsis thaliana]

NCBI Description



```
173252
Seq. No.
Seq. ID
                  jC-atXLIB327413P2h09b1
                  BLASTN
Method
NCBI GI
                  g2529657
BLAST score
                  44
                  2.0e-15
E value
                  71
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T30B22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  173253
Seq. No.
Seq. ID
                  jC-atXLIB327413P3a01b1
                  BLASTX
Method
NCBI GI
                  g99736
BLAST score
                  58
                  7.0e-10
E value
                  125
Match length
                  43
% identity
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                  Arabidopsis thaliana >gi 16187 emb CAA46814 (X66016)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                  173254
Seq. ID
                  jC-atXLIB327413P3a02b1
                  BLASTN
Method
                  g3941523
NCBI GI
BLAST score
                  42
E value
                  3.0e-14
                  50
Match length
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  173255
Seq. No.
                   jC-atXLIB327413P3a03b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2582640
BLAST score
                   51
                   1.0e-19
E value
Match length
                   59
                   97
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                   173256
Seq. ID
                   jC-atXLIB327413P3a05b1
Method
                   BLASTN
NCBI GI
                   g3395937
BLAST score
                   271
                   1.0e-151
E value
Match length
                   301
                   97
% identity
```

homolog (PTB) mRNA, complete cds

Arabidopsis thaliana polypyrimidine tract-binding protein



Seq. No. 173257

Seq. ID jC-atXLIB327413P3a07b1

Method BLASTN
NCBI GI g3800746
BLAST score 52
E value 4.0e-20
Match length 52
% identity 100

NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,

complete cds

Seq. No. 173258

Seq. ID jC-atXLIB327413P3a10b1

Method BLASTN
NCBI GI g2582640
BLAST score 50
E value 5.0e-19
Match length 50

% identity 100
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173259

Seq. ID jC-atXLIB327413P3a11b1

Method BLASTN
NCBI GI g2582640
BLAST score 56
E value 2.0e-22
Match length 76
% identity 93

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173260

Seq. ID jC-atXLIB327413P3b01b1

Method BLASTN
NCBI GI g2582640
BLAST score 37
E value 3.0e-11
Match length 45
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173261

Seq. ID jC-atXLIB327413P3b02b1

Method BLASTN
NCBI GI g2582640
BLAST score 37
E value 3.0e-11
Match length 45
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173262

Seq. ID jC-atXLIB327413P3b07b1



```
Method
                  BLASTN
NCBI GI
                  g4468976
BLAST score
                  122
                  6.0e-62
E value
                  126
Match length
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18
NCBI Description
                  (ESSA project)
                  173263
Seq. No.
Seq. ID
                  jC-atXLIB327413P3b10b1
```

Method BLASTN
NCBI GI 94580365
BLAST score 162
E value 8.0e-86
Match length 170

% identity 99
NCBI Description Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No. 173264

Seq. ID jC-atXLIB327413P3c01b1

Method BLASTN
NCBI GI g4753195
BLAST score 120
E value 9.0e-61
Match length 127
% identity 99

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 173265

Seq. ID jC-atXLIB327413P3c02a1

Method BLASTN
NCBI GI g2462264
BLAST score 43
E value 5.0e-15

E value 5.0e-1
Match length 43
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173266

Seq. ID jC-atXLIB327413P3c03a1

Method BLASTN
NCBI GI g3046854
BLAST score 82
E value 5.0e-38
Match length 109
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No. 173267

Seq. ID jC-atXLIB327413P3c08a1

Method BLASTN NCBI GI g531828 BLAST score 33



E value 9.0e-09 Match length 41 95 % identity Cloning vector pSport1, complete cds NCBI Description Seq. No. 173268 jC-atXLIB327413P3c08b1 Seq. ID Method BLASTN q4558656 NCBI GI BLAST score 108 1.0e-53 E value 115 Match length % identity 99 Arabidopsis thaliana chromosome II BAC T10F5 genomic NCBI Description sequence, complete sequence Seq. No. 173269 Seq. ID jC-atXLIB327413P3c09b1 Method BLASTN g2582640 NCBI GI BLAST score 43 8.0e-15 E value 50 Match length % identity 96 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 173270 Seq. No. Seq. ID jC-atXLIB327413P3c10b1 Method BLASTN NCBI GI q2582640 BLAST score 46 E value 1.0e-16 Match length 58 95 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 Seq. No. 173271 Seq. ID jC-atXLIB327413P3c11b1 Method BLASTN NCBI GI g2264317 BLAST score 61 1.0e-25 E value Match length 84 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 173272

Seq. ID jC-atXLIB327413P3c12b1

Method BLASTX
NCBI GI g3386613
BLAST score 717
E value 5.0e-76
Match length 144
% identity 99



```
(AC004665) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                  173273
Seq. No.
Seq. ID
                  jC-atXLIB327413P3d05a1
                  BLASTN
Method
                  q531828
NCBI GI
BLAST score
                  44
                  2.0e-15
E value
                  44
Match length
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
                  173274
Seq. No.
Seq. ID
                  jC-atXLIB327413P3d05b1
                  BLASTN
Method
                  g3941523
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
Match length
                  51
                  100
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  173275
Seq. No.
                   jC-atXLIB327413P3d06a1
Seq. ID
                  BLASTN
Method
                  g2462264
NCBI GI
                   38
BLAST score
                   9.0e-12
E value
                   50
Match length
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   173276
Seq. ID
                   jC-atXLIB327413P3d06b1
                   BLASTN
Method
                   g2894591
NCBI GI
                   99
BLAST score
E value
                   3.0e-48
                   114
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                   (ESSAII project)
Seq. No.
                   173277
                   jC-atXLIB327413P3d08a1
Seq. ID
                   BLASTN
```

Method g2462264 NCBI GI BLAST score 39 1.0e-12 E value Match length 43 % identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

173278 Seq. No.

jC-atXLIB327413P3d09b1 Seq. ID



```
Method BLASTN
NCBI GI g3292807
BLAST score 171
E value 4.0e-91
Match length 217
% identity 94
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
(ESSAII project)
```

Seq. No. 173279

Seq. ID jC-atXLIB327413P3d11a1

Method BLASTN
NCBI GI g2462264
BLAST score 47
E value 3.0e-17
Match length 47
% identity 100

% identity 100 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173280

Seq. ID jC-atXLIB327413P3d12b1

Method BLASTN
NCBI GI g4757414
BLAST score 46
E value 1.0e-16
Match length 94
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 173281

Seq. ID jC-atXLIB327413P3e02b1

Method BLASTN
NCBI GI g2582640
BLAST score 41
E value 1.0e-13
Match length 49
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173282

Seq. ID jC-atXLIB327413P3e03a1

Method BLASTN
NCBI GI 94220628
BLAST score 336
E value 0.0e+00
Match length 457
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24C1, complete sequence [Arabidopsis thaliana]

Seq. No. 173283

Seq. ID jC-atXLIB327413P3e04b1

Method BLASTN NCBI GI g2582640

BLAST score 53



E value 8.0e-21 Match length 61 % identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173284

Seq. ID jC-atXLIB327413P3e06b1

Method BLASTN
NCBI GI g2582640
BLAST score 50
E value 6.0e-19
Match length 50

Match length 50 % identity 100

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173285

Seq. ID jC-atXLIB327413P3e08b1

Method BLASTN
NCBI GI g3941523
BLAST score 43
E value 9.0e-15

E value 9.0e-Match length 43 % identity 100

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 173286

Seq. ID jC-atXLIB327413P3e10a1

Method BLASTN
NCBI GI g2462264
BLAST score 33
E value 8.0e-09
Match length 33
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173287

Seq. ID jC-atXLIB327413P3e10b1

Method BLASTN
NCBI GI g2582640
BLAST score 36
E value 1.0e-10
Match length 55
% identity 91

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173288

Seq. ID jC-atXLIB327413P3f01b1

Method BLASTN
NCBI GI g2232147
BLAST score 81
E value 2.0e-37
Match length 143

% identity 97



```
Arabidopsis thaliana 14-3-3-like protein GF14 upsilon
NCBI Description
                   (GRF5) gene, complete cds
Seq. No.
                  173289
Seq. ID
                  jC-atXLIB327413P3f02a1
                  BLASTN
Method
                  q531828
NCBI GI
BLAST score
                   44
                  2.0e-15
E value
                  44
Match length
                  100
% identity
                  Cloning vector pSport1, complete cds
NCBI Description
                  173290
Seq. No.
                   jC-atXLIB327413P3f02b1
Seq. ID
                  BLASTN
Method
                  g2582640
NCBI GI
BLAST score
                   53
E value
                   9.0e-21
                   75
Match length
                   92
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   173291
Seq. No.
                   jC-atXLIB327413P3f03b1
Seq. ID
                   BLASTN
Method
                   q4204173
NCBI GI
BLAST score
                   102
E value
                   5.0e-50
Match length
                   142
                   92
% identity
                  Arabidopsis thaliana chromosome 1 BAC T2K10 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   173292
Seq. No.
                   jC-atXLIB327413P3f04a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2462264
BLAST score
                   49
                   2.0e-18
E value
                   57
Match length
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   173293
Seq. No.
                   jC-atXLIB327413P3f05a1
Seq. ID
                   BLASTN
Method
```

g3869069 NCBI GI BLAST score 103 E value 1.0e-50 Match length 122 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MEB5, complete sequence [Arabidopsis thaliana]

173294 Seq. No.



```
Seq. ID
                  jC-atXLIB327413P3f05b1
Method
                  BLASTN
NCBI GI
                  q3869069
BLAST score
                  71
E value
                  1.0e-31
Match length
                  121
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173295
Seq. ID
                  jC-atXLIB327413P3f06b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  39
                  2.0e-12
E value
Match length
                  47
% identity
                  98
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173296
Seq. No.
Seq. ID
                  jC-atXLIB327413P3f07b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  60
                  6.0e-25
E value
Match length
                  75
% identity
                  95
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  173297
                  jC-atXLIB327413P3f08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  52
E value
                  4.0e-20
                  56
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173298
                  jC-atXLIB327413P3f08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  48
E value
                  1.0e-17
Match length
                  76
% identity
                  91
```

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173299

Seq. ID jC-atXLIB327413P3f09b1

Method BLASTN NCBI GI g2582640



```
43
BLAST score
                  8.0e-15
E value
                  47
Match length
                  98
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173300
Seq. No.
Seq. ID
                  jC-atXLIB327413P3f10b1
                  BLASTN
Method
                  g3941523
NCBI GI
                  40
BLAST score
                  3.0e-13
E value
                  48
Match length
                  98
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  173301
Seq. No.
Seq. ID
                  jC-atXLIB327413P3g02a1
Method
                  BLASTN
                  g3510339
NCBI GI
                  139
BLAST score
                  5.0e-72
E value
                  264
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K7, complete sequence [Arabidopsis thaliana]
                  173302
Seq. No.
                  jC-atXLIB327413P3g02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2443751
                  644
BLAST score
E value
                  1.0e-70
                  146
Match length
                  95
% identity
                 (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
                  173303
Seq. No.
Seq. ID
                  jC-atXLIB327413P3g04a1
Method
                  BLASTN
NCBI GI
                  g3449323
BLAST score
                  171
                  3.0e-91
E value
Match length
                  298
                  89
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZA15, complete sequence [Arabidopsis thaliana]
```

Seq. No. 173304

Seq. ID jC-atXLIB327413P3g05a1 Method BLASTN

Method BLASTN
NCBI GI g4559344
BLAST score 96
E value 2.0e-46



Match length 127 % identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F27C12 genomic

sequence, complete sequence

Seq. No. 173305

Seq. ID jC-atXLIB327413P3g09b1

Method BLASTN
NCBI GI g2582640
BLAST score 39
E value 2.0e-12

Match length 66 % identity 91

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173306

Seq. ID jC-atXLIB327413P3h02b1

Method BLASTN
NCBI GI g3800746
BLAST score 46
E value 1.0e-16
Match length 50
% identity 98

NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,

complete cds

Seq. No. 173307

Seq. ID jC-atXLIB327413P3h05b1

Method BLASTN
NCBI GI g2582640
BLAST score 46

E value 1.0e-16
Match length 50
% identity 98

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173308

Seq. ID jC-atXLIB327413P3h07b1

Method BLASTN
NCBI GI g2582640
BLAST score 54
E value 2.0e-21
Match length 62
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173309

Seq. ID jC-atXLIB327413P4a01b1

Method BLASTX
NCBI GI g99737
BLAST score 663
E value 1.0e-69
Match length 150
% identity 89



NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No. 173310

Seq. ID jC-atXLIB327413P4a02a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 5.0e-19
Match length 58
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173311

Seq. ID jC-atXLIB327413P4a04a1

Method BLASTN
NCBI GI g3510343
BLAST score 43
E value 5.0e-15
Match length 47
% identity 52

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 173312

Seq. ID jC-atXLIB327413P4a04b1

Method BLASTX
NCBI GI g2129608
BLAST score 762
E value 3.0e-81
Match length 154
% identity 99

NCBI Description GTP-binding protein, 68K - Arabidopsis thaliana >gi 807577

(L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 173313

Seq. ID jC-atXLIB327413P4a05a1

Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 4.0e-15
Match length 56
% identity 95

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173314

Seq. ID jC-atXLIB327413P4a07b1

Method BLASTN
NCBI GI g4589424
BLAST score 52
E value 4.0e-20
Match length 80
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K8E10, complete sequence



```
173315
Seq. No.
Seq. ID
                  jC-atXLIB327413P4a09b1
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                  49
                  2.0e-18
E value
Match length
                  69
% identity
                  93
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173316
Seq. No.
Seq. ID
                  jC-atXLIB327413P4a10a1
Method
                  BLASTN
NCBI GI
                  g540252
BLAST score
                  34
                  4.0e-09
E value
                  38
Match length
                  97
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
                  173317
Seq. No.
Seq. ID
                  jC-atXLIB327413P4a10b1
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  38
                  8.0e-12
E value
Match length
                   42
                   98
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                   173318
Seq. No.
                   jC-atXLIB327413P4b02a1
Seq. ID
Method
                  BLASTN
                  q3763944
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
Match length
                   111
% identity
NCBI Description
                 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                   173319
Seq. ID
                   jC-atXLIB327413P4b02b1
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   34
```

2.0e-09 E value Match length 45 93 % identity

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

173320 Seq. No.

Seq. ID jC-atXLIB327413P4b03b1

Method BLASTN



NCBI GI g2582640
BLAST score 59
E value 2.0e-24
Match length 71
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173321

Seq. ID jC-atXLIB327413P4b04b1

Method BLASTN
NCBI GI g2582640
BLAST score 60
E value 6.0e-25
Match length 72
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173322

Seq. ID jC-atXLIB327413P4b05a1

Method BLASTN
NCBI GI g4512656
BLAST score 48
E value 2.0e-17
Match length 283

Match length 283 % identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No. 173323

Seq. ID jC-atXLIB327413P4b06a1

Method BLASTN
NCBI GI g2462264
BLAST score 38
E value 7.0e-12
Match length 54
% identity 93

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173324

Seq. ID jC-atXLIB327413P4b08a1

Method BLASTN
NCBI GI g2182286
BLAST score 166
E value 4.0e-88
Match length 199
% identity 95

NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 173325

Seq. ID jC-atXLIB327413P4b12a1

Method BLASTN
NCBI GI g2462264
BLAST score 46
E value 1.0e-16



```
46
Match length
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  173326
Seq. No.
                  jC-atXLIB327413P4b12b1
Seq. ID
Method
                  BLASTN
                  g2582640
NCBI GI
                  63
BLAST score
                  1.0e-26
E value
                  75
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  173327
Seq. No.
Seq. ID
                  jC-atXLIB327413P4c02a1
                  BLASTN
Method
NCBI GI
                  g2290120
BLAST score
                  43
                  9.0e-15
E value
                  65
Match length
                  94
% identity
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  173328
Seq. No.
                  jC-atXLIB327413P4c03a1
Seq. ID
Method
                  BLASTN
                  g2642152
NCBI GI
BLAST score
                  72
E value
                  8.0e-32
Match length
                  174
                  87
% identity
                  Arabidopsis thaliana chromosome II BAC T517 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  173329
Seq. ID
                  jC-atXLIB327413P4c03b1
Method
                  BLASTN
NCBI GI
                  q2642152
                   105
BLAST score
                  9.0e-52
E value
Match length
                  109
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T517 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   173330
                   jC-atXLIB327413P4c05a1
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g531828
BLAST score 42
E value 5.0e-14
Match length 61
% identity 93

NCBI Description Cloning vector pSport1, complete cds

Seq. No.

Seq. ID

173336

jC-atXLIB327413P4c11b1



```
173331
Seq. No.
Seq. ID
                  jC-atXLIB327413P4c06b1
Method
                  BLASTN
                  g4220638
NCBI GI
BLAST score
                  229
                  1.0e-126
E value
                  253
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  173332
Seq. No.
Seq. ID
                  jC-atXLIB327413P4c09a1
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  110
                  1.0e-54
E value
                  114
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
                  173333
Seq. No.
Seq. ID
                  jC-atXLIB327413P4c10a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  45
                  1.0e-15
E value
Match length
                  57
% identity
                  95
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173334
Seq. No.
Seq. ID
                  iC-atXLIB327413P4c10b1
Method
                  BLASTN
                  g3800746
NCBI GI
BLAST score
                  33
                  6.0e-09
E value
Match length
                  48
                  96
% identity
NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                  complete cds
Seq. No.
                   173335
Seq. ID
                   jC-atXLIB327413P4c11a1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  57
E value
                  5.0e-23
Match length
                  65
% identity
                  97
NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                  gene, partial cds
```



Method BLASTN
NCBI GI g2582640
BLAST score 66
E value 2.0e-28
Match length 74
% identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173337

Seq. ID jC-atXLIB327413P4d01b1

Method BLASTN
NCBI GI g4510360
BLAST score 62
E value 4.0e-26
Match length 90
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 173338

Seq. ID jC-atXLIB327413P4d02b1

Method BLASTN
NCBI GI g3941523
BLAST score 33
E value 8.0e-09
Match length 44

Match length 44 % identity 93

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 173339

Seq. ID jC-atXLIB327413P4d04a1

Method BLASTN
NCBI GI g4589410
BLAST score 161
E value 5.0e-85
Match length 269
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 173340

Seq. ID jC-atXLIB327413P4d04b1

Method BLASTN
NCBI GI g4589410
BLAST score 92
E value 4.0e-44
Match length 100
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 173341

Seq. ID jC-atXLIB327413P4d05a1

Method BLASTN NCBI GI g4678266



```
BLAST score 41
E value 2.0e-13
Match length 76
% identity 88
NCBI Description Arabidop
```

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No. 173342

Seq. ID jC-atXLIB327413P4d06a1

Method BLASTN
NCBI GI g2462264
BLAST score 43
E value 9.0e-15
Match length 43

% identity 100 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173343

Seq. ID jC-atXLIB327413P4d06b1

Method BLASTN
NCBI GI g2582640
BLAST score 41
E value 1.0e-13
Match length 49
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173344

Seq. ID jC-atXLIB327413P4d09b1

Method BLASTX
NCBI GI g1872500
BLAST score 531
E value 4.0e-54
Match length 111
% identity 95

NCBI Description (U80605) farnesyl diphosphate synthase precursor

[Arabidopsis thaliana]

Seq. No. 173345

Seq. ID jC-atXLIB327413P4d11b1

Method BLASTN
NCBI GI g2582640
BLAST score 54
E value 2.0e-21
Match length 72
% identity 95

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173346

Seq. ID jC-atXLIB327413P4d12a1

Method BLASTN
NCBI GI g4519194
BLAST score 40
E value 8.0e-13
Match length 76



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                  173347
Seq. No.
Seq. ID
                  jC-atXLIB327413P4e01b1
                  BLASTN
Method
NCBI GI
                  g1402897
BLAST score
                  75
                  6.0e - 34
E value
                  107
Match length
                  93
% identity
NCBI Description A.thaliana gst6 gene
                  173348
Seq. No.
Seq. ID
                  jC-atXLIB327413P4e02a1
                  BLASTN
Method
                  g2264317
NCBI GI
BLAST score
                  127
E value
                  5.0e-65
Match length
                  191
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
                  173349
Seq. No.
Seq. ID
                  jC-atXLIB327413P4e06a1
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  34
                  3.0e-09
E value
                  38
Match length
% identity
                  97
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  173350
Seq. No.
                  jC-atXLIB327413P4e07a1
Seq. ID
Method
                  BLASTN
                  g2462264
NCBI GI
BLAST score
                  33
                  8.0e-09
E value
Match length
                  45
% identity
                  93
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173351
                   jC-atXLIB327413P4e07b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3108025
BLAST score
                  36
E value
                   4.0e-11
Match length
                  40
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC T13D8, complete
                  sequence [Arabidopsis thaliana]
```

23780

173352

Seq. No.



```
jC-atXLIB327413P4e08a1
Seq. ID
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  50
                  2.0e-19
E value
                  66
Match length
                  95
% identity
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                   173353
Seq. No.
                   jC-atXLIB327413P4e09b1
Seq. ID
Method
                   BLASTN
                  q3928074
NCBI GI
                   162
BLAST score
                   9.0e-86
E value
Match length
                   205
% identity
                  Arabidopsis thaliana chromosome II BAC T7F6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   jC-atXLIB327413P4e12a1
Seq. ID
Method
                   BLASTN
                   g4589432
NCBI GI
BLAST score
                   257
E value
                   1.0e-142
                   269
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MMJ24, complete sequence
Seq. No.
                   173355
                   jC-atXLIB327413P4f02b1
Seq. ID
Method
                   BLASTN
                   g2335089
NCBI GI
BLAST score
                   40
                   5.0e-13
E value
Match length
                   40
% identity
                   100
                   Arabidopsis thaliana chromosome II BAC T11A7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   173356
Seq. No.
                   jC-atXLIB327413P4f03b1
Seq. ID
                   BLASTX
Method
                   g3834312
NCBI GI
                   779
BLAST score
                   3.0e-83
E value
Match length
                   156
```

94 % identity

(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 NCBI Description Daucus carota and a member of S locus glycoprotein family

PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815,

gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248,

gb AA728536, gb Z30816 an



```
173357
Seq. No.
                  jC-atXLIB327413P4f04b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                  55
E value
                  6.0e-22
                  79
Match length
                  92
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  173358
Seq. No.
Seq. ID
                  jC-atXLIB327413P4f05a1
                  BLASTN
Method
                  g2290120
NCBI GI
                  50
BLAST score
                   8.0e-19
E value
Match length
                   65
% identity
                   94
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                   gene, partial cds
                   173359
Seq. No.
Seq. ID
                   jC-atXLIB327413P4f05b1
                   BLASTN
Method
                   g2582640
NCBI GI
                   64
BLAST score
                   2.0e-27
E value
Match length
                   72
% identity
                   97
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   173360
                   jC-atXLIB327413P4f07b1
Seq. ID
                   BLASTX
Method
                   g4056502
NCBI GI
                   420
BLAST score
E value
                   4.0e-41
                   91
Match length
                   97
% identity
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                   173361
Seq. No.
                   jC-atXLIB327413P4f08b1
Seq. ID
                   BLASTX
Method
                   g267073
NCBI GI
                   167
BLAST score
                   2.0e-11
E value
                   38
Match length
                   84
% identity
NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
```

beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

173362 Seq. No.



```
jC-atXLIB327413P4f09a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g16249
BLAST score
                  90
                  1.0e-42
                                   - ~
E value
                  98
Match length
                  98
% identity
NCBI Description A.thaliana mRNA for Cu, Zn superoxide dismutase
                  173363
Seq. No.
Seq. ID
                  jC-atXLIB327413P4f10b1
                  BLASTN
Method
NCBI GI
                  q2582640
                  33
BLAST score
                  6.0e-09
E value
                  55
Match length
                  91
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  173364
Seq. No.
Seq. ID
                  jC-atXLIB327413P4g01a1
                  BLASTN
Method
                  q2232147
NCBI GI
BLAST score
                  113
E value
                  2.0e-56
                  193
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana 14-3-3-like protein GF14 upsilon
                   (GRF5) gene, complete cds
                  173365
Seq. No.
                   jC-atXLIB327413P4g02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3024697
BLAST score
                   160
                   1.0e-10
E value
Match length
                   100
% identity
                   45
                  T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
NCBI Description
                   (CCT-EPSILON) >gi 2213618 (AC000103) F21J9.12 [Arabidopsis
                   thaliana]
Seq. No.
                   173366
Seq. ID
                   jC-atXLIB327413P4g03b1
Method
                   BLASTX
NCBI GI
                   g2833460
```

Method BLASTX
NCBI GI g2833460
BLAST score 503
E value 7.0e-51
Match length 148
% identity 61

NCBI Description RIBOFLAVIN-SPECIFIC DEAMINASE >gi_1001153_dbj_BAA10295_ (D64001) riboflavin biosynthesis protein [Synechocystis

sp.]

Seq. No. 173367

Seq. ID jC-atXLIB327413P4g05b1



Method BLASTN
NCBI GI g2582640
BLAST score 59
E value 3.0e-24
Match length 71
% identity 96

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 173368

Seq. ID jC-atXLIB327413P4g06a1

Method BLASTN
NCBI GI g2462264
BLAST score 39
E value 4.0e-12

E value 4.0e-12 Match length 47 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173369

Seq. ID jC-atXLIB327413P4h04b1

Method BLASTN
NCBI GI g2795802
BLAST score 69
E value 2.0e-30
Match length 77
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F17A14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173370

Seq. ID jC-atXLIB327413P4h05a1

Method BLASTN
NCBI GI g3335331
BLAST score 230
E value 1.0e-126
Match length 292
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 173371

Seq. ID jC-atXLIB327413P4h06a1

Method BLASTN
NCBI GI 94220633
BLAST score 76
E value 2.0e-34
Match length 96
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7J8, complete sequence [Arabidopsis thaliana]

Seq. No. 173372

Seq. ID jC-atXLIB327413P4h07b1

Method BLASTN NCBI GI g3800746

BLAST score 38



8.0e-12 E value Match length 49 94 % identity Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, NCBI Description complete cds 173373 Seq. No. Seq. ID jC-atXLIB327413P4h09a1 BLASTN Method g2832639 NCBI GI 75 BLAST score E value 7.0e - 34103 Match length % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 NCBI Description (ESSAII project) 173374 Seq. No. jC-atXLIB327413P4h11a1 Seq. ID BLASTN Method g2290120 NCBI GI 46 BLAST score 2.0e-16 E value 66 Match length 92 % identity HIV-1 strain MO2 from USA, envelope glycoprotein (env) NCBI Description gene, partial cds Seq. No. 173375 jC-atXLIB327413P4h12a1 Seq. ID BLASTN Method g1399264 NCBI GI 101 BLAST score 3.0e-49E value Match length 101 % identity 100 Arabidopsis thaliana calmodulin-domain protein kinase CDPK NCBI Description isoform 9 (CPK9) mRNA, complete cds Seq. No. 173376 jC-atXLIB327413P4h12b1 Seq. ID BLASTX Method q1399265 NCBI GI 776 BLAST score 6.0e - 83E value 149 Match length 99 % identity (U31751) calmodulin-domain protein kinase CDPK isoform 9 NCBI Description [Arabidopsis thaliana]

173377 Seq. No.

jC-atXLIB327414P1a02a1 Seq. ID

BLASTN Method g4006885 NCBI GI BLAST score 122 3.0e-62 E value 245 Match length



% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 173378

Seq. ID jC-atXLIB327414Pla09a1

Method BLASTN
NCBI GI g3319339
BLAST score 42
E value 3.0e-14

Match length 65 % identity 92

NCBI Description Arabidopsis thaliana BAC F9D12

Seq. No. 173379

Seq. ID jC-atXLIB327414P1a11b1

Method BLASTN
NCBI GI g531828
BLAST score 58
E value 9.0e-24
Match length 69
% identity 97

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 173380

Seq. ID jC-atXLIB327414P1b04b1

Method BLASTN
NCBI GI g531828
BLAST score 43
E value 9.0e-15
Match length 69
% identity 93

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 173381

Seq. ID jC-atXLIB327414P1b09a1

Method BLASTN
NCBI GI 94325285
BLAST score 288
E value 1.0e-161
Match length 330
% identity 97

NCBI Description Arabidopsis thaliana NAC domain protein NAM mRNA, complete

cds

Seq. No. 173382

Seq. ID jC-atXLIB327414P1b10a1

Method BLASTN
NCBI GI g4220645
BLAST score 46
E value 9.0e-17
Match length 78
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 173383

Seq. ID jC-atXLIB327414P1c03b1 BLASTN Method g540252 NCBI GI 39 BLAST score 2.0e-12 E value 60 Match length 92 % identity Cloning vector pSVSport1 beta-lactamase gene, complete cds NCBI Description 173384 Seq. No. jC-atXLIB327414P1c05a1 Seq. ID Method BLASTN g4262221 NCBI GI 138 BLAST score E value 2.0e-71 Match length 150 % identity 98 Arabidopsis thaliana chromosome II BAC F10A8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 173385 Seq. No. jC-atXLIB327414P1c11a1 Seq. ID Method BLASTN q2995989 NCBI GI 85 BLAST score 8.0e-40 E value 117 Match length % identity 94 Arabidopsis thaliana dormancy-associated protein (DRM1) NCBI Description mRNA, complete cds 173386 Seq. No. Seq. ID jC-atXLIB327414P1e09a1 BLASTX Method g99681 NCBI GI BLAST score 341 7.0e-32 E value 93 72

Match length % identity

cold-regulated protein cor47 - Arabidopsis thaliana NCBI Description (fragment) $>gi_388259_{emb}_{CAA42483}_{AE}$ (X59814) Cold and ABA

regulated gene [Arabidopsis thaliana]

173387 Seq. No.

jC-atXLIB327414P1f02b1 Seq. ID

Method BLASTN g303565 NCBI GI BLAST score 79 3.0e-36 E value 111 Match length % identity 94

NCBI Description Escherichia coli Transposon gamma delta tnpA, tnpR and tnpX

genes for transposase, resolvase and ORF, complete cds

173388 Seq. No.

jC-atXLIB327414P1f10a1 Seq. ID

Method BLASTN



```
NCBI GI
                  g4589434
BLAST score
                  121
                  2.0e-61
E value
Match length
                  133
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ7, complete sequence
                  173389
Seq. No.
                  jC-atXLIB327414P1g03a1
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
BLAST score
                  33
                  7.0e-09
E value
                  33
Match length
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  173390
                  iC-atXLIB327414P1g03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2924514
BLAST score
                  253
E value
                  1.0e-21
                   49
Match length
% identity
NCBI Description (AL022023) protein kinase-like [Arabidopsis thaliana]
Seq. No.
                   173391
                   jC-atXLIB327414P1h01b1
Seq. ID
Method
                   BLASTN
                   q4519791
NCBI GI
BLAST score
                   61
                   2.0e-25
E value
                   77
Match length
                   95
% identity
NCBI Description Arabidopsis thaliana mRNA for Aspl, complete cds
Seq. No.
                   173392
                   jC-atXLIB327414P1h04b1
Seq. ID
                   BLASTN
Method
                   g1061039
NCBI GI
BLAST score
                   77
                   4.0e-35
E value
                   85
Match length
                   98
% identity
NCBI Description A.thaliana mRNA for sterol-C-methyltransferase
Seq. No.
                   173393
                   jC-atXLIB327414P1h05a1
Seq. ID
                   BLASTN
Method
                   g4539331
NCBI GI
                   67
BLAST score
E value
                   4.0e-29
Match length
                   104
% identity
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13



(ESSA project)

```
Seq. No.
                  173394
Seq. ID
                  jC-atXLIB327414P1h06a1
                  BLASTN
Method
                  g1755175
NCBI GI
                  97
BLAST score
                  5.0e-47
E value
Match length
                  128
% identity
                  Arabidopsis thaliana germin-like protein (GLP4) mRNA,
NCBI Description
                  complete cds
                  173395
Seq. No.
                  jC-atXLIB327414P1h06b1
Seq. ID
Method
                  BLASTX
                  g3482931
NCBI GI
BLAST score
                  131
                  3.0e-27
E value
                  79
Match length
                  89
% identity
                  (AC003970) germin-like protein [Arabidopsis thaliana]
NCBI Description
                  173396
Seq. No.
Seq. ID
                  jC-atXLIB327414P1h07a1
                  BLASTN
Method
                  q2462264
NCBI GI
                  34
BLAST score
E value
                  2.0e-09
Match length
                  38
                  97
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  173397
                   jC-atXLIB327414P1h07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  38
                  8.0e-12
E value
Match length
                   42
                   98
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
Seq. No.
                   173398
                   jC-atXLIB327414P1h09b1
Seq. ID
                   BLASTN
Method
                   g2264309
NCBI GI
                   76
BLAST score
                   2.0e-34
E value
                   91
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJJ3, complete sequence [Arabidopsis thaliana]
```

23789

173399

jC-atXLIB327414P1h10a1

Seq. No.

Seq. ID



```
BLASTN
Method
                  g2351062
NCBI GI
BLAST score
                  140
                  1.0e-72
E value
                  253
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                  173400
Seq. No.
                  jC-atXLIB327414P2a01a1
Seq. ID
                  BLASTX
Method
                  g4455159
                  564
```

NCBI GI g4455159 BLAST score 564 E value 4.0e-58 Match length 122 % identity 90

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 173401 Seq. ID jC-atXLIB327414P2a08a1 Method BLASTN NCBI GI g2462264

BLAST score 49
E value 2.0e-18
Match length 53
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173402

Seq. ID jC-atXLIB327414P2a10a1

Method BLASTN
NCBI GI g2290120
BLAST score 54
E value 2.0e-21
Match length 65
% identity 95

NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 173403

Seq. ID jC-atXLIB327414P2a12a1

Method BLASTN
NCBI GI g598848
BLAST score 41
E value 1.0e-13
Match length 65
% identity 91

NCBI Description Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No. 173404

Seq. ID jC-atXLIB327414P2a12b1

Method BLASTN
NCBI GI g4415905
BLAST score 87
E value 4.0e-41
Match length 259



% identity Arabidopsis thaliana chromosome II BAC F13K3 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 173405 jC-atXLIB327414P2b09a1 Seq. ID BLASTN Method NCBI GI q2462264 42 BLAST score 3.0e-14E value 50 Match length % identity 96 Cucumis sativus mRNA for patatin-like protein, partial NCBI Description 173406 Seg. No. Seq. ID jC-atXLIB327414P2b09b1 Method BLASTN NCBI GI g2723476 BLAST score 44 2.0e-15 E value 211 Match length % identity Arabidopsis thaliana AtRab mRNA for GTP-binding protein, NCBI Description complete cds 173407 Seq. No. jC-atXLIB327414P2c01a1 Seq. ID BLASTX Method NCBI GI q4455159 BLAST score 321 4.0e-31 E value Match length 113 66 % identity NCBI Description (AL021687) putative protein [Arabidopsis thaliana] 173408 Seq. No. jC-atXLIB327414P2c01b1 Seq. ID BLASTN Method NCBI GI g2582640 BLAST score 47 E value 3.0e-17 63 Match length 95 % identity NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40 173409 Seq. No. jC-atXLIB327414P2c10a1 Seq. ID BLASTX Method NCBI GI g3243274 616 BLAST score 4.0e-64 E value 147 Match length 83 % identity (AF072134) TCP3 [Arabidopsis thaliana]

173410 Seq. No.

NCBI Description



jC-atXLIB327414P2d01b1 Seq. ID BLASTN Method q2582640 NCBI GI BLAST score 50 5.0e-19E value 70 Match length 93 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 173411 Seq. No. Seq. ID jC-atXLIB327414P2d02a1 BLASTX Method g2911078 NCBI GI BLAST score 162 6.0e-11 E value 120 Match length 38 % identity (AL021960) putative protein [Arabidopsis thaliana] NCBI Description 173412 Seq. No. jC-atXLIB327414P2d02b1 Seq. ID BLASTN Method g2582640 NCBI GI BLAST score 42 E value 3.0e-14 70 Match length % identity Arabidopsis thaliana mRNA for `arginine/serine-rich splicing NCBI Description factor, RSp40 173413 Seq. No. iC-atXLIB327414P2e11a1 Seq. ID BLASTN Method NCBI GI g2290120 BLAST score 35 2.0e-10 E value Match length 43 95 % identity NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env) gene, partial cds Seq. No. 173414 Seq. ID jC-atXLIB327414P2f03a1 BLASTX Method NCBI GI q4581162 BLAST score 381 1.0e-36 E value 117 Match length % identity 66 (AC006220) putative symbiosis-related protein [Arabidopsis NCBI Description thaliana]

Seq. No. 173415

Seq. ID jC-atXLIB327414P2f05a1

Method BLASTN NCBI GI g603055



BLAST score 121 E value 2.0e-61 Match length 423 % identity 84 Arabidopsis thaliana inner mitochondrial membrane protein NCBI Description mRNA, complete cds Seq. No. 173416 Seq. ID jC-atXLIB327414P2g03a1 BLASTX Method g2231312 NCBI GI BLAST score 737 E value 2.0e-78 145 Match length 99 % identity (U75603) AtRab18 [Arabidopsis thaliana] NCBI Description Seq. No. 173417 Seq. ID jC-atXLIB327414P2g05a1 BLASTX Method NCBI GI q3789911 BLAST score 146 4.0e-09 E value Match length 117 31 % identity (AF081802) developmental protein DG1118 [Dictyostelium NCBI Description discoideum] Seq. No. 173418 Seq. ID jC-atXLIB327414P2g11a1 BLASTN Method NCBI GI q4454447 BLAST score 34 E value 7.0e-10 50 Match length 92 % identity Arabidopsis thaliana chromosome II BAC F5H14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 173419 jC-atXLIB327414P2g12a1 Seq. ID BLASTX Method q1871180 NCBI GI BLAST score 179 6.0e-13E value Match length 110 45 % identity NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

173420

Seq. No.

jC-atXLIB327414P2g12b1 Seq. ID

BLASTN Method g1871173 NCBI GI BLAST score 53 8.0e-21 E value 306 Match length 83 % identity



```
Arabidopsis thaliana chromosome II BAC T06D20 genomic
NCBI Description
                  sequence, complete sequence
                  173421
Seq. No.
                  iC-atXLIB327414P3b01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455159
BLAST score
                  153
                  6.0e-15
E value
Match length
                  100
                  53
% identity
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
                  173422
Seq. No.
                  jC-atXLIB327414P3b05a1
Seq. ID
                  BLASTX
Method
                  q2088654
NCBI GI
BLAST score
                  593
E value
                  2.0e-61
                  129
Match length
                  91
% identity
                  (AF002109) 60S acidic ribosomal protein P0 isolog
NCBI Description
                  [Arabidopsis thaliana]
                  173423
Seq. No.
                  jC-atXLIB327414P3c03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2316090
BLAST score
                  174
                  2.0e-12
E value
                  132
Match length
% identity
                  34
NCBI Description (AF007549) golgi SNARE [Rattus norvegicus]
                  173424
Seq. No.
                  jC-atXLIB327414P3c04a1
Seq. ID
                  BLASTN
Method
                  g4455168
NCBI GI
                  78
BLAST score
                  1.0e-35
E value
                  229
Match length
                  88
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                  (ESSAII project)
                  173425
Seq. No.
                   jC-atXLIB327414P3c06a1
Seq. ID
                  BLASTX
Method
```

q3273196 NCBI GI BLAST score 190 3.0e-14E value

78 Match length % identity 53

(AB010915) responce regulator1 [Arabidopsis thaliana] NCBI Description >gi 3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_ (AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. ID



```
173426
Seq. No.
                  jC-atXLIB327414P3c12b1
Seq. ID
                  BLASTN
Method
                  g4589428
NCBI GI
                  59
BLAST score
                  2.0e-24
E value
                  298
Match length
% identity
                  83
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
                  173427
Seq. No.
                  jC-atXLIB327414P3f12a1
Seq. ID
                  BLASTN
Method
                  g2290120
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
Match length
                  65
% identity
                  95
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
                  173428
Seq. No.
Seq. ID
                   jC-atXLIB327414P3g09a1
                  BLASTN
Method
                  g2290120
NCBI GI
BLAST score
                  57
                   4.0e-23
E value
                  65
Match length
                  97
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                   gene, partial cds
                   173429
Seq. No.
Seq. ID
                   jC-atXLIB327414P3h01b1
                   BLASTN
Method
                   g3413696
NCBI GI
                   56
BLAST score
E value
                   1.0e-22
                   140
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T19L18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   173430
                   jC-atXLIB327414P3h06a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2462264
BLAST score
                   48
E value
                   8.0e-18
Match length
                   56
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   173431
```

jC-atXLIB327414P3h12a1



```
BLASTN
Method
NCBI GI
                  q468770
                  177
BLAST score
                  9.0e-95
E value
Match length
                  410
                  86
% identity
                  A.thaliana genes for chloroplast ribosomal protein L12 and
NCBI Description
                  tRNA-Pro
                  173432
Seq. No.
                   jC-atXLIB327414P4a03b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2864617
                   268
BLAST score
                   2.0e-23
E value
                   69
Match length
% identity
                   84
                   (ALO21811) H+-transporting ATP synthase chain9 - like
NCBI Description
                  protein [Arabidopsis thaliana]
                   173433
Seq. No.
                   jC-atXLIB327414P4a04b2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2864607
BLAST score
                   61
                   1.0e-25
E value
                   226
Match length
                   88
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                   (ESSAII project)
                   173434
Seq. No.
Seq. ID
                   jC-atXLIB327414P4a05a2
Method
                   BLASTX
                   g3426062
NCBI GI
                   342
BLAST score
                   2.0e-48
E value
                   132
Match length
% identity
                   83
                  (AJ007587) monooxygenase [Arabidopsis thaliana]
NCBI Description
                   173435
Seq. No.
                   jC-atXLIB327414P4a06a2
Seq. ID
                   BLASTX
Method
                   q3426062
NCBI GI
                   366
BLAST score
                   7.0e-35
E value
Match length
                   144
                   63
% identity
NCBI Description (AJ007587) monooxygenase [Arabidopsis thaliana]
                   173436
Seq. No.
                   jC-atXLIB327414P4a07a2
Seq. ID
                   BLASTX
Method
                   g3426062
NCBI GI
```

101

6.0e-04

BLAST score

E value